



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 126550

TO: Phuong Bui
Location: REM-2A15/2C18
Art Unit: 1638
Monday, July 12, 2004

Case Serial Number: 09/857522

From: Toby Port
Location: Biotech-Chem Library
Remsen 1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Bui,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port



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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 08:38:29 ; Search time 7664 Seconds
(without alignments)
11016.731 Million cell updates/sec

Title: US-09-857-522B-3
Perfect score: 1948
Sequence: 1 gtcgaccacgcgcgtccggac.....taaaaaaaaaaaaaaaaa 1948

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
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17: em_hum:*
18: em_in:*
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20: em_om:*
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38: em_sy:*
39: em_hcgo_hum:*
40: em_hcgo_mus:*
41: em_hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|-----------|----------------------|
| 1 | 1195.8 | 61.4 | 1838 | 8 | D82035 | D82035 Oryza sativ |
| 2 | 1195.8 | 61.4 | 2213 | 8 | AK100591 | AK100591 Oryza sat |
| 3 | 1195.8 | 61.4 | 2245 | 8 | AK072723 | AK072723 Oryza sat |
| 4 | 1195.6 | 61.4 | 1899 | 8 | BT009004 | BT009004 Triticum |
| 5 | 1186.8 | 60.9 | 1872 | 8 | D82038 | D82038 Oryza sativ |
| 6 | 1186.8 | 60.9 | 2161 | 8 | D82036 | D82036 Oryza sativ |
| 7 | 1164 | 59.8 | 1770 | 8 | OSU55768 | OSU55768 Oryza sativ |
| 8 | 1159.6 | 59.5 | 2927 | 8 | AK069206 | AK069206 Oryza sat |
| 9 | 1037.8 | 53.3 | 1542 | 8 | HVU7990 | AJ007990 Hordeum v |
| 10 | 1026.2 | 52.7 | 1539 | 8 | HVBKIN12M | X65604 H.vulgare B |
| 11 | 988.2 | 50.7 | 1809 | 8 | RYERKIN1 | M74113 Secale cere |
| 12 | 817.4 | 42.0 | 2073 | 8 | AK067158 | AK067158 Oryza sat |
| 13 | 815.8 | 41.9 | 2209 | 8 | D82039 | D82039 Oryza sativ |
| 14 | 795 | 40.8 | 1453 | 8 | HVBKIN2 | X82548 H.vulgare m |
| 15 | 791.2 | 40.6 | 1948 | 8 | AF143743 | AF143743 Lycopersi |
| 16 | 784.2 | 40.3 | 2100 | 8 | AF062479 | AF062479 Oryza sat |
| 17 | 780.8 | 40.1 | 1929 | 6 | AR184289 | AR184289 Sequence |
| 18 | 780.2 | 40.1 | 1539 | 6 | AX505467 | AX505467 Sequence |
| 19 | 780.2 | 40.1 | 1539 | 8 | AY149927 | AY149927 Arabidops |
| 20 | 780.2 | 40.1 | 1809 | 8 | AY070468 | AY070468 Arabidops |
| 21 | 780.2 | 40.1 | 1834 | 8 | ATNPK | X99279 A.thaliana |
| 22 | 778.6 | 40.0 | 1825 | 6 | AX497023 | AX497023 Sequence |
| 23 | 778.6 | 40.0 | 1852 | 8 | ATSKIN1 | X94755 A.thaliana |
| 24 | 777 | 39.9 | 1778 | 8 | CSSNFIAPK | Y10036 C.sativus m |
| 25 | 777 | 39.9 | 1825 | 6 | AX497027 | AX497027 Sequence |
| 26 | 769.4 | 39.5 | 1966 | 8 | STU83797 | U83797 Solanum tub |
| 27 | 757.2 | 38.9 | 1869 | 8 | ATSKIN2 | X94757 A.thaliana |
| 28 | 756.2 | 38.8 | 1536 | 6 | E05288 | E05288 DNA encodin |
| 29 | 756.2 | 38.8 | 2028 | 8 | TOBNPK5 | D26602 Tobacco mRN |
| 30 | 756 | 38.8 | 1608 | 8 | BT010386 | BT010386 Arabidops |
| 31 | 756 | 38.8 | 2209 | 8 | AY093170 | AY093170 Arabidops |
| 32 | 755.4 | 38.8 | 1539 | 6 | AX507962 | AX507962 Sequence |
| 33 | 746.4 | 38.3 | 1941 | 8 | AF128443 | AF128443 Glycine m |
| 34 | 744.4 | 38.2 | 2006 | 8 | BT009349 | BT009349 Triticum |
| 35 | 695 | 35.7 | 2138 | 8 | D82037 | D82037 Oryza sativ |
| 36 | 607.6 | 31.2 | 1188 | 8 | AK069613 | AK069613 Oryza sat |
| 37 | 488 | 25.1 | 504 | 8 | AY146586 | AY146586 Zea may |
| 38 | 478.8 | 24.6 | 915 | 6 | AX755326 | AX755326 Sequence |
| 39 | 438 | 22.5 | 697 | 8 | AK121034 | AK121034 Oryza sat |
| 40 | 418.4 | 21.5 | 1175 | 8 | STSNFIAPK | X95996 S.tuberosum |
| 41 | 405.4 | 20.8 | 1203 | 8 | AK104868 | AK104868 Oryza sat |
| 42 | 371.6 | 19.1 | 196216 | 8 | AF165818 | AF165818 Guillard |
| 43 | 330.6 | 17.0 | 2292 | 5 | AF340021 | AF340021 Xenopus 1 |
| 44 | 329.8 | 16.9 | 1647 | 10 | RNU40819 | U40819 Rattus norv |
| 45 | 329.8 | 16.9 | 1653 | 12 | AY335587 | AY335587 Synthetic |

ALIGNMENTS

RESULT 1
D82035
LOCUS D82035 1838 bp mRNA linear PLN 06-FEB-1999
DEFINITION Oryza sativa mRNA for OSK4, complete cds.
ACCESSION D82035
VERSION D82035.1 GI:4107000
KEYWORDS OSK4.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS 1 (sites)
TITLE Takano,M., Kajiya-Kanegae,H., Funatsuki,H. and Kikuchi,S.
Rice has two distinct classes of protein kinase genes related to

Pred. No. is the number of results predicted by chance to have a

SNF1 of Saccharomyces cerevisiae, which are differently regulated in early seed development
Mol. Gen. Genet. 260 (4), 388-394 (1998)
JOURNAL 99086251
MEDLINE 9870704
REFERENCE 2 (bases 1 to 1838)
AUTHORS Takano,M.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1995) Makoto Takano, National Institute of Agrobiological Resources, Department of Molecular Genetics, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:mtakano@abr.affrc.go.jp, Tel:81-298-38-7446, Fax:81-298-38-7408)

FEATURES
source 1..1838
Location/Qualifiers
/organism="Oryza sativa"
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SLIMNGDVNGRLLPAVIKFEIQLYKSRDEKYLDMQRTVGPQLFLDFCAAFITKLRV
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polyA_site 1838
/gene="osk4"

ORIGIN
Query Match 61.4%; Score 1195.8; DB 8; Length 1838;
Best local Similarity 85.9%; Pred. No. 3.9e-309;
Matches 1326; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

Qy 161 GTAAGAGTGAAGTGGATGGAAGTAGTAAAGGAGTGGCATTCTGAAGCATTAAAGAAC 220
Db 80 GTCACTGTGAAGTGAAGAAATGCTAGAGCGGTGGCATTCTGAGGCACTGAAGAAC 139
Qy 221 TACAACCTGGAGAACTTTAGGTATCGTACATTGGAAAAGTGAAGATTGCAGAGCAT 280
Db 140 TACAATCTAGAGAACTTTAGGTATGGTTCAATTGAAAAGTGAAGATTGCAGAGCAT 199
Qy 281 AAGCTTACTGACATAGGGTGTCTATAAGATCATCACTGCCGCAATGAGAAATATG 340
Db 200 AAGCTTACAGGCGACAGAGTGTCTATAAGATCCTGAACCGTCGCCAAATGAGAAATATG 259
Qy 341 GAAATGGAAGAAAGCAAGAGAGAAATTCAGAGATTGAAGTTGTTCAATTCACCCCAT 400
Db 260 GAAATGGAAGAAAGCAAGAGAGAAATTCAGAGATTGAAGTTGTTCAATTCACCCCAT 319
Qy 401 ATCATTCGGCTTTATGAGGTATATACACACCTACAGATATATATGTTGATGGAATAT 460
Db 320 ATCATTCGGCTTTATGAGGTATATACACCTACAGATATATATGTTGATGGAATAT 379
Qy 461 TGTAGTATGGCAGTTATTGATTACATTGTTGAGAAAGCAGATTACAGAAAGATGAA 520
Db 380 TGCAAGTTTGGAACCTGTTGATTACATTGTTGAGAAAGCAGATTGAGAAAGATGAG 439
Qy 521 GCTGTCGAATCTTCCAGCAGATCATATCTGCGTCGAATACTGCCATAGAAAACATGTT 580
Db 440 GCTGCGCAATCTTCCAGCAGATCATATCTGCGGTTGAATACTGCCACAGAAAACATGTTG 499

Qy 581 GTCCACCGTGACCTAAAGCCGGAACCTTGTTACTTGATTCAAAGTATATATGTAACCTT 640
Db 500 GTTCATCGTATCTGAAGCCAGAAAACCTTGCTACTGATTCAAAGTATTAACGTTAAAGCTT 559
Qy 641 GCGAATTTTGGTCTGAGCAATGTCATGCATGATGGCCATTTTCTGAAGACTAGCTGTGG 700
Db 560 GCTGACTTTGGTTTGAAGTATGTCATGCATGATGGCCATTTTAAAGACAAGCTGCGGG 619
Qy 701 AGTCCGAATATGCTGCTCCAGAGTAAATATCTGTAACATATATGCTGAGCCTGAGGTC 760
Db 620 AGTCCGAATATGCTGCTCCAGAGTATCTCTGTAATATATATGCTGAGCCTGAGGTC 679
Qy 761 GATGATGGAAGTTGTGGGTGATCTTTATGCTCTTGTGGAACCTCTCCATTGAT 820
Db 680 GATGATGGAAGCTGTGAGTGAATCTTTATGCTCTCTTGTGTAACCTCTCCATTGAT 739
Qy 821 GATGAGAAATATCCCAATCTGTTCAAAAAATTAAAGGAGTATCTACACACTTCCAGT 880
Db 740 GACGAGAAATATCCCAACTATTCAAAAAGATAAAGGGTGTATATATACTCTCCCAAGT 799
Qy 881 CATTTGCTGCTTTGGCCAGGATTTGATCCCAAGATGCTTGTGTTGAGCCTATGAAG 940
Db 800 CATTTATCTGCTCTGGCCAGGATTTGATCCCAAGATGCTTGTGTTGATCCCAATGAAG 859
Qy 941 AGAATCACAATTTAGGAAATTCGGAGCATCAATGTTCCAGATTGCGCTTCCAGCTTAC 1000
Db 860 AGAATCACAATTCGTAATTCAGAGCATCAATGTTTCAGATTGCGCTTCTCGTTAC 919
Qy 1001 TTGGCAGTGCCTCCACAGATACGACACAACAAGCCAAAATGATGATGAAGATACACTT 1060
Db 920 TTAGCAGTGCCTCCACAGACACAGACAGCAAGCCAAAATGATGATGAAGATACCTT 979
Qy 1061 CGAGATGTTGTTAATATGAGGATTAAACAAGAACCATGTGTGTAATCACTGTGCAGAGA 1120
Db 980 CAAGACGTTGTTAACTTGGGTATGAAGAAAGCAACCATGTGTGTAATCTCTGCGCAATAGA 1039
Qy 1121 CTTCAAAATGAGGCAACTGTTGCATATTATTACTATTGACAAATCGGTTAGAGCAACT 1180
Db 1040 CTGCAAAATGAGGCAACTGTTGCATATTATTGCTATTGACAAATCGATCCGAGCTAAC 1099
Qy 1181 AGTGCATCTTGGGCGAGATTAACAAGAAATCAATGAACAGAAATTTAAATCAGCTGGCG 1240
Db 1100 AGTGCATCTTGGGCGAGACACTATCAAGAAATCATTGAGAGAAATCTTAATCGCTTGGCT 1159
Qy 1241 TCATCTGAATCATCTAGTTCTGTGTAAGGAATTAATGTTCCAGAAAGCAGTATCTCTCAT 1300
Db 1160 TCATCAGAAATCAAGCAAGTTCAAAATACAAGCATTATCTCCAGAAAGCAGTATCTCTCAT 1219
Qy 1301 AGCAGTGTGTTGGGCCATATTATCTGTTGAAAGAAATGGCGCTTGACTTCAGTCT 1360
Db 1220 GCCAGTGTGTTGGGCCACATTTATCTGTTGAAGAAATGGGCTCTTGACTTCAGTCT 1279
Qy 1361 CGGCGCCACCTCTGTAATTAATGTTGAGGCTTTAAAGCACTTCAAGAAATTAACGTC 1420
Db 1280 CGAGCTCAGCCTCGCGAGATTAATGATGAGGCTCTAAAGGCACTTGAAGACTTAAATGTC 1339
Qy 1421 AGATGAAGAAGATGGGCACTTCAACGTTGAAATGCAAGATGGTCCCAAGGTTTCCTGAA 1480
Db 1340 TGCTGAAGAAGATGACAGTCAACATGAAGTGACAGATGAGCGTTGGTATCTCTCAG 1399
Qy 1481 GTTAATGACACGTTAGATGCAGAACAGCTTTCTTGTACTCTAACCATCATGATTAAT 1540
Db 1400 GCCACTGATATGTTAGATGTCAACACAGCTTTGTTGATGATCAATTATATGATTAAT 1459
Qy 1541 GATGATGCTAATGGAGGCTACCTAAGTATGATCAAGTTTGAATTCAGCTTTACAAGAGC 1600
Db 1460 GCGGATGTAACCGGAGGTTACCTGCTGATCAAGTTTGAATTCAGCTTTACAAGAGC 1519
Qy 1601 AAGGACGACAAGTACCTCTTGAATATGCAAGAGATTACTGACCTCAGCTGCTCTTCTT 1660
Db 1520 AGAGACGAGAAGTATCTGCTGATATGCAAGAGATTACGCGGCTCAGCTCTTTCTCTG 1579
Qy 1661 GACTTCTGTGCGGCTTCTTACCAAGCTTAGGGTTCTATAGT 1703

|||||
Db 1580 GACTTCTGTGACGCTTCTTACCAACTGAGGTTCTATAGT 1622

RESULT 2
AKI00591
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J023106J08, full insert sequence.
AKI00591 2213 bp mRNA linear PLN 24-JUL-2003

ACCESSION AKI00591
VERSION AKI00591.1 GI:32985800
KEYWORDS FLI_CDNA; CAP trapper.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS
1 The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team:

Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:; Otsuo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., NIKURA,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN:; Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
Science 301 (5631), 376-379 (2003)
JOURNAL
MEDLINE 22752273
PUBMED 12869764

2 (bases 1 to 2213)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., NIKURA,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otsuo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.

Direct Submission
Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/NIAS_Rice_Full-length_cDNA_Project_Team:Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,

Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otsuo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., NIKURA,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
location/Qualifiers
1. 2213
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ORIGIN

Query Match 61.4%; Score 1195.8; DB 8; Length 2213;
Best Local Similarity 85.9%; Pred. No. 4e-309;
Matches 1326; Conservative 0; Mismatches 217; Indels 0; Gaps 0;
OY 161 GTAAGTGAATAATGATGAAGTGAAGTGAAGGAGTGGGCAATTCGAAGCATTGAAGAAC 220
DB 216 GTCACTGTGAATAATGAAGAAATGCTAGAGCGGTGGCAATTCGAGGCACTGAAGAAC 275
OY 221 TACAACCTGGGAAGAACTTTAGGTATCGGTACATTGTTGAAAAGTGAAGATTGCAGAGCAT 280
DB 276 TACAATCTGAAGAAGAACTTTAGGTATGTTGTTCAATTTGGAAGAAGTGAAGAGCAT 335
OY 281 AAGCTTACTGACATAGGCGTTCCTATAAAGATCATCACTGCCGCCAAATGAGAATATG 340
DB 336 AAGCTTACAGGGCACAAGATTGCTATAAAGATCTGAACCGTGCCTCAATGAGAATATG 395
OY 341 GAAATGGAAGAAAGCAAGAGAAATTCAGATATTGAAGTTGTTCAATTCACCCCAT 400
DB 396 GAAATGGAAGAAAGCAAGAGAAATTCAGATATTGAAGTTGTTCAATTCACCCCAT 455
OY 401 ATCATTCGCTTTATGAGGTCAATATACACACCTACAGATATATATGTTGTGATGAATAT 460
DB 456 ATCATTCGCTTTATGAGGTCAATATACACCTACAGATATATATGTTGTGATGAATAT 515
OY 461 TGTAAGTATGGCGAGTTATTTGATTACATTTGTTGAAAAGCGAGATTACAGAGAAGTAA 520
DB 516 TGCAGATTGGAGAACTGTTGATTACATTTGTTGAAAAGCGAGTTGCAAGAAGATGAG 575
OY 521 GCTCGTGAATCTTCCAGCAGATCATATCTGGCGTGAATATCTCCATAGAAACATGTT 580
DB 576 GCTCGCGGAATCTTCCAGCAGATCATATCTGGCGTGAATATCTCCATAGAAACATGTT 635
OY 581 GTCACCGGTGACCTAAAGCCGGAACCTTGTACTGTTGTTGTTGTTGTTGTTGTTGTT 640
DB 636 GTTCATGTGATCTGAAGCCAGAAACTTGTCTACTGATTCATCAAGTATTAACGTAAGCTT 695
OY 641 GCGGATTTTGGTCTGAGCAATGTCATGATGAGCCATTTTCTGAAGACTAGCTGTGGG 700
DB 696 GCTGATTTTGGTCTGAGCAATGTCATGATGAGCCATTTTCTGAAGACTAGCTGTGGG 755
OY 701 AGTCCGAATATGCTGCTCCAGAGTAATATCTGTTAACTATATGCTGAGCCTGAGGTC 760

| | | | |
|----|------|---|------|
| Db | 756 | AGTCGGAATTATGCTGCTCCAGAGGTGATCTCTGTAATATATATGTCGAGACCCGAGCTT | 815 |
| Qy | 761 | GATGTATGAGTTGTGGGGTATTCTTTATGCTCTTCTTTGTGAACCTCTCCATTGTGAT | 820 |
| Db | 816 | GATGTATGAGCTGTGGAGTGATCCTTATGCTCTCCTTTGTGTACTCTTCCATTGTGAT | 875 |
| Qy | 821 | GATGAGAATATTTCCCAATCTGTTCAAAAAAATTAAAGGAGGTATACACACTTCCAAGT | 880 |
| Db | 876 | GACGAGAATATCCCAACTATTCAAAAAGATAAAGGGTGTATATATACTCTCCAAGT | 935 |
| Qy | 881 | CATTGTCTGCTTTGGCCAGGAGTTGATCCCAAGATGCTTGTGTGAGCCTATGAAG | 940 |
| Db | 936 | CATTATCTGCTCTGGCCAGGAGTTGATCCCAAGAGTGTGTTGTGATCCAATGAAG | 995 |
| Qy | 941 | AGAATCACAAATTAGGAAATTCGGAGACATCAATGTTCCAGATTGCGCTTCCACGTTAC | 1000 |
| Db | 996 | AGAATCACAAATTCGTAATTCGAGAGCATCAATGTTTCCAGATTGCGCTTCCGTTAC | 1055 |
| Qy | 1001 | TTGGCAGTGCCTCCACCAGATACGACACAACAAGCCAAATGATGTGTAAGATACACTT | 1060 |
| Db | 1056 | TTAGCAGTGCCTCCACCAGACACAGCAGCAGCAAGCCAAATGATGTGTAAGATACACTT | 1115 |
| Qy | 1061 | CGAGATGTTGTTAATATATGGATTTAACAGAAACCATGTGTGTGAATCACTGTGCAGCAGA | 1120 |
| Db | 1116 | CAAGACGTTGTAACCTTGGGTTATGAAAAGCACATGTGTGTGAATCTCTGCGCAATAGA | 1175 |
| Qy | 1121 | CTTCAAAATGAGGCAACTGTGTGATATATTATTACTATTGGACAATCGGTTTAGACCAACT | 1180 |
| Db | 1176 | CTGCAAAATGAGGCAACTGTGTGATATATTGCTATTGGACAATCGATTCGAGCTACC | 1235 |
| Qy | 1181 | AGTGGCTATCTTGGGGCAGATTATCAAGATCAATGACAGAGAAATTTAAATCAGCTGCGG | 1240 |
| Db | 1236 | AGTGGCTATCTTGGGAGCAGACTATCAAGATCAATGAGAGAAATTTAAATCGCTTGTCT | 1295 |
| Qy | 1241 | TCATCTGAATCATCTAGTTCTGTACGAGAAATATGTTCCAGAGCAGTGTATCTTCAT | 1300 |
| Db | 1296 | TCATCAGAATCAGCAAGTCAATATCAAGCATTATCTCCAGAGAAAGTGTATCTTCAT | 1355 |
| Qy | 1301 | AGCAGTGTGTCGGCCATATATCTCTGTGAAGAATAATGGGCGCTTGGACTTCAGTCT | 1360 |
| Db | 1356 | GCCAGTGTGTCGGCCACATATCTCTGTGAAGAATAATGGGCGCTTGGACTTCAGTCT | 1415 |
| Qy | 1361 | CGGGCCACCTCGTGAATATATGTTGAGTCTTAAAGCAGCTTCAAGATTTAAACGTC | 1420 |
| Db | 1416 | CGAGCTCAGCCTCGCGAGATATGATGAGTCTTAAAGGCAGCTTGAAGACTTAAATGTC | 1475 |
| Qy | 1421 | AGATGAAGAAGATGGGCATCAACGTTGAATGCAGATGTTGCCAGGGTTTCTTGAA | 1480 |
| Db | 1476 | TGCTGAAGAAGATGAGACAGTACCAACATGAAGTGACAGTGGAGCGTGGGTATCCTCAG | 1535 |
| Qy | 1481 | GTTAATGACACGTTAGATGCCAGCAACGCTTCTTGGTACTCTTACCATCATGATTAAT | 1540 |
| Db | 1536 | GCCACTGATATGTTAGATGTCAACACACAGCTTGTGATGACTCAATTAATGATTAAT | 1595 |
| Qy | 1541 | GATGATGCTAATGGAGGCTACCTACTGTGATCAAGTTTGAATTCAGCTTTACAAGACG | 1600 |
| Db | 1596 | GGCGATGTAAACGGAGGTTACCTGCTGTGATCAAGTTTGAATTCAGCTTTACAAGACG | 1655 |
| Qy | 1601 | AAGGACGACAACTACTCTTAGATATGCAGAGAGTTACTGACCTCAGCTGCTCTTCTT | 1660 |
| Db | 1656 | AGAGACGAGAAATATCTGCTGATATGCAGAGAGTTACGGGGCGCTCAGCTCTTCTCTG | 1715 |
| Qy | 1661 | GACTTCTGTGCGGCTTCTTACCAGCTTAGGGTTCTATAGT | 1703 |
| Db | 1716 | GACTTCTGTGACGCTTCTTACCAAACTGAGGGTTCTATAGT | 1758 |

RESULT 3
AK072723
LOCUS AK072723 2245 bp mRNA linear PLN 24-JUL-2003
DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:J023135H07, full insert sequence.

| | |
|-----------|---|
| ACCESSION | AK072723 |
| VERSION | AK072723.1 GI:32982746 |
| KEYWORDS | FLI cDNA; CAP trapper. |
| SOURCE | Oryza sativa (japonica cultivar-group) |
| ORGANISM | Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrharcoideae; Oryzeae; Oryza. |
| REFERENCE | 1 |
| AUTHORS | The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team; Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN; Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y. Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice Science 301 (5631), 376-379 (2003) 22752273 12869764 |
| TITLE | 2 (bases 1 to 2245) |
| JOURNAL | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A. |
| JOURNAL | Direct Submission |
| AUTHORS | Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007) |
| TITLE | This clone is one of the 28k full-length cDNA clones from japonica rice. |
| COMMENT | URL : http://cdna01.dna.affrc.go.jp/cDNA/ NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M. FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K. |

Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hirooka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.

location/Qualifiers

1. 2245
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J023135H07"

ORIGIN

Query Match 61.4%; Score 1195.8; DB 8; Length 2245;
Best Local Similarity 85.9%; Pred. No. 4e-309;
Matches 1326; Conservative 0; Mismatches 217; Indels 0; Gaps 0;

OY 161 GTAAGAGTGAATAATGATGGAAGTAAAGGAGTGGCATTCTGAAGCATTAAGAAC 220
DB 212 GTCACTGTAAATGGAAGAAATGCTAGAGCGGTGGCATTCTGAGGCACTGAAGAAC 271
OY 221 TACAACCTGGAGAAGACTTTAGTATCGGTACATTTTGAAAAGTGAAGATTGCAGAGCAT 280
DB 272 TACAATCTAGAGAAGACTTTAGTATCGGTACATTTTGAAAAGTGAAGATTGCAGAGCAT 331
OY 281 AAGCTTACTGACATAGGGTGTCTATTAAGATCATCAACTGCCGCAATGAGAAATATG 340
DB 332 AAGCTTACAGGGCACAGAGTGTCTATTAAGATCCTGAACCGTCCCAATGAGAAATATG 391
OY 341 GAAATGGAAGAAAAGCAAGAGAGAAATCAAGATATTGAAGTTGTCATTCACCCCAT 400
DB 392 GAAATGGAAGAAAAGCAAGAGAGAAATCAAGATATTGAAGTTGTCATTCACCCCAT 451
OY 401 ATCATTCGGCTTTATGAGGTCAATACACACTACAGATATATATGTGTGATGAATAT 460
DB 452 ATCATTCGGCTTTATGAGGTCAATACACTCCTACGATATATATGTGTGATGAATAT 511
OY 461 TGTAGTATGGCGAGTATTGTATACATTTGTGAGAAAGGCAATTAAGAGATGAA 520
DB 512 TGTAGTATGGCGAGTATTGTATACATTTGTGAGAAAGGCAATTAAGAGATGAG 571
OY 521 GCTCGTGAATCTTCCAGCAGATCATCTGCGGTGCAATATCTGCCATAGAAACATGCTT 580
DB 572 GCTCGCGGAATCTTCCAGCAGATTAATCTGGGGTTGAATATCTGCCACAGAAAATGCTG 631
OY 581 GTCCACCGTGACCTAAAGCCGGAACCTGTTACTTGATTCAAAGTATATGTAAACCTT 640
DB 632 GTTCATCTGATCTGAAGCCAGAAAATCTGCTACTGATTCAAAGTATATGTAAGCTT 691
OY 641 GCGGATTTGGTCTGAGCAATGTCAATGATGAGCCATTTCTGAAGACTAGCTGTGG 700
DB 692 GCTGACTTTGGTTGAGTAATGTCAATGATGAGCCATTTTAAAGACAAAGCTGCGG 751
OY 701 AGTCCGAATATAGTCTGCCAGAGGTATATCTGTTAACTATATGCTGAGCTGAGGTC 760
DB 752 AGTCCGAATATAGTCTGCCAGAGGTATCTCTGTTAAATATATGCTGAGCCGAGGTT 811
OY 761 GATGTATGAGTGTGGGGTATCTTTATGCTCTTGTGGAACCTCTTCATTTGAT 820
DB 812 GATGTATGAGCTGTGAGTATCTTTATGCTCTCTTGTGTGTAATCTTCCATTTGAT 871
OY 821 GATGAGATATTTCCCAATCTGTTCAAAAAATTAAGGAGGTATCTACACACTTCCAAGT 880

DB 872 GACGAGATATATCCCAACCTATTCAAAAAGATAAAGGTGTATATATACTCTCCCAAGT 931
OY 881 CATTTGTCTGCTTTGGCCAGGAAATTTGATCCCAAGAAATGCTGTGTGAGCCTATGAG 940
DB 932 CATTTATCTGCTCTGGCCAGGAAATTTGATCCCAAGAAATGCTGTGTGATCCCAATGAG 991
OY 941 AGAATCAATATTAGGAAATTTGGAGCATCAATGTTCCGATTCGCTCCAGCTTAC 1000
DB 992 AGAATCAATATTGTAATTTGAGAGCATCAATGTTTTCAGATTGCTTCTCTGTTAC 1051
OY 1001 TTGGAGTGCCTCCACAGATACGACACAAAGCCAAATGATTTGATGAAGATACACTT 1060
DB 1052 TTAGCAGTGCCTCCACAGACACGACACAAAGCCAAATGATTTGATGAAGATACCTT 1111
OY 1061 CGAGATGTTGTTAATATGGAATTTAAAGAAACCATGTGTGTAATCACTGTGACAGACA 1120
DB 1112 CAAGACGTTGTAACCTTGGTTATGAAGAAAGACCATGTGTGTAATCTCTGCGCAATAGA 1171
OY 1121 CTTCAAAATGAGCAACTGTTGCAATATTATTTACTATTGCAATCGGTTTAGAGCAACT 1180
DB 1172 CTGCAAAATGAGCAACTGTTGCAATATTATTTGCTATTGGAATCGATTCCGAGCTACC 1231
OY 1181 AGTGGCTATCTTGGGCAAGATTAACAAGATCAATGACAGCAATTTAAATCAGCTGGCC 1240
DB 1232 AGTGGCTATCTGGGCAAGATTAACAAGATCAATGACAGCAATTTAAATCAGCTGGCT 1291
OY 1241 TCATCTGAATCATCTAGTTCTGGTAAGGAAATTAATGTTCCAGGAAGCAGTATCCTCAT 1300
DB 1292 TCATCAGAAATCAGCAAGTTCAAAATCAAGGATTAATCTCCAGGAAGCAGTATCCTCAT 1351
OY 1301 AGCAGTGTGTTGCGCCATATTATCTGTTGAAAGAAAATGCGGCTTGACTTCAGTCT 1360
DB 1352 GCCAGTGTGTTGCGCCATATTATCTGTTGAAAGAAAATGCGGCTTGACTTCAGTCT 1411
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DB 1412 CGAGCTCAGCCTCGGAGATATGATGAGTCTTAAAGCACTTGAAGACTTAATATGTC 1471
OY 1421 AGATGGAAGAAGATGGGCACTAACAGTGAATGCAATGCTGCCAGGTTTCTGAA 1480
DB 1472 TGTGGAAGAAGATGGAACAGTACCAATGAAGTGCAGATGGAAGCTTGGGATCTCAG 1531
OY 1481 GTTAATGACACGTTAGATGCCAGCAACAGCTTCTTGTTGACTCTCAATCATGATTAAT 1540
DB 1532 GCCACTGATATGTTAGATGTCACACAGACTTGTGTGATGACTCAATTAATGATTAAT 1591
OY 1541 GATGATGCTAATGGAGGCTTACTGATCAAGTTGAATTCAGCTTTACAGAGCG 1600
DB 1592 GCGGATGTAAACGAGGTTACTGCTGTGATCAAGTTGAATTCAGCTTTACAGAGCG 1651
OY 1601 AAGGACGACAAGTACCTTTAGATATGACAGAGATTACTGCACTCAGCTGCTTCTT 1660
DB 1652 AGAGACGAGAAGTATCTGCTGATATGACAGAGATTACGGGGCTCAGCTCCTTCTCTG 1711
OY 1661 GACTTCTGTGGCGCTTCTTACCAAGCTTAGGGTTCTATAGT 1703
DB 1712 GACTTCTGTGCAAGCTTCTTACCAACTGAGGTTCTATAGT 1754

RESULT 4
BT009004 1899 bp mRNA linear PLN 20-JUN-2003
LOCUS BT009004
DEFINITION Triticum aestivum clone wdk2c.pk018.c16.fis, full insert mRNA
sequence.
ACCESSION BT009004
VERSION BT009004.1 GI:32128555
KEYWORDS FLI CDNA.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Triticum.
REFERENCE 1 (bases 1 to 1899)

AUTHORS Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H., Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
 TITLE Direct Submission
 JOURNAL Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

FEATURES
 source Location/Qualifiers
 1. 1899
 /organism="Triticum aestivum"
 /mol_type="mRNA"
 /db_xref="taxon:4565"
 /clone="wdk2c.pk018.c16.fis"

ORIGIN

Query Match 61.4%; Score 1195.6; DB 8; Length 1899;
 Best Local Similarity 85.8%; Pred. No. 4.5e-309;
 Matches 1327; Conservative 0; Mismatches 219; Indels 0; Gaps 0;

QY 166 AGTGAATGATGGAAGTAGTAAGGAGTGGGCATCTGAAGCATTAAGAACTACAA 225
 DB 60 AGTGAATGGAAGGGAACACTAGAGAGTGGGCATCTGACGCATTAAGAACTACAA 119
 QY 226 CCTGGGAAGACTTTAGTATCGTACATTTGGAAGAAGTGAAGATTCAGAGCATTAAGCT 285
 DB 120 TGTGGGCAACATTAAGTATAGGACATTTGGAAGAAGTGAAGATTCAGAGCATTAAGCA 179
 QY 286 TACTGACATAGGCTTGCTATAAAGATCACTGCCGCAAAATGAAGAATATGAAAT 345
 DB 180 TACAGGGCATAAAGTGTCTATAAAGATCTGAACCGTGTCAATGAGAATATGAAAT 239
 QY 346 GGAAGAGAAGCAAAAGAGAATTCAGATTTGAAGTGTTCATCAACCCCATATCAT 405
 DB 240 GGAAGAGAAGCAAAAGAGAAGATCAAGATTTGAAGTGTTCATCAACCCCATATCAT 299
 QY 406 TCGGCTTTATGAGGTCTATATACACACCTTACAGATATATGTTGATGGAATATTGTA 465
 DB 300 CCGGCTTTATGAGGTCTATTAACACCTTACAGATATATGTTGATGGAATATTGCAA 359
 QY 466 GTATGCGGATTTATTTGATTACATTTGAGAAAGGAGATTAAGAGATGAAGCTCG 525
 DB 360 GTATGCTGAGTATTGCACTGATTTGTAAGAAAGGCGGTTACAGAAAGATGAGCTCG 419
 QY 526 TCGAATCTTCAGAGATCATATCTGGCGTGAATATCTGCCATGAAACATGTTGTCCA 585
 DB 420 TCGAATCTTCAGAGATCATATCTGGGTGGAATACTGCCACAGAAACATGTTGTCTCA 479
 QY 586 CCGTGACCTAAAGCCGGAACCTGTTACTGATTCAAGTAAATGTAAGCTTGCGGA 645
 DB 480 TCGTGATCTAAAGCCAGAGAACCTGTTACTGATTCCAATATCAATGTGAACCTTGCGGA 539
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 QY 706 GAACTATGCTGCTCCAGAGTAATATCTGTTAACTATATGCTGAGCTGAGCTGATGT 765
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 QY 766 ATGAGTTGTTGGGTGATTTCTTATGCTCTCTTTGTTGAACTCTTCCATTGATGATGA 825
 DB 660 TTGAGCTGCGGGGTGATCTTATGCTCTCTTTGTTGCACTCTTCCATTGATGATGA 719
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 DB 780 ATCTGCTCTTGCAGAGGATTTGATCCCAAGATGCTTGTGTTGATCTATGAAGAAAT 839
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 DB 840 CACAATTGTTGAATTCGAGAAACACCAATGTTTCAGAATGCGCTTCTGCTACCTGCGC 899

QY 1006 AGTGCTCCACAGATACGACACAACAAAGCCAAAATGATGATGAAGATACACTTGCAGA 1065
 DB 900 AGTGCTCCACAGACACGCGGACAGCAAGCCAAAATGATGATGAAGATACACTTGAAGA 959
 QY 1066 TGTGTTAATATGGATTTTAAACAAGAACCATGTGTGTGAATCACTGTGCAGCACTTCA 1125
 DB 960 GATTGTCAACCTGGGATATGATTAAGAACCATGTGTGTGAATCATGTGTGCAATAGCTGCA 1019
 QY 1126 AAATGAGGCAACTGTGTCATATTTACTATTGGACAAATCGGTTTAGAGCAACTAGTGG 1185
 DB 1020 AAATGAGGCAACTGTGTCATATTTACTCTTGGACAAATCGGTTCCGGCCACTAGTGG 1079
 QY 1186 CTATCTGGGCGAGATTATCAAGAATCAATGACAGCAAAATTAATCAGCTGCGCTCATC 1245
 DB 1080 CTATTTGGGGCTGACTATCTTAACAATCAATGAGGTAGAGTTTAAATCAGTTTACTTCAATT 1139
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 QY 1606 CGACAAGTACCTCTAGATATGAGAGAGTACTGGAAGCTGAGCTCTCTCTGACTT 1665
 DB 1500 TGACAAGTACCTGCTAGATATGAGAGAGTACTGGAAGCTGAGCTCTCTCTGACTT 1559
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 DB 1560 TTGCGGCGCTTCTCTTACCAAGCTTAGGTTCTATAGTGTGTGCC 1605

RESULT 5
 DB82038
 LOCUS Oryza sativa mRNA for OSK3, complete cds. 1872 bp mRNA linear PLN 06-FEB-1999
 DEFINITION
 ACCESSION DB82038
 VERSION DB82038.1 GI:4107006
 KEYWORDS OSK3.
 SOURCE Oryza sativa
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 REFERENCE 1 (sites)
 AUTHORS Takano,M., Kajiya-Kanegae,H., Funatsuki,H. and Kikuchi,S.
 TITLE Rice has two distinct classes of protein kinase genes related to SNF1 of Saccharomyces cerevisiae, which are differently regulated in early seed development
 JOURNAL Mol. Gen. Genet. 260 (4), 388-394 (1998)
 MEDLINE 99086251
 PUBMED 9870704
 REFERENCE 2 (bases 1 to 1872)
 AUTHORS Takano,M.
 TITLE Direct Submission

| | | | | | |
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| LOCUS | D82036 | 2161 bp | mRNA | linear | PLN 06-FEB-1999 |
| DEFINITION | Oryza sativa mRNA for OSK5, complete cds. | | | | |
| ACCESSION | D82036 | | | | |
| VERSION | D82036.1 | GI:4107002 | | | |
| KEYWORDS | OSK5. | | | | |
| SOURCE | Oryza sativa | | | | |
| ORGANISM | Oryza sativa | | | | |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza. | | | | |
| REFERENCE | 1 (sites) | | | | |
| AUTHORS | Takano, M., Kajiya-Kanegae, H., Funatsu, H. and Kikuchi, S. | | | | |
| TITLE | Rice has two distinct classes of protein kinase genes related to SNF1 of Saccharomyces cerevisiae, which are differentially regulated in early seed development | | | | |
| JOURNAL | Mol. Gen. Genet. 260 (4), 388-394 (1998) | | | | |
| MEDLINE | 99086251 | | | | |
| PUBMED | 9870704 | | | | |
| REFERENCE | 2 (bases 1 to 2161) | | | | |
| AUTHORS | Takano, M. | | | | |
| TITLE | Direct Submission | | | | |
| JOURNAL | Submitted (15-DEC-1995) Makoto Takano, National Institute of Agrobiological Resources, Department of Molecular Genetics; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan | | | | |
| | (E-mail: mtakano@abr.affrc.go.jp, Tel: 81-298-38-7446, Fax: 81-298-38-7408) | | | | |

| FEATURES | Location/Qualifiers |
|----------|--|
| source | 1..2161 /organism="Oryza sativa" /mol_type="mRNA" /db_xref="taxon:4530" |
| gene | 1..2161 /gene="osk5" |
| CDS | 127..1653 |

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ORIGIN

| | | | | |
|----------------------------|--------|-------------------|-----------|--------------|
| Query Match | 60.9%; | Score 1186.8; | DB 8; | Length 2161; |
| Best Local Similarity | 85.3%; | Pred. No. 1e-306; | | |
| Matches 1336; Conservative | 0; | Mismatches 227; | Indels 3; | Gaps 1; |

[illegible]

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| Q | y | 743 | TATG | CTG | ACCTG | AGTCG | ATGAT | GATG | AGTTG | TGGG | GTATCTT | ATGCTCT | TTGT | 802 | |
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| D | b | 817 | ATAT | ATACT | CTCC | AAGTC | ATTAT | CTGCT | TGG | CCAG | AGATTG | ATCC | CAAGATG | 876 | |
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| Q | y | 1163 | AATC | GTTT | AGACA | CTAGT | GCTAT | CTTGG | GGCAG | ATTAT | CAAG | AATCA | ATG | GACAG | 1222 |
| D | b | 1117 | AATC | GATT | CCG | AGTAC | AGTGG | CTATT | GGG | AGCACT | ATCA | AGAA | CTTTG | GAGAG | 1176 |
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| Q | y | 1403 | CTT | CAAG | AATTAA | CGTCAG | ATGGA | AGAA | TGGG | CACTA | CAACG | TGA | ATG | CAGATG | 1462 |
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Oy 1703 TGGTCT 1708
Db 1654 TACCCT 1659

RESULT 7
LOCUS OSU55768 1770 bp mRNA linear PLN 02-AUG-1996
DEFINITION Oryza sativa SNF1-related protein kinase (RSK1) mRNA, complete cds.
ACCESSION U55768
VERSION U55768.1 GI:1477683
KEYWORDS
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 1770)
AUTHORS Tsai, T.-H. and Le, H.-T.
TITLE SNF1-related protein kinase of rice
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1770)
AUTHORS Tsai, T.-H.
TITLE Direct Submission
JOURNAL Submitted (19-APR-1996) Teh-Huei Tsai, Life Science, National
Tsing-Hua University, Hsinchu 30043, Republic of China

FEATURES
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ORIGIN
Query Match 59.8%; Score 1164; DB 8; Length 1770;
Best Local Similarity 85.2%; Pred. No. 1.3e-300;
Matches 1312; Conservative 0; Mismatches 225; Indels 3; Gaps 1;

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Db 7 GTGAAATGATGGAATGCTAAAGGCGGTGGCATTTCTGAGGCACTGAAGAACTACAAT 66
Oy 227 CTGGGAAGAACTTTAGGTATCGGTACATTTGGAAAAAGTGAAGATTGCAGAGCATTAAGCTT 286
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Oy 287 ACTGACATAGGTTGCTATTAAGATCACTGCGCCCAATGAGAAATATGAAATG 346
Db 127 ACAGACACAGAGTTGCTATTAAGATCTGAACCGCCCAATGAGAAATATGAAATG 186
Oy 347 GAAGAGAAAGCAAGAGAGAAATTCAGATATTTGAAGTTGTTCAATCAACCCCATATCATT 406
Db 187 GAGAGAAAGCAAGAGAGAAATTCAGATATTTGAAGTTGTTCAATCAATCCCATATCATT 246
Oy 407 CGGCTTATGAGGTCATATACACACCTACAGATATATATGTTGATGGAATATTTGAAG 466
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Oy 467 TATGCGAGTTATTTGATTTACATTTGTTGAGAAAGGCGAGATTACAGAAAGT--GAAGCT 523
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Oy 584 CACCGTACCTAAAGCCGAAACCTGTTACTTGTATCAAGATTAATGTAAGAACTTGGC 643
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Oy 644 GATTTGTTGATGAGCAATGTCATGATGAGGCCATTTCTGAAGCTAGCTGTGGAGT 703
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Oy 704 CCGAATATGCTGCTCCAGAGGTAATATCTGTAACATATATGCTGGAACCTGAGTGCAT 763
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Oy 824 GAGATATTTCCCAATCTGTTCAAAAAATTAAAGGAGTATCTACACTTCCAAAGTCAT 883
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Oy 884 TTGTGCTTTGGCCAGGATTTGATCCCAAGATGCTTGTGTTGAGCCTATGAAGAGA 943
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Oy 1244 TCTGAATCATTAAGTTCTGTTGACGAAATTAATGTTCCAGAAAGCAAGTATCCTCATAGC 1303

| | | | | | | |
|----|------|-------------------|------------------|---------------------|------------------|-------------------|
| Db | 1087 | TCGGAATCAGCAAGTTC | AAATACAGGCA | TTATCTTCCAGGAAGCAGT | ATCCTCATGCC | 1146 |
| Qy | 1304 | AGTGTTCGGCCATAT | TATCTGTGAAAGAAAT | TGGCGCTTGACT | CTCAGTCCG | 1363 |
| Db | 1147 | AGTGTTCGGCCACAT | TATCTGTGAAAGAAAT | TGGCGCTTGACT | CTCAGTCCG | 1206 |
| Qy | 1364 | GCCACCCCTCGTGA | AATATGTTGAGGCTT | AAAGCAGCTTCA | GAATTAAACGTCAGA | 1423 |
| Db | 1207 | GCTCAACCTCGCAG | ATAATGATTGAGGCT | TAAAGCAGCTTCA | GAAGCTTAAATGCTCC | 1266 |
| Qy | 1424 | TGGAAGAAGATGGG | CACACTACACG | TGAATGCAGATG | TGTCGCCAGGTTTCC | TGAAGTT 1483 |
| Db | 1267 | TGGAAGAAGATGG | ACAGTACACATGA | GTGCAGATGAGC | CGTTGGGTATCCTC | CAGGCC 1326 |
| Qy | 1484 | AATGACACGTTAG | ATGCCAGCACAGC | TTTCTTGCTGACT | CTTACCATCATG | GAATGAT 1543 |
| Db | 1327 | ACTGATATTTAG | ATGTCAACCA | CAGCTTTGTTGAT | GACTCAATTATTA | TGATAATGCC 1386 |
| Qy | 1544 | GATGCTAATGGAG | GCTACTACTGTG | ATCAAGTTGAAT | TCAGCTTTACA | GAGCAG 1603 |
| Db | 1387 | GATGTAACGGAG | GTTACCTGCTGT | GATCAAGTTGA | AAATCCAGCTTT | TACAAGAGCAGA 1446 |
| Qy | 1604 | GACGACAAGTACT | CTTAGATATG | CAGAGTTACTG | ACCTCAGCTGCT | CTTCTGAC 1663 |
| Db | 1447 | GACGAGAAGTAT | CTGTGATATG | CAGAGTTACG | GGCCTCAGCTC | CTTTCTGAGC 1506 |
| Qy | 1664 | TTCTGTGGCGCT | TCTTACCAAGC | TTAGGTTCTAT | AGT 1703 | |
| Db | 1507 | TTCTGTGACGCT | TCTTACCAACT | GAGGTTCTAT | AGT 1546 | |

| | | | | | |
|------------|--|---------|------|--------|-----------------|
| RESULT 8 | AK069206 | 2927 bp | mRNA | linear | PLN 24-JUL-2003 |
| LOCUS | Oryza sativa (japonica cultivar-group) cDNA clone:J023008117, full insert sequence. | | | | |
| DEFINITION | AK069206 AK069206.1 GI:32979230 | | | | |
| ACCESSION | AK069206.1 GI:32979230 | | | | |
| VERSION | FLI CDNA; CAP trapper. | | | | |
| KEYWORDS | Oryza sativa (japonica cultivar-group) | | | | |
| SOURCE | Oryza sativa (japonica cultivar-group) | | | | |
| ORGANISM | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. | | | | |
| REFERENCE | 1 The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team; Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotte,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Ootomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN; Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y. | | | | |
| TITLE | Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice | | | | |
| JOURNAL | Science 301 (5631), 376-379 (2003) | | | | |
| MEDLINE | 22752273 | | | | |
| PUBMED | 12869764 | | | | |
| REFERENCE | 2 (bases 1 to 2927) | | | | |
| AUTHORS | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotte,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y. | | | | |

| | | | | | | | |
|----|------|-------------------|------------------|---------------------|------------------|-------------------|--|
| Qy | 1087 | TCGGAATCAGCAAGTTC | AAATACAGGCA | TTATCTTCCAGGAAGCAGT | ATCCTCATGCC | 1146 | Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,C., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Ootomo,Y., Ryu,R., Satoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toyoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A. |
| Qy | 1304 | AGTGTTCGGCCATAT | TATCTGTGAAAGAAAT | TGGCGCTTGACT | CTCAGTCCG | 1363 | FAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K. |
| Qy | 1364 | GCCACCCCTCGTGA | AATATGTTGAGGCTT | AAAGCAGCTTCA | GAATTAAACGTCAGA | 1423 | Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toyoda,Y., Waki,K., Yasunishi,A. and Hayashizaki,Y. |
| Qy | 1207 | GCTCAACCTCGCAG | ATAATGATTGAGGCT | TAAAGCAGCTTCA | GAAGCTTAAATGCTCC | 1266 | location/Qualifiers |
| Qy | 1424 | TGGAAGAAGATGGG | CACACTACACG | TGAATGCAGATG | TGTCGCCAGGTTTCC | TGAAGTT 1483 | 1.2927 |
| Qy | 1267 | TGGAAGAAGATGG | ACAGTACACATGA | GTGCAGATGAGC | CGTTGGGTATCCTC | CAGGCC 1326 | /organism="Oryza sativa (japonica cultivar-group)" |
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| Qy | 1604 | GACGACAAGTACT | CTTAGATATG | CAGAGTTACTG | ACCTCAGCTGCT | CTTCTGAC 1663 | |
| Qy | 1447 | GACGAGAAGTAT | CTGTGATATG | CAGAGTTACG | GGCCTCAGCTC | CTTTCTGAGC 1506 | |
| Qy | 1664 | TTCTGTGGCGCT | TCTTACCAAGC | TTAGGTTCTAT | AGT 1703 | | |
| Qy | 1507 | TTCTGTGACGCT | TCTTACCAACT | GAGGTTCTAT | AGT 1546 | | |

COMMENT

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotte,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kamondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28k full-length cDNA clones from japonica rice.

| | | | | | | | |
|----|------|-----------------|----------------|---------------|-------------------|---------------|---|
| Qy | 155 | CGTAACTAAGAGTGA | AAATGATGCAAGT | AGTAAGGAGGAGT | GGCATTCTGAAGCATTA | 214 | Query Match 59.5%; Score 1159.6; DB 8; length 2927; Best local Similarity 85.1%; Pred. No. 2.1e-299; Matches 1323; Conservative 0; Mismatches 219; Indels 12; Gaps 2; |
| Qy | 1174 | CGTTGGTTCAAA | GTGAAGATGATGA | AAATGCTAAAGG | CGGTGGCATTCTGAGG | CACGTG 1233 | |
| Qy | 215 | AGGAACCTAAC | CACTGGGAAGACTT | TAGGTATCGGTAC | ATTGGAAAAGTGAAG | ATTGCA 274 | |
| Qy | 1234 | AAAGAACTACA | ATCTTGAAGAACTT | TAGTATTGGCTCA | ATTGGAAAAGTGAAG | ATTGCA 1293 | |
| Qy | 275 | GAGCATTAAGCTT | ACTGACATGAGG | TTGCTATTAAGAT | CACTCAACTGCCG | CCAAATGGA 334 | |

Db 1294 GAGCATAAGCTTACAGGACACAGAGTTGCTATTAAGATCCTGNAACCGCCCAATGAGA 1353

Qy 335 AATATGAAATGGAAGAGAAAGCAAGAGAAATTCAGATATTTGAAGTTGTCATTAC 394

Db 1354 AATATGAAATGGAAGAGAAAGCAAGAGAAATTCAGATATTTGAAGTTGTCATTAC 1413

Qy 395 CCCCATATCATTCGGCTTTATGAGTCAATACACCTACAGATATATATGTTGATG 454

Db 1414 CCCCATATCATTCGGCTTTATGAGTCAATACACCTACAGATATATATGTTGATG 1473

Qy 455 GAATATTGTAAGTATGCGGAGTATTTGATTACATTTGTTGAGAAAGGCAGATTACAGAA 514

Db 1474 GAGTACTGCAAGTTTGAGAACTGTTGATTACATTTGTTGAGAAAGGCAGTTGCAAGAA 1533

Qy 515 GATGAAGCTCGTGAATCTTCCAGCAGATCATATCTGGCGTGAATACTGCCATAGAAAC 574

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Qy 575 ATGTTGTCCACCGTGACCTTAAGCCGGAACCTGTTACTTGATTCAAGTAAATGTA 634

Db 1594 ATGTTGTTCATCGTGAATCTGAAGCCAGAAACTTGCTACTGATTCAAAGTAAATGTA 1653

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Db 1774 GAGTTGATGTATGAGAGCTGTGAGTGAATCCTTTATGCTCTTCTTTGTTGTAATCTTCCA 1833

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Db 1894 CCAAGTCATTTATCTGCTCTGGCCAGAGATTGATCCCAAGATGCTTTGTTGATCCA 1953

Qy 935 ATGAAGAGAATCACAATTAGGGAATTCGGAGCATCAATGTTCCAGATTGCCCTTCCA 994

Db 1954 ATGAAGAGAATCACAATTCGTAATTCGAGAGCATCAGTGTTCCAGATTGCCCTTCTC 2013

Qy 995 CGTTACTTGGCAGTGCTCCACCAGATACGACACAACAAGCCAAATGATGTGAAGAT 1054

Db 2014 CGTTACTTAGCAGTGCTCCACCAGACAGACAGCAAGCCAAATGATGTGAAGAT 2073

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Db 2134 AATAGACTGCAGAATGAGGCAACTGTGCAATATATTACTCTTGACAAATCGATTCCGA 2193

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Db 2194 GCTACCAAGTGGCTATTTGGGAGCAGACTATCAAGAATCTTTGAGAGGAATTTTAATCGC 2253

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Db 2434 AATGTCCTCGAAGAGAAATGGACAGTACCAACATGAATGCAGATGAGCGTTGG--- 2490

Qy 1475 CCTGAAGTTAATGACACCGTTAGATGCGACCAACAGCTTCTTGGTGAATCTACCATCATG 1534

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Db 2603 -AGACCAGAGACGAGAAGTATCTGCTGATATGACAGAGATTACGGGGCTCAGCTCCTT 2661

Qy 1655 TTCCTGACTTCTGTGCGGCTTCCCTTACCAAGCTTAGGGTTCTATAGTGTCT 1708

Db 2662 TTCCTGACTTCTGTGACAGCTTCTTACCAAGCTGAGGGTTCTATAGTACCCT 2715

RESULT 9

HVU7990

LOCUS HVU7990 1542 bp mRNA linear PLN 22-JUL-1998

DEFINITION Hordeum vulgare mRNA for SnRK1-type protein kinase, partial.

ACCESSION AJ007990

VERSION AJ007990.1 GI:3341451

KEYWORDS kin12a gene; SnRK1-type protein kinase.

SOURCE Hordeum vulgare subsp. vulgare

ORGANISM Hordeum vulgare subsp. vulgare

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticaceae; Hordeum.

REFERENCE 1

AUTHORS Slocombe,S.P., Bertini,L., Beaudoin,F., Dickinson,J.R. and Halford,N.G.

TITLE Molecular cloning of Bsnr1p, a novel putative SNF4-related protein identified in a two-hybrid screen with barley seed SnRK1 protein kinase

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1542)

AUTHORS Slocombe,S.P.

TITLE Direct Submission

JOURNAL Submitted (21-JUL-1998) Slocombe S.P., Salamini Department, Max Planck Institut fuer Zuechtungsforshung, Carl-von-Linne Weg 10, D-50829 Koeln, GERMANY

FEATURES

source location/Qualifiers

1. .1542

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/mol_type="mRNA"

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1. .1542

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WAIGLSGAHPRDIIMEVLKALKEINVCWKNGLYNMKCRWCPGFPQVSDMLDSNHN
EVDNSTIMDNGNADGRLEPAVVKFEIQLYKTKDNKYLDIQRVTGPOLLFLFECCGAFLT
NLRVL"

ORIGIN

Query Match 53.3%; Score 1037.8; DB 8; Length 1542;
Best Local Similarity 80.6%; Pred. No. 9e-267;
Matches 1242; Conservative 0; Mismatches 287; Indels 12; Gaps 2;
QY 173 ATGATGGAAGTAGTAAGGAGGTGGGCACTTCTGAAGCATTGAAGAACTACAACCTGGGA 232
DB 1 ATGATGGGAACAACAGAGAGGTGACATCTGAAGTGTAAAGAACTACAATCTAGGC 60
QY 233 AGAAGCTTAGGTATCGGTACATTGTGAAAAGTGAAGATTGCAGAGCAATAAGCTTACTGGA 292
DB 61 AAAACATTAGGTTTAGAACAATTGGAGATGTGAAGTTGCAGAGCAATAAGCTTACGGGA 120
QY 293 CATAGGTTGCTATAAGATCATCACTGCCGCCAATGAGAAATAAGAAATGGAAGAG 352
DB 121 CAGAGAGTTGCTATAAGATTCTGAACCGTCGTAATAATGGAACATAAGAAATGGAAGAG 180
QY 353 AAAGCAAAAGAGAAATTCAGATATTGAAGTTG-----TTCAATTCACCCCATATC 403
DB 181 AAAGCAAAATAGAGAAATCAAGATTAATGAGATTGTTCATTGACTTCATTCACTCATATC 240
QY 404 ATTCGGCTTTATGAGGTCTATATACACACCTTACAGATATATATGTTGATGGAATATTGT 463
DB 241 ATCCGGTTTATGAGGTCTATAGAGACACCTTAAAGATATATTGTTGATGGAATATTGC 300
QY 464 AAGTATGGCGAGTTATTGATTACATTGTGAAAAGCGAGATTACAGAAAGATGAAGCT 523
DB 301 AATAATGGCGAGCTATTGGAATACATTATGGAATGGCCGGTTACAGAGATGAGGCT 360
QY 524 CGTGAATCTTCAGACAGATCATATCTGGCGTCGAATACTGCCATAGAAAACATGTTGTC 583
DB 361 CGTGAATCTTCAGACAGATTTTAGCTGGTGTGAATACCTGCCACAGATAATGTTGTT 420
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QY 644 GATTTGGTCTGAGCAATGTCATGATGAGCCATTTCTGAAGACTAGCTGTGGAGT 703
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QY 704 CCGAAGTATGCTGCTCCAGAGGTAATCTGTTAACTATATGCTGAGCTGAGGTCGAT 763
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QY 1124 CAAATGAGGCAACTGTTGCAATATTACTATTGCAATCGGTTAGAGCACTAGT 1183
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QY 1184 GGTATCTTTGGGCGAGATTATCAAGAATCAATGACAGAAATTTAATCAGCTGGCTCA 1243
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DB 1141 GGTGGCTTACGGCCATATTACCTGTACAAAGAAATGGGCTATTGGGTGCAGTCCGGA 1200
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QY 1424 TGAAGAAGAAATGGGCACTACACAGTGAATGCAGATGTGCCAGGGTTCTGAGTT 1483
DB 1261 TGAAGAAGAAATGACTCTACACATGAATGCAGGTGTGCCCTGGGTTCTCAGGTC 1320
QY 1484 AATGACA---CGTTAGATGCCAACAAGCCTTCTTGTGACTCTACCATCATGATTAAT 1540
DB 1321 AGCGATATGTTGTTAGATTCCAAACAACCTTGTGATGACTCTACCATCATGATTAAT 1380
QY 1541 GATGATGCTAATGGAGGCTACCTACTGTGATCAAGTTTGAATTCAGCTTTACAAGACG 1600
DB 1381 GGCATGCTGATGGAGGCTACCCGCCGTAGTCAAGTTGAAATCCAGCTTTACAAGACC 1440
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QY 1661 GACTTCTGTGCGGCTTCTTACCAAGCTTAGGTTCTATA 1701
DB 1501 GAATTTGTGGGCGTTCCTTACCAACCTTAGGGTTCTATA 1541

RESULT 10
HVBKIN12M 1539 bp mRNA linear PLN 05-MAY-1995
LOCUS HVBKIN12M
DEFINITION H.vulgare BKIN12 mRNA for protein kinase (partial).
ACCESSION X65604
VERSION X65604.1 GI:18933
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
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/organism="Hordeum vulgare subsp. vulgare"
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Hordeum vulgare subsp. vulgare
protein kinase.
X65604.1, GI:18933
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Hordeum.
1 (bases 1 to 1539)
Halford,N.G., Vicente-Carabajosa,J., Sabelli,P.A., Shewry,P.R.,
Hannappel,U. and Kreis,M.
Molecular analyses of a barley multigene family homologous to the
yeast protein kinase gene SNF1
Plant J. 2 (5), 791-797 (1992)
93258420
1302632
2 (bases 1 to 1539)
Halford,N.G.
Direct Submission
Submitted (16-APR-1992) N.G. Halford, Long Ashton Research Station,
University of Bristol, Dept of Agricultural Sciences, Long Ashton,
Bristol BS18 9AF, UK
Location/Qualifiers
1. 1539
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Sundance"
/sub_species="vulgare"

TITLE Kreis,M., Shewry,P.R. and Halford,N.G.
Complementation of snfl, a mutation affecting global regulation of
carbon metabolism in yeast, by a plant protein kinase cDNA
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (19), 8602-8605 (1991)
MEDLINE 92020901
PUBMED 1924320
COMMENT Original source text: Secale cereale (cultivar Gazelle) seed
endosperm cDNA to mRNA.

FEATURES
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ORIGIN

Query Match 50.7%; Score 988.2; DB 8; Length 1809;
Best Local Similarity 80.7%; Pred. No. 1.8e-253;
Matches 1235; Conservative 0; Mismatches 248; Indels 48; Gaps 5;

QY 190 AGGAGTGGGCATTCTGAAGCATTGAAGAACTACAACCTGGGAAGACTTTAGGTATCGG 249
DB 118 AGGAGCGGAACATTCTGAAGCATTGAAGAACTACTATCTGGTAAATATTAGGTAGG 177
QY 250 TACATTGGAAAAGTGAAGATTGCAGAGCATTAAGCTTACTGCACATAGGGTTGCTATAA 309
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QY 421 CATATACACACCTACAGATATATATGTTGTGATGGAATATTGTAAGTATGCCAGTTATT 480
DB 358 CATGTGACACCGAAGATATTTTGTGTGATGGAATATTGCCAAATGGTGAACCTATT 417
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QY 541 GATCATATCTGGCGTCGAATACTGCGCATAGAAACATGGTTGCCACCGTGAACCTTAAAGCC 600
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QY 1552 TGGAGGCTACCTACTGTGATCAAGTTTGAATTCAGCTTCAAGAGCAAGAGAGAGCAAA 1611
DB 1468 TAGTAGGCTACCTGCTGTGATCAAGTTTGAATTCAGCTTCAAGAGCAAGAGAGAGCAAA 1527
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DB 1588 GGGCTTCTTACCAACCTTAGGGTTCTATAG 1618

RESULT 12
AK067158
LOCUS AK067158 2073 bp mRNA linear PLN 24-JUL-2003

| | |
|------------|---|
| DEFINITION | Oryza sativa (japonica cultivar-group) cDNA clone:J013094M16, full insert sequence. |
| ACCESSION | AK067158 |
| VERSION | AK067158.1 GI:32977176 |
| KEYWORDS | FLI CDNA; CAP trapper. |
| SOURCE | Oryza sativa (japonica cultivar-group) |
| ORGANISM | Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza. |
| REFERENCE | 1 |
| AUTHORS | The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team; Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN; Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y. Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice |
| TITLE | Science 301 (5631), 376-379 (2003) |
| JOURNAL | 22752273 |
| MEDLINE | 12869764 |
| PUBMED | 2 (bases 1 to 2073) |
| REFERENCE | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007) |
| COMMENT | This clone is one of the 28K full-length cDNA clones from japonica rice. URL : http://cdna01.dna.affrc.go.jp/cdna/NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M. FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S., |

| | |
|----------|--|
| FEATURES | Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y. Location/Qualifiers |
| source | 1. 2073 /organism="Oryza sativa (japonica cultivar-group)" /mol_type="mRNA" /cultivar="Nippobare" /db_xref="taxon:39947" /clone="J013094M16" |

ORIGIN

Query Match 42.0%; Score 817.4; DB 8; Length 2073;
Best Local Similarity 72.4%; Pred. No. 1.1e-207;
Matches 1074; Conservative 0; Mismatches 406; Indels 3; Gaps 1;

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| DB | 229 TACCGGATTTGCCAAA | ACCCTAGGGATTTGGTCATTTGGCAAAGTGAAGATCGCGGAGCAT | 288 |
| QY | 281 AAGCTTACTGGA | CATAGGGTTCCTATTAAGATCATCAACTGCCCCCAATGAGAATATG | 340 |
| DB | 289 ATATTGACTGGTCA | CAAGGTGGCAATCAAGATCCTCAATCGCCGTAAGATCAAGAGCATG | 348 |
| QY | 341 GAAATGGAAGAAAG | CAAGAGAAATTCAGATATTGAAGTTGTCATTCAACCCCAT | 400 |
| DB | 349 GAGATGGAAGAAAG | ATTAAAGAAATCAAGATACCTTAGATTATTATGCACCCACAT | 408 |
| QY | 401 ATCATTCGCTTAT | GAGTGCATATACACACCTACAGATATATATGTTGTGATGAATAT | 460 |
| DB | 409 ATCATTCGCTTAT | GAGTGCATATACACACCTACAGATATATATGTTGTGATGAATAT | 468 |
| QY | 461 TGTAAGTATGGCGA | GTATTGATTATCATTTGTTGAGAAAGCAGATTACAGAAAGATGAA | 520 |
| DB | 469 GTCAAATCTGGA | AGATTGTTGATTATCATTCGTTGAGAAAGCAGATTACAGAAAGATGAA | 528 |
| QY | 521 GCTCGTGAATCTT | CCAGCAGATCATCTGCGGTGGAATACCTGCCATAGAAACATGTT | 580 |
| DB | 529 GCTCGAGCTTTT | TCAGCAGATCATCTGCGGTGGAATATGCGCATAGAAACATGTTG | 588 |
| QY | 581 GTCCACCGTGAC | CTTAAAGCCGGAACCTGTTACTTGTGATCAAGTATATGTAATAACTT | 640 |
| DB | 589 GTTCATGCTGAT | CTTAAAGCCAGAAACCTTCTTTGACTCCAAATGCAATGTTAAGATT | 648 |
| QY | 641 GCGGATTTGGTCT | GAGCAATGCATGATGGCCATTTTCTGAAGACTAGCTGTGG | 700 |
| DB | 649 GCAGACTTTGGCT | TGAGTAATGTATGCGTGATGTCACCTTCTGAAGACAAGTTGTGT | 708 |
| QY | 701 AGTCGAACTATG | CTGCTCCAGAGTAATATCTGTAAGTATATATGCTGACCTGAGGTC | 760 |
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| QY | 761 GATGTATGAGAGT | TGTGGGTGATCTTTATGCTCTTCTTTGTGGAACCTCTCCATTGAT | 820 |
| DB | 769 GATGTATGAGAGT | TGTGTGTATTTATTTATGCTCTTCTTTGTGGAACCTCTCCATTGAT | 828 |
| QY | 821 GATGAGATATAT | TCCCAATCTGTTCAAAAAATTAAAGGAGGATATCTACACACTTCCAGT | 880 |
| DB | 829 GACGAGATATAT | TCCCAACCTTTTAAAGAAATAAAGGGTGCAATATATACCTTCCAGT | 888 |

OY 701 AGTCCGAACCTATGCTGCTCCAGAGGTAATATCTGGTAAACTATATGCTGACCTGAGGTC 760
DB 703 AGCCCAATATGACAGACCTGAGGTGATATCTGTAAACTATATGCTGGCCCTGAAGTT 762
OY 761 GATGATGAGTGTGGGGTGATTTCTTATGCTCTTCTTGTGAACTCTTCCATTGGAT 820
DB 763 GATGTGTGAGTGTGGTGTATTTCTTATGCTCTTGTGTGACCCCTTCATTGGAT 822
OY 821 GATGAGATATTTCCCAATCTGTCAAAAAAATTAGGAGGTATCTACACACTTCCAAGT 880
DB 823 GACGAGAATATTTCCCACTTTTAAAGAAATAAGGGTGCCATATATACCTTCCAGT 882
OY 881 CATTTGCTGCTTTGGCCAGGGATTGATCCCAAGTCTTGTGTGAGCCTATGAAG 940
DB 883 CATTTGCTGCTTTGGCCAGGGATTGATCCCAAGTCTTGTGTGAGCCTATGAAG 942
OY 941 AGAATCACAATTAGGAAATTGGGAGCATCAATGGTTCCAGATTGCGCTTCCAGCTTAC 1000
DB 943 AGGATCACCATACTGAAATCCGTGAACATCAGTGTTCACAGTTGCTTCCGCGTTAT 1002
OY 1001 TTGGCAGTGCCTCCACAGATACGACACAACAAGCAAAATGATTGATGAAGATACACTT 1060
DB 1003 TTAGCTGTGCCACTCTTGACACTGACACAACAGGTTAAAAAGCTCGACGATGAACCTCTG 1062
OY 1061 CGAGATGTTGTTAATATGGGATTTAACAAGAACCAATGTGTGAATCACTGTGACAGACA 1120
DB 1063 AATGATGTATCAATATGGGGTTTGACAAGAAATCACTAATCGAATCACTTCAAGAGA 1122
OY 1121 CTTCAAAATGAGGCAACTGTGGCATATTTACTATTGGACAATCGGTTTAGACCAACT 1180
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DB 1303 GGGTTTGGCTGAGGCATCATTTGCAAGCTGACAGGAAATGGGCCCTTGGTCTTCACTCT 1362
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DB 1483 CATGAGATGATGATGATTAACAACCATGGCTTGTGTCAGAAATCTGTAATTAATTGAAACT 1542
OY 1541 GATGATGCTAAATGGGAGGCTACTACTGTGATCAAGTTTGAATTCAGCTTAAACAAGAG 1600
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OY 1601 AAGAGCAAGATACCTCTTAGATATGACAGAGTACTGACCTCAGCTCTTCTCTT 1660
DB 1600 AGGATGAAAAAATACCTTCTGACTTGCAAAAGGTCAGTGACCAACAGCTTCTTCTTG 1659
OY 1661 GACTTCTGTGCGCTTCTTACCAAGCTTAGGCTTCTATAGT 1703
DB 1660 GACCTGTGCTGTGCTTCTTAATCTCAGCTGAGAGTCTTTAAT 1702

RESULT 14
HVBKIN2 HVBKIN2 1453 bp mRNA linear PLN 18-SEP-1995
LOCUS
DEFINITION H.vulgare mRNA for SNF1-related protein kinase.

ACCESSION X82548
VERSION X82548.1 GI:575291
KEYWORDS BKIN2 gene; SNF1 protein kinase.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 Hannappel,U., Vicente-Carabajosa,J., Barker,J.H., Shewry,P.R. and
Halford,N.G.
TITLE Differential expression of two barley SNF1-related protein kinase
genes
JOURNAL Plant Mol. Biol. 27 (6), 1235-1240 (1995)
MEDLINE 95284374
PUBMED 7766906
REFERENCE 2 (bases 1 to 1453)
AUTHORS Halford,N.G.
TITLE Direct Submission
JOURNAL Submitted (07-NOV-1994) N.G. Halford, Institute of Arable Crops
Research, Long Ashton Research Station, University of Bristol,
Bristol BS18 9AF, UK
FEATURES
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LSPLRDLIPRMLVVDPMKRTIREIREHSWFKARLPRLVPPPTAOQVKLDET
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ORIGIN

Query Match 40.8%; Score 795; DB 8; Length 1453;
Best Local Similarity 72.9%; Pred. No. 1.1e-201;
Matches 1071; Conservative 0; Mismatches 380; Indels 18; Gaps 3;
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DB 2 GGCAAAACCTCGGCATCGGTCTTGGCAAGGTCAAGATCGCGAGCATATAATTACG 61
OY 290 GGACATAGGGTGTCTATAAAGATCACTCACTGCCGCCAAATGAGAAATATGAAATGAA 349
DB 62 GGACACAAGGTGCAATCAAGATCCTCAATCGCCGCAAGATCAAGACATGAGATGAA 121
OY 350 GAGAAAGCAAGAGAAATCAAGATTAATGAAGTGTTCATTCACCCCATATCATTCGG 409
DB 122 GAGAAAGTGAAGAGAAATCAAGATACTGAGATTATTATGCAATCTCATATCATACGG 181
OY 410 CTTTATGAGTCAATATACACACCTACAGATATATATGTTGTGATGCAATATTTGAAGTAT 469
DB 182 CTTTATGAGTCAATATACCCCGCGGATATTATATGTTGTATGAGATGTTAAATCT 241

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 08:27:59 ; Search time 834 Seconds
(without alignments)
9922.650 Million cell updates/sec

Title: US-09-857-522B-3
Perfect score: 1948
Sequence: 1 gtcgaccacgcgcgcgcgcac.....taaaaaaaaaaaaaaaaa 1948

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: Geneseqn19908:*
3: Geneseqn20008:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
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| 1 | 1948 | 100.0 | 1948 | 3 | AAA52768 | Aaa52768 Corn puta |
| 2 | 1948 | 100.0 | 1948 | 7 | ACC00743 | Acc00743 Zea mays |
| 3 | 1195.6 | 61.4 | 1899 | 7 | ACC00753 | Acc00753 Triticum |
| 4 | 804.2 | 41.3 | 2107 | 3 | AAA52769 | Aaa52769 Corn puta |
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| 6 | 793.4 | 40.7 | 2052 | 7 | ACC00745 | Acc00745 Zea mays |
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| 9 | 780.8 | 40.1 | 1929 | 4 | AAF62011 | Aaf62011 Tomato le |
| 10 | 780.2 | 40.1 | 1539 | 6 | ABZ12357 | Abz12357 Arabidops |
| 11 | 780.2 | 40.1 | 1792 | 3 | AAC44825 | Aac44825 Arabidops |
| 12 | 778.6 | 40.0 | 1825 | 6 | AA146639 | Aa146639 A thalian |
| 13 | 777 | 39.9 | 1825 | 6 | AA146642 | Aa146642 A thalian |
| 14 | 776.6 | 39.9 | 1539 | 6 | AA171048 | Aa171048 Arabidops |
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| 17 | 756.2 | 38.8 | 1536 | 2 | AAQ47789 | Aaq47789 SHP gene |
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| 19 | 744.4 | 38.2 | 2006 | 3 | AAA52777 | Aaa52777 Wheat put |
| 20 | 744.4 | 38.2 | 2006 | 7 | ACC00754 | Acc00754 Triticum |
| 21 | 591.4 | 30.4 | 817 | 3 | AAA52776 | Aaa52776 Wheat put |
| 22 | 548.2 | 28.1 | 1485 | 3 | AAC46066 | Aac46066 Arabidops |
| 23 | 489.6 | 25.1 | 944 | 9 | ADC75707 | Adc75707 DNA homol |

| | | | | | | |
|----|-------|------|------|---|----------|--------------------|
| 24 | 478.8 | 24.6 | 915 | 9 | ADC07761 | Adc07761 Rice DNA |
| 25 | 329.8 | 16.9 | 1647 | 2 | AAT85525 | Aat85525 Mammalian |
| 26 | 329.8 | 16.9 | 1647 | 9 | ADB52890 | Adb52890 Primary r |
| 27 | 305.6 | 15.7 | 2761 | 2 | AAQ76197 | Aaq76197 CDNA of r |
| 28 | 304 | 15.6 | 1783 | 2 | AAQ76198 | Aaq76198 CDNA of h |
| 29 | 304 | 15.6 | 3079 | 4 | AAS60973 | Aas60973 Human can |
| 30 | 297.8 | 15.3 | 1902 | 7 | ACC60983 | Acc60983 Gene sequ |
| 31 | 296.8 | 15.2 | 986 | 6 | ABN98495 | Abn98495 Arabidops |
| 32 | 284.2 | 14.6 | 754 | 9 | ADC08744 | Adc08744 Wheat DNA |
| 33 | 283 | 14.5 | 503 | 3 | AAA75813 | Aaa75813 A 503 bp |
| 34 | 278.8 | 14.3 | 301 | 7 | ABX89774 | Abx89774 Corn ear- |
| 35 | 274.8 | 14.1 | 1698 | 9 | ADB61362 | Adb61362 Clone of |
| 36 | 270.2 | 13.9 | 2663 | 4 | ABL05573 | Ab105573 Drosophil |
| 37 | 243.6 | 12.5 | 410 | 2 | AAT76751 | Aat76751 SEQ.ID.No |
| 38 | 238.8 | 12.3 | 615 | 9 | ADC76322 | Adc76322 DNA homol |
| 39 | 234 | 12.0 | 1590 | 3 | AAC36536 | Aac36536 Arabidops |
| 40 | 231.6 | 11.9 | 334 | 3 | AAC39681 | Aac39681 Zea mays |
| 41 | 229.2 | 11.8 | 1869 | 3 | AAA52775 | Aaa52775 Soybean p |
| 42 | 229.2 | 11.8 | 1869 | 7 | ACC00752 | Acc00752 Glycine m |
| 43 | 229.2 | 11.8 | 4719 | 4 | AAD18822 | Aad18822 Human kin |
| 44 | 228.8 | 11.7 | 1338 | 3 | AAC42994 | Aac42994 Arabidops |
| 45 | 228 | 11.7 | 1341 | 3 | AAC50382 | Aac50382 Arabidops |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | |
| AAA52768 | AAA52768 standard; cDNA; 1948 BP. |
| XX | |
| AC | AAA52768; |
| XX | |
| DT | 03-JAN-2001 (first entry) |
| XX | |
| DE | Corn putative catabolite repression protein SNF1 coding sequence #2. |
| XX | |
| KW | Corn; carbon catabolite repression; sucrose non-fermenting protein 1; |
| KW | SNF1; plant growth; ss. |
| XX | |
| OS | Zea mays. |
| XX | |
| FH | Key |
| FT | CDS |
| FT | Location/Qualifiers |
| FT | 173..1702 |
| FT | /*tag= a |
| FT | /product= "SNF1" |
| XX | |
| PN | WO200036115-A2. |
| XX | |
| PD | 22-JUN-2000. |
| XX | |
| PF | 15-DEC-1999; 99WO-US029824. |
| XX | |
| PR | 16-DEC-1998; 98US-0112563P. |
| XX | |
| PA | (DUPO) DU PONT DE NEMOURS & CO E I. |
| XX | |
| PI | Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ; |
| PI | Miao G; |
| XX | |
| DR | WPI; 2000-431593/37. |
| DR | P-PSDB; AAB03416. |
| XX | |
| PT | New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins |
| PT | involved in carbon catabolite repression in plants and seeds, useful for |
| PT | controlling carbon and nitrogen partitioning pathways during plant growth |
| PT | and development. |
| XX | |
| PS | Claim 2; Page 34-35; 59pp; English. |
| XX | |
| CC | The present sequence is a putative sucrose non-fermenting protein SNF1 |
| CC | coding sequence from corn. The sequence was isolated by searching a corn |
| CC | tassel shoot cDNA library for sequences similar to those encoding SNF1 in |

CC Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The
CC protein is involved in carbon catabolite repression, and so the gene and
CC protein can be used in plants to control the nitrogen and carbon
CC partitioning pathways during plant growth and development. They can also
CC be used to alter the accumulation of carbohydrates, lipids and proteins
CC during plant growth

XX Sequence 1948 BP; 572 A; 380 C; 461 G; 535 T; 0 U; 0 Other;

Query Match 100.0%; Score 1948; DB 3; Length 1948;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 GTCGACCCACGCGTCCGACCAAAAGCCGGGATACGCCCCCAAGTCCAAAAGCCCTCTCC 60
QY 61 GCCCCGCTCTCCCACTCGTAGGTGTTCTCCCGTCTCCGCCGCACTCGCTCGTCCGCGC 120
DB 61 GCCCCGCTCTCCCACTCGTAGGTGTTCTCCCGTCTCCGCCGCACTCGCTCGTCCGCGC 120
QY 121 GCAGGAAGGTTGACCTGTCGAGGGGCCGCCAACCCGGTAAGTAAGAGTGAATAATGATGG 180
DB 121 GCAGGAAGGTTGACCTGTCGAGGGGCCGCCAACCCGGTAAGTAAGAGTGAATAATGATGG 180
QY 181 AAGTAGTAAGGAGGTGGGCATTTGGAAGCAATTAAGGAATCAACCTGGGAAGAACTTT 240
DB 181 AAGTAGTAAGGAGGTGGGCATTTGGAAGCAATTAAGGAATCAACCTGGGAAGAACTTT 240
QY 241 AGGTATCGGTACATTTGGAAGAGTGAAGATGCAGAGCATTAAGCTTAAGTGAATAGGT 300
DB 241 AGGTATCGGTACATTTGGAAGAGTGAAGATGCAGAGCATTAAGCTTAAGTGAATAGGT 300
QY 301 TGCTATAAAGATCATCAACTGCCGCCAAATGAGAATATGGAATGGAAGAGAAAGCAAA 360
DB 301 TGCTATAAAGATCATCAACTGCCGCCAAATGAGAATATGGAATGGAAGAGAAAGCAAA 360
QY 361 GAGAGAATTCAGATATTTGAAGTGTTCATCACCCCCATATCATTCGCTTTATGAGGT 420
DB 361 GAGAGAATTCAGATATTTGAAGTGTTCATCACCCCCATATCATTCGCTTTATGAGGT 420
QY 421 CATATACACACCTACAGATATATGTGTGTGATGGAATATGTAAGTATGGCGATTATT 480
DB 421 CATATACACACCTACAGATATATGTGTGTGATGGAATATGTAAGTATGGCGATTATT 480
QY 481 TGATTACATTGTTGAGAAAGGCAGATTACAGAGAAGTGAAGCTCGTGAATCTTCCAGCA 540
DB 481 TGATTACATTGTTGAGAAAGGCAGATTACAGAGAAGTGAAGCTCGTGAATCTTCCAGCA 540
QY 541 GATCATATCTGGCGTGAATACTGCCATAGAAACATGGTGTCCACCGTGAACCTAAAGCC 600
DB 541 GATCATATCTGGCGTGAATACTGCCATAGAAACATGGTGTCCACCGTGAACCTAAAGCC 600
QY 601 GGAAGAACTTGTACTTGAATCAAGTATATAAAGCTTGCGATTGTTGTTGAGCAA 660
DB 601 GGAAGAACTTGTACTTGAATCAAGTATATAAAGCTTGCGATTGTTGTTGAGCAA 660
QY 661 TGTTCATGTCATGAGCCATTCTTGAAGACTAGCTGTGGAGTCCGAACATATGCTGCTCC 720
DB 661 TGTTCATGTCATGAGCCATTCTTGAAGACTAGCTGTGGAGTCCGAACATATGCTGCTCC 720
QY 721 AGAGGTAATATCTGGTAAACTATATGCTGAGCTGAGGTGATGATGAGATTGTTGGGT 780
DB 721 AGAGGTAATATCTGGTAAACTATATGCTGAGCTGAGGTGATGATGAGATTGTTGGGT 780
QY 781 GATTCTTTATGCTCTTCTTGTGGAAGTCTTCAATTTGATGATGAGAAATATCCCAATCT 840
DB 781 GATTCTTTATGCTCTTCTTGTGGAAGTCTTCAATTTGATGATGAGAAATATCCCAATCT 840
QY 841 GTTCAAAAAAATTAAAGGAGGTATCTACACACTTCCAAGTCATTTGCTGCTTTGGCCAG 900
DB 841 GTTCAAAAAAATTAAAGGAGGTATCTACACACTTCCAAGTCATTTGCTGCTTTGGCCAG 900

QY 901 GGATTGTATCCACGAATGCTTGTGTGAGCCCTATGAAAGAAATCACAATTAGGGAAT 960
DB 901 GGATTGTATCCACGAATGCTTGTGTGAGCCCTATGAAAGAAATCACAATTAGGGAAT 960
QY 961 TCGGAGCATCAATGTTCCAGATTGCGCTTCCACGTTACTTGCGAGTGCCCTCCACAGA 1020
DB 961 TCGGAGCATCAATGTTCCAGATTGCGCTTCCACGTTACTTGCGAGTGCCCTCCACAGA 1020

QY 1021 TACGACACAACAAGCCAAAATGATGTAAGATACACTTCGAGATGTTGTTAATATGG 1080
DB 1021 TACGACACAACAAGCCAAAATGATGTAAGATACACTTCGAGATGTTGTTAATATGG 1080
QY 1081 ATTTAACAAGAACCATGTGTGTAATCACTGTGACGACAGCTTCAAAATGAGGCACTGT 1140
DB 1081 ATTTAACAAGAACCATGTGTGTAATCACTGTGACGACAGCTTCAAAATGAGGCACTGT 1140
QY 1141 TGCATATTATTACTATTGGACAATCGGTTAGAGCACTAGTGCGCTATCTTGGGGCAGA 1200
DB 1141 TGCATATTATTACTATTGGACAATCGGTTAGAGCACTAGTGCGCTATCTTGGGGCAGA 1200
QY 1201 TTATCAAGAATCAATGACAGGAATTTAATCAGCTGGCGTCATCTGAATCATCTAGTTC 1260
DB 1201 TTATCAAGAATCAATGACAGGAATTTAATCAGCTGGCGTCATCTGAATCATCTAGTTC 1260
QY 1261 TGGTACGAGGAATTATGTTCCAGGAAGCAGTGAATCCTCAAGCAGTGTGTTGCGCCATA 1320
DB 1261 TGGTACGAGGAATTATGTTCCAGGAAGCAGTGAATCCTCAAGCAGTGTGTTGCGCCATA 1320
QY 1321 TTATCCTGTGAAGAAAATGGGCGCTTGACCTTCAGTCTCGGGCCCACTCGTGAAT 1380
DB 1321 TTATCCTGTGTGAAGAAAATGGGCGCTTGACCTTCAGTCTCGGGCCCACTCGTGAAT 1380
QY 1381 AATGTTGAGGCTTTAAAGCACTTCAAGAAATTAACGTCAGATGGAAGAAGATGGGCA 1440
DB 1381 AATGTTGAGGCTTTAAAGCACTTCAAGAAATTAACGTCAGATGGAAGAAGATGGGCA 1440
QY 1441 CTACAAAGTGAATGACAGATGGTCCAGGGTTTCTGTAAGTTAATGACACGTTAGATGC 1500
DB 1441 CTACAAAGTGAATGACAGATGGTCCAGGGTTTCTGTAAGTTAATGACACGTTAGATGC 1500
QY 1501 CAGCAAGCTTCTTGTTGACTCTACCATCATGATGATATGATGCTAATGGAGGCT 1560
DB 1501 CAGCAAGCTTCTTGTTGACTCTACCATCATGATGATATGATGCTAATGGAGGCT 1560
QY 1561 ACCTACTGTATCAAGTTGAAATCCAGCTTTACAAAGCAGAAAGCAGCAAGTACTCTT 1620
DB 1561 ACCTACTGTATCAAGTTGAAATCCAGCTTTACAAAGCAGAAAGCAGCAAGTACTCTT 1620
QY 1621 AGATATGACAGAGATTACTGAGCTCAGCTGCTCTTCTGCACTTCTGTGCGGCTTCT 1680
DB 1621 AGATATGACAGAGATTACTGAGCTCAGCTGCTCTTCTGCACTTCTGTGCGGCTTCT 1680
QY 1681 TACCAAGCTTAGGGTCTATATAGTGTCTACCATGTGCAAAATTTTCACTGTGTGATGAAT 1740
DB 1681 TACCAAGCTTAGGGTCTATATAGTGTCTACCATGTGCAAAATTTTCACTGTGTGATGAAT 1740
QY 1741 AACCGAAGCATGTAAATAGGAACCTGTTCTCGTCTTTGGACAACGAAACATGTTGAG 1800
DB 1741 AACCGAAGCATGTAAATAGGAACCTGTTCTCGTCTTTGGACAACGAAACATGTTGAG 1800
QY 1801 TGAAGTCTTGTGTTGAGCGCGTAAAGTCAATGATATACCTTAGGTAGTACTATTTTCT 1860
DB 1801 TGAAGTCTTGTGTTGAGCGCGTAAAGTCAATGATATACCTTAGGTAGTACTATTTTCT 1860
QY 1861 TCTTAATAATTTGCTGCTGCTAGTGAATAGTTCAATTTTGAACCTAAACGTTACGAATAA 1920
DB 1861 TCTTAATAATTTGCTGCTGCTAGTGAATAGTTCAATTTTGAACCTAAACGTTACGAATAA 1920
QY 1921 AAAAAAGTAAAAAATTTTAAAAA 1948
DB 1921 AAAAAAGTAAAAAATTTTAAAAA 1948

RESULT 2
ACC00743
ID ACC00743 standard; cDNA; 1948 BP.
XX
AC ACC00743;
XX
DT 16-MAY-2003 (first entry)
XX
DE Zea mays oil trait related cDNA sequence SEQ ID NO:235.
XX
KW plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CKC-like transcription factor; antisense inhibition; co-suppression;
KW transgenic plant; gene; ss.
XX
OS Zea mays.
XX
PN WO2003002751-A2.
XX
PD 09-JAN-2003.
XX
PF 27-JUN-2002; 2002WO-US020152.
XX
PR 29-JUN-2001; 2001US-0301913P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI (PION-) PIONEER HI-BRED INT INC.
PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczynski MC;
XX
DR WPI; 2003-201509/19.
DR P-PSDB; ABR40708.
XX
PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
PS Claim 18; Page 272-273; 542pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV) or
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 1948 BP; 572 A; 380 C; 461 G; 535 T; 0 U; 0 Other;
Query Match 100.0%; Score 1948; DB 7; Length 1948;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 121 GCAGGAAGTTGACCTGTCGAGGCGCGCGAACC CGGTAACTAAGATGAAAATGATGG 180
Db |||||||
121 GCAGGAAGTTGACCTGTCGAGGCGCGCGAACC CGGTAACTAAGATGAAAATGATGG 180
QY 181 AAGTAGTAAAGGAGTGGGCACTTGAAGCATTAAGGAATCAACCTGGGAAGACTTT 240
Db |||||||
181 AAGTAGTAAAGGAGTGGGCACTTGAAGCATTAAGGAATCAACCTGGGAAGACTTT 240
QY 241 AGGTATCGGTACATTTGAAAAAGTGAAGATTGCAGAGCATTAAGCTTAAGCATAGGGT 300
Db |||||||
241 AGGTATCGGTACATTTGAAAAAGTGAAGATTGCAGAGCATTAAGCTTAAGCATAGGGT 300
QY 301 TGCTATTAAGATCATCACTGCGCCCAATGAGAAATATGAAATGGAAGAAAGCAAA 360
Db |||||||
301 TGCTATTAAGATCATCACTGCGCCCAATGAGAAATATGAAATGGAAGAAAGCAAA 360
QY 361 GAGAGATTCAAGATATTTGAAGTTGTCATTCAACCCCAATCATTCGGCTTATGAGGT 420
Db |||||||
361 GAGAGATTCAAGATATTTGAAGTTGTCATTCAACCCCAATCATTCGGCTTATGAGGT 420
QY 421 CATATACACACCTACAGATATATATGTTGTGATGGAATATTTGAAGTATGGCGAGTTATT 480
Db |||||||
421 CATATACACACCTACAGATATATATGTTGTGATGGAATATTTGAAGTATGGCGAGTTATT 480
QY 481 TGATTAATTTGTTGAGAAAGGCAAGTTACAGGAAGTGAAGCTGTCGAATCTTCCAGCA 540
Db |||||||
481 TGATTAATTTGTTGAGAAAGGCAAGTTACAGGAAGTGAAGCTGTCGAATCTTCCAGCA 540
QY 541 GATCATATCTGGCGTCGAATATCTGCCATAGAAACATGTTGTGCCACCGTAAAGCC 600
Db |||||||
541 GATCATATCTGGCGTCGAATATCTGCCATAGAAACATGTTGTGCCACCGTAAAGCC 600
QY 601 GGAATACTTGTACTTGTGATTCAAAGTATATGTAAACTTGGCGAATTTTGGTCTGAGCAA 660
Db |||||||
601 GGAATACTTGTACTTGTGATTCAAAGTATATGTAAACTTGGCGAATTTTGGTCTGAGCAA 660
QY 661 TGTATGATGATGAGCCATTTTCTGAAGACTAGCTGTGGAGTCCGAATATGCTGCTCC 720
Db |||||||
661 TGTATGATGATGAGCCATTTTCTGAAGACTAGCTGTGGAGTCCGAATATGCTGCTCC 720
QY 721 AGAGTAATATCTGTAACATAATATGCTGAGCCTGAGTGAATGATGAGTTGTGGGT 780
Db |||||||
721 AGAGTAATATCTGTAACATAATATGCTGAGCCTGAGTGAATGATGAGTTGTGGGT 780
QY 781 GATTCTTATGCTCTTCTTTGGAACCTTCCATTGATGATGAGATATTTCCCAATCT 840
Db |||||||
781 GATTCTTATGCTCTTCTTTGGAACCTTCCATTGATGATGAGATATTTCCCAATCT 840
QY 841 GTTCAAAAAATTAAGGAGTATCTACACACTTCCAAGTCAATTTGTCTGTTGGCAG 900
Db |||||||
841 GTTCAAAAAATTAAGGAGTATCTACACACTTCCAAGTCAATTTGTCTGTTGGCAG 900
QY 841 GTTCAAAAAATTAAGGAGTATCTACACACTTCCAAGTCAATTTGTCTGTTGGCAG 900
Db |||||||
841 GTTCAAAAAATTAAGGAGTATCTACACACTTCCAAGTCAATTTGTCTGTTGGCAG 900
QY 901 GGATTGATCCACGAATGCTTGTGAGCCTATGAAGAAATCACAATTAGGGAAT 960
Db |||||||
901 GGATTGATCCACGAATGCTTGTGAGCCTATGAAGAAATCACAATTAGGGAAT 960
QY 901 GGATTGATCCACGAATGCTTGTGAGCCTATGAAGAAATCACAATTAGGGAAT 960
Db |||||||
901 GGATTGATCCACGAATGCTTGTGAGCCTATGAAGAAATCACAATTAGGGAAT 960
QY 961 TCGGAGCATCAATGTTCCAGATTGCGCTTCCACGTTACTTGGCAGTGCTCCACCAGA 1020
Db |||||||
961 TCGGAGCATCAATGTTCCAGATTGCGCTTCCACGTTACTTGGCAGTGCTCCACCAGA 1020
QY 961 TCGGAGCATCAATGTTCCAGATTGCGCTTCCACGTTACTTGGCAGTGCTCCACCAGA 1020
Db |||||||
961 TCGGAGCATCAATGTTCCAGATTGCGCTTCCACGTTACTTGGCAGTGCTCCACCAGA 1020
QY 1021 TAGGACACAACAAGCCAAAATGATGATGAAGATACACTTCGAGATGTTGTTAATATGGG 1080
Db |||||||
1021 TAGGACACAACAAGCCAAAATGATGATGAAGATACACTTCGAGATGTTGTTAATATGGG 1080
QY 1081 ATTTAACAAGAACCATGTGTGGAATCACTGTGCAGCAGACTTCAAAATGAGGCACTGT 1140
Db |||||||
1081 ATTTAACAAGAACCATGTGTGGAATCACTGTGCAGCAGACTTCAAAATGAGGCACTGT 1140
QY 1141 TGCATATTAATTTACTATTGAGCAATCGGTTAGAGCAACTAGTGCTATCTTGGGGCAGA 1200
Db |||||||
1141 TGCATATTAATTTACTATTGAGCAATCGGTTAGAGCAACTAGTGCTATCTTGGGGCAGA 1200

| | | | |
|----|------|---|------|
| QY | 1201 | TTATCAAGAATCAATGACAGGAATTTAAATCAGCTGGCGTCATCTGAATCATCTAGTTC | 1260 |
| Db | 1201 | TTATCAAGNAATCAATGACAGGAATTTAAATCAGCTGGCGTCATCTGAATCATCTAGTTC | 1260 |
| QY | 1261 | TGCTACGAGGAATTTATGTTCCAGGAAGCAGTGAATCTCATAGCAGTGGTTTGGCGCAT | 1320 |
| Db | 1261 | TGGTACGAGGAATTTATGTTCCAGGAAGCAGTGAATCTCTCATAGCAGTGGTTTGGCGCAT | 1320 |
| QY | 1321 | TTATCCTGTTGAAGAANAATGGGCGCTTGACCTTCAGTCTCGGGCCACCTCGTGAAT | 1380 |
| Db | 1321 | TTATCCTGTTGAAGAANAATGGGCGCTTGACCTTCAGTCTCGGGCCACCTCGTGAAT | 1380 |
| QY | 1381 | AATGGTTGAGGTCCTTAAAGCACTTCAAGAATTTAAACGTACAGATGGAAGAATGGCA | 1440 |
| Db | 1381 | AATGGTTGAGGTCCTTAAAGCACTTCAAGAATTTAAACGTACAGATGGAAGAATGGCA | 1440 |
| QY | 1441 | CTACAACGTGAATGCAGATGGTGCCAGGGTTTCCTGAAGTTAATGACACGTTAGATGC | 1500 |
| Db | 1441 | CTACAACGTGAANAATGCAGATGGTGCCAGGGTTTCCTGAAGTTAATGACACGTTAGATGC | 1500 |
| QY | 1501 | CAGCAACAGCTTCTTGCTGCACTCTACCATCATGATATATGATGCTAATGGAGGCT | 1560 |
| Db | 1501 | CAGCAACAGCTTCTTGCTGCACTCTACCATCATGATATATGATGCTAATGGAGGCT | 1560 |
| QY | 1561 | ACCTACTGTGATCAAGTTGAATTCAGCTTTACAAGAAGAAAGACGACAAGTACCTCTT | 1620 |
| Db | 1561 | ACCTACTGTGATCAAGTTGAATTCAGCTTTACAAGAAGAAAGACGACAAGTACCTCTT | 1620 |
| QY | 1621 | AGATATGCAGAGATTACTGCACTCAGCTGCTCTTCTTGCACTTCTGTGCGGCTTCT | 1680 |
| Db | 1621 | AGATATGCAGAGATTACTGCACTCAGCTGCTCTTCTTGCACTTCTGTGCGGCTTCT | 1680 |
| QY | 1681 | TACCAAGCTTAGGGTTCTAATAGTGCTCTACCATGTGCAAAATTTCACTGTGTGATGAAT | 1740 |
| Db | 1681 | TACCAAGCTTAGGGTTCTAATAGTGCTCTACCATGTGCAAAATTTCACTGTGTGATGAAT | 1740 |
| QY | 1741 | AACCGAAGCATGTAAATAGGAACCTTGTTCTCGTCTTTGGACAACGAACATGTTGAG | 1800 |
| Db | 1741 | AACCGAAGCATGTAAATAGGAACCTTGTTCTCGTCTTTGGACAACGAACATGTTGAG | 1800 |
| QY | 1801 | TGACTGCTTGTGTTGAGCGCGTAAGGTCATGTATACTTAGGTTAGTACTATTTTCGT | 1860 |
| Db | 1801 | TGACTGCTTGTGTTGAGCGCGTAAGGTCATGTATACTTAGGTTAGTACTATTTTCGT | 1860 |
| QY | 1861 | TCTTAAATATTTGTGCTGCTGCTAGTGATAGTTCATTTTGAACCTAAAACGTTACGAATTA | 1920 |
| Db | 1861 | TCTTAAATATTTGTGCTGCTGCTAGTGATAGTTCATTTTGAACCTAAAACGTTACGAATTA | 1920 |
| QY | 1921 | AAAAAGAGTAAAAAAAAAAAAAAAAAAAA 1948 | |
| Db | 1921 | AAAAAGAGTAAAAAAAAAAAAAAAAAAAA 1948 | |

| | |
|----------|--|
| RESULT | 3 |
| ACC00753 | |
| ID | ACC00753 standard; cDNA; 1899 BP. |
| XX | |
| AC | ACC00753; |
| XX | |
| DT | 16-MAY-2003 (first entry) |
| XX | |
| DE | Triticum aestivum oil trait related cDNA sequence SEQ ID NO:255. |
| XX | |
| KW | Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; |
| KW | LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1; |
| KW | CKC-like transcription factor; antisense inhibition; co-suppression; |
| KW | transgenic plant; gene; ss. |
| XX | |
| OS | Triticum aestivum. |
| XX | |
| PN | WO2003002751-A2. |
| XX | |

| | | | |
|----|---|---|---------|
| PD | | 09-JAN-2003. | |
| XX | | | |
| PF | - | 27-JUN-2002; 2002WO-US020152. | |
| XX | | | |
| PR | - | 29-JUN-2001; 2001US-0301913P. | |
| XX | | | |
| PA | (DUPO) DU PONT DE NEMOURS & CO E I. | | |
| PI | (PION-) PIONEER HI-BRED INT INC. | | |
| XX | | | |
| PI | Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT; | | |
| PI | Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B; | | |
| PI | Tarczynski MC; | | |
| XX | | | |
| DR | WPI, 2003-201509/19. | | |
| DR | P-PsDB; ABR40718. | | |
| PT | | | |
| PT | Novel nucleotide fragment encoding polypeptides having receptor-like | | |
| PT | protein kinase activity, caleosin-like activity, useful for altering oil | | |
| PT | phenotypes in plants such as sunflower, coconut, soybean, wheat and rice. | | |
| XX | | | |
| PS | Claim 18; Page 296; 542pp; English. | | |
| XX | | | |
| CC | The present invention describes an isolated nucleotide fragment (I) | | |
| CC | comprising a nucleic acid sequence (NS) chosen from a NS encoding a | | |
| CC | polypeptide (PP) having receptor-like protein kinase activity, mitogen | | |
| CC | activated protein (MAP)-kinase activity, LIP15-like transcription factor | | |
| CC | activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like | | |
| CC | activity and CKC-like transcription factor activity. Also described: (1) | | |
| CC | complement (II) of (I); (2) a chimeric construct (III) comprising (I) or | | |
| CC | (II), operably linked to a regulatory sequence; (3) a plant (IV) | | |
| CC | comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5) | | |
| CC | oil obtained from (V). (I) or its part can be used in antisense | | |
| CC | inhibition or co-suppression in a transformed plant. (III) is useful for | | |
| CC | altering the oil phenotype in a plant such as corn, soybean, wheat, rice, | | |
| CC | canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for | | |
| CC | creating transgenic plants having altered lipid profiles. (I) can also be | | |
| CC | used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to | | |
| CC | ABR40879 represent sequences used in the exemplification of the present | | |
| CC | invention | | |
| XX | | | |
| SQ | Sequence 1899 BP; 572 A; 364 C; 462 G; 501 T; 0 U; 0 Other; | | |
| | | | |
| | Query Match | 61.4%; Score 1195.6; DB 7; Length 1899; | |
| | Best Local Similarity | 85.8%; Pred. No. 4.1e-308; | |
| | Matches 1327; Conservative | 0; Mismatches 219; Indels | 0; Gaps |
| OY | 166 AGTGAATAATGAGTAGTAAGTAAGGAGTGCGCATTCCTGAAGCATTAAAGAACTACAA | 225 | |
| Db | 60 AGTGAATAATGAGGAGAACAAC TAGAGAGGTGGGCATTCTGACGCATTAAAGAACTACAA | 119 | |
| OY | 226 CCTGGAGAAGACTTTAGCGTATCGGTACATTTGAAAAAGTGAAGATTGCAGAGCATTAAGCT | 285 | |
| Db | 120 TGTGGGCAAGAACATTAGGTATAGGCACATTTGAAAAGTGAAGATTGCAGAGCATTAAGCA | 179 | |
| OY | 286 TACTGACATAGGGGTGCTATTAAGATCATCACTGCCGCCAATGAGAAATATGGAAT | 345 | |
| Db | 180 TACAGGGCATAAAGTTGCTATTAAGATTCTGAACCGTCTCAATGAGAACTATGGAAT | 239 | |
| OY | 346 GGAAGAGAAAGCAAAGAGAGAAATTCAGATATGGAAGTGTTCATTCACCCCCATATCAT | 405 | |
| Db | 240 GGAGAGAAAGCAAAGAGAGAGATCAAGATATGAGGTGTTCAACCCTCATATCAT | 299 | |
| OY | 406 TCGGCTTATGAGGTATATACACACCTACAGATATATATGTTGTGATGGAATATTGTA | 465 | |
| Db | 300 CCGGCTTATGAGGTATATACACACCTACAGATATATGTTGTGATGGAATATTGCA | 359 | |
| OY | 466 GTATGGCAGTATTGATTACATTTGTTGAGAAAGCAGATTACAGGAAGATGAAGCTCG | 525 | |
| Db | 360 GTATGGTGAAGTATTGCACTGCATTGTTGAGAAAGGCGGTTACAGGAAGATGAAGCTCG | 419 | |
| OY | 526 TCGAATCTTCCAGCAGATCATATCTGGCGTCGAATACTGCCATAGAAACATGTTGTCCA | 585 | |
| Db | 420 TCGAATCTTCCAGCAGATCATATCTGGTGTGTAATCTGCCACAGAAACATGTTGTCTCA | 479 | |

QY 586 CCGTGACCTTAAGCCGGAAGAACTTGTACTTGAATTCAGATATAATGTAAGAACTTGCGGA 645
 DB 480 TCGTATCTAAGCCAGAGAACCTGTACTTGAATTCAGATATAATGTAAGAACTTGCGGA 539
 QY 646 TTTGGTCTGAGCAATGTCATGATGAGGCCATTTTCTGAAGACTAGCTGTGGAGTCC 705
 DB 540 CTTGGGTTAAGTAATGTCATGATGAGGCCATTTTCTGAAGACTAGCTGTGGAGTCC 599
 QY 706 GAACTATGCTGCTCCAGAGGTAATATCTGTAACCTATATGCTGAGCTGAGGTGATGT 765
 DB 600 AAATATGCTGACAGAGGTTATCTCAGTAATAATACGCTGAGACCTGAGGTGATGT 659
 QY 766 ATGAGTTGGGGTGAATCTTATGCTCTTGTGGAACCTTCCATTGATGATGA 825
 DB 660 TTGAGCTGCGGGTGATACTTATGCTCTTGTGGAACCTTCCATTGATGATGA 719
 QY 826 GAATATTCCTCAATCTGTTCAAAAAATTAGGAGGTATCTACACACTTCCAGTCATTT 885
 DB 720 CAATATTCCTCAACTGTTCAAAAAATTAGGAGGTATCTATATCTTCCAGTCATTT 779
 QY 886 GTCTGCTTTGGCCAGGGATTGATCCCAAGATGCTTGTGAGCCTTATGAGAGAAAT 945
 DB 780 ATCTGCTTTGCAAGGATTGATCCCAAGATGCTTGTGATCTTATGAGAGAAAT 839
 QY 946 CACAATTAGGAAATTCGGGAGCATCAATGTTCCAGATTGCGCTTCCAGTTACTTGGC 1005
 DB 840 CACAATTGTAATTCGGAAGAACCCATGTTTCAGAATGCGCTTCCAGTTACTTGGC 899
 QY 1006 AGTGCCTCCACCAAGATACAGACACAACAAGCCAAATGATTGATGAAGATACACTTCGAGA 1065
 DB 900 AGTGCCTCCACCAAGATACAGACACAACAAGCCAAATGATTGATGAAGATACACTTCGAGA 959
 QY 1066 TGTGTTAATATGGGATTTAACAAGAACCATGTTGTAATCACTGTGACAGCACTTCA 1125
 DB 960 GATTGTCAACCTGGGATATGATAAGAACCATGTTGTAATCACTGTGACAGCACTTCA 1019
 QY 1126 AAATGAGGCACTGTTGCATATTTATTTACTTATGGAACAATCGGTTTATGAGCAACTAGTGG 1185
 DB 1020 AAATGAGGCACTGTTGCATATTTACTTACTTGTGGAACAATCGGTTTATGAGCAACTAGTGG 1079
 QY 1186 CTATCTTGGGCGAGATTATCAAGAAATCAATGACAGGAATTTAAATCAGCTGCGTCATC 1245
 DB 1080 CTATTTGGGGCTGACTATCTACAAATCAATGAGGTAAGAGTTTAAATCAGTTTACTTCAAT 1139
 QY 1246 TGAATCATCTAGTTCTGCTACAGGAATTTATGTTCCAGGAAGCAGTGAATCTCATAGCAG 1305
 DB 1140 GGAATCAGCAAGCCCAAGTACAGGCACTATCTTCCAGCAAGCAATGATTTCTCAAGCAG 1199
 QY 1306 TGGTTGGCGGCAATATATCTGTTGAAGAAATGGGCGCTTGACCTTCACTCTCGGC 1365
 DB 1200 TGGCTTGGCGGCAATATATCTGTTGAAGAAATGGGCGCTTGACCTTCACTCTCGGC 1259
 QY 1366 CCACCTCTGTAATAATGTTGAGGTCTTAAAGCACTTCAAGAAATTAACGTCAGATG 1425
 DB 1260 TCAACCTCTGTAATAATGATGAGGTTCTTAAAGCACTTCAAGAAATTAATGTCGCTG 1319
 QY 1426 GAAGAAGATGGGCACTACAACGTAAGATGAGTGGCCAGGGTTTCTGAAGTTAA 1485
 DB 1320 GAAGAAGATGGGCACTACAACGTAAGATGAGTGGCCAGGGTTTCTGAAGTTAA 1379
 QY 1486 TGACACGTTAGATGCGCAGCAACAGCTTCTTGGTGAATCTTACCATCATGGAATATGATGA 1545
 DB 1380 TGATATGTTAGATGCGCAGCAACAGCTTCTTGGTGAATCTTACCATCATGGAATATGATGA 1439
 QY 1546 TGCTAATGGAGGCTTACTGATCAAGTTTGAATTCAGCTTTTCAAGACGAAGGA 1605
 DB 1440 TGCTAATGGAGGCTTACTGATCAAGTTTGAATTCAGCTTTTCAAGACGAAGGA 1499
 QY 1606 CGACAAGTACTCTTAGATATGACAGAGTTACTGACCTCAGCTGCTCTTCTGACTT 1665
 DB 1500 TGACAAGTACTCTTAGATATGACAGAGTTACTGACCTCAGCTGCTCTTCTGACTT 1559

QY 1666 CTGTCGGGCTTCTTACCAAGCTTAGGGTCTATAGTGTCTACC 1711
 DB 1560 TTGCGCGGCTTCTTACCAACCTTAGGGTCTATAGTGTGTC 1605

RESULT 4
 AAA52769
 ID AAA52769 standard; cDNA; 2107 BP.
 XX
 AC AAA52769;
 XX
 DT 03-JAN-2001 (first entry)
 XX
 DE Corn putative catabolite repression protein SNF1 coding sequence #3.
 XX
 KW Corn; carbon catabolite repression; sucrose non-fermenting protein 1;
 KM SNF1; plant growth; ss.
 XX
 OS Zea mays.
 XX
 FT Key Location/Qualifiers
 FT CDS 2..1739
 FT /*tag= a
 FT /product= "SNF1"
 FT /partial
 PN MO200036115-A2.
 XX
 PD 22-JUN-2000.
 XX
 PF 15-DEC-1999; 99MO-US029824.
 XX
 PR 16-DEC-1998; 98US-0112563P.
 XX
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 PI Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ;
 PI Miao G;
 XX
 DR WPI; 2000-431593/37.
 DR P-PSDB; AAB03417.
 XX
 PT New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
 PT involved in carbon catabolite repression in plants and seeds, useful for
 PT controlling carbon and nitrogen partitioning pathways during plant growth
 PT and development.
 XX
 PS Claim 2; Page 37; 59pp; English.
 XX
 CC The present sequence is a putative sucrose non-fermenting protein SNF1
 CC coding sequence from corn. The sequence was isolated by searching a corn
 CC stem cDNA library for sequences similar to those encoding SNF1 in
 CC Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The
 CC protein is involved in carbon catabolite repression, and so the gene and
 CC protein can be used in plants to control the nitrogen and carbon
 CC partitioning pathways during plant growth and development. They can also
 CC be used to alter the accumulation of carbohydrates, lipids and proteins
 CC during plant growth
 XX
 SQ Sequence 2107 BP; 578 A; 454 C; 484 G; 591 T; 0 U; 0 Other;

Query Match 41.3%; Score 804.2; DB 3; Length 2107;
 Best Local Similarity 71.7%; Pred. No. 1.1e-203;
 Matches 1084; Conservative 0; Mismatches 418; Indels 9; Gaps 2;

QY 190 AGGAGTGGGCAATCTGAAGCATTAAGAACTACAACTGGGAAGAACTTAGGTATCGG 249
 DB 238 AGCGGAAGAGATGCCAACCTTGAAGCGGTTACAGATTGGCAAAACCTGGGAATTGG 297
 QY 250 TACATTGGAAAAAGTGAAGATTGCAGACATTAAGCTTACTGACATAGGGTGTATATA 309
 DB 298 GTGCTTCGTTAAAGTGAAGATCGCGGAACATATATTTGACTGTGTCATTAAGGTGGCATCA 357

QY 310 GATCATCACTGCCCGCAATGAGAAATATGGAATGGAAGAGAAAGCAAGAGAGAAATT 369
DB 358 GATTCTCAATCCGCAAGAGATCAGAGCATGATATGGAAGAGAAAGTTAAGAGAGAAAT 417
QY 370 CAAGATATTGAAGTTGTTCAATCACCCTCATATCGGCTTTATGAGGTATATACAC 429
DB 418 CAAGATATGAGATTATTATGATCCTCATATCATACGCCCTTTATGAGGTATAGATAC 477
QY 430 ACCTACAGATATATATGTTGTGATGGAATATTGAAGTATGCGAGTTATTGATTACAT 489
DB 478 ACCTGCTGATATCTGTGTTGTTATGAGATGTTAAATCTGAGAGTTGTTGATTACAT 537
QY 490 TGTGAGAAAGCAGATTACAGAGAGATGAAGCTCGTGAATCTTCAGCAGATCATATC 549
DB 538 CGTTGAGAAAGGAGGCTACACGAGAGAGAGAGCCGACACTTTTTCAGCAGATCATATC 597
QY 550 TGGCGTCGATACTGCCATAGAAACATGGTTGCCACCGTGACCTTAAAGCCGAAAACTT 609
DB 598 TGGTGTGAATATTGCCATAGGAACATGGTTGCTCACCGTGAATTTAAAGCAGAGAAATCT 657
QY 610 GTTACTTGATTCAGAAATATATATGTTAAACTTCCGAAATTTTGTCTGAGCAATGTCATGCA 669
DB 658 TCTTTGATTCAGAAATGCAATGTTAAGATTGCCGATTTTGCTTAAATATTATGCG 717
QY 670 TGATGCCAATTTCTGAAGACTAGCTGTGGAGTCCGAATATGCTGCTCCAGAGTAAT 729
DB 718 TGATGTCATTTCTTAAGACGAGTGTGTAGCCCGAATTATGACAGACCTGAGTCAAT 777
QY 730 ATCTGTAACATATATGCTGAGACCTGAGTCGATGATGAGTTGTGGGTGATCTTTA 789
DB 778 ATCTGTAACATATATGCTGCTGCTGAGTGAAGTCAAGTCTGAGCTGTGAGTTATTCTTTA 837
QY 790 TGCTCTTCTTTGTGGAACTCTTCCATTTGATGATGAGAAATTTCCCAATCTGTTCAAAA 849
DB 838 TGCTCTTCTTTGTGGCACTCTCCCATTTGAGATGAGAAATTTCCAAACCTTTTCAAGAA 897
QY 850 AATTAAAGGAGTATCTACACACTTCCAAGTCATTTGCTGCTTTGGCCAGGATTTGAT 909
DB 898 AATAAAGGTGAATATATACCTTCCATGATTTGTCAACCTTCAGGAGGGAATTTGAT 957
QY 910 CCCACGAATGCTGTGTTGAGCCTATGAAGAAATCACAATTAGGAAATTCGGAGCA 969
DB 958 TCCCAGAAATGCTGTGTTGATCCAATGAAGAAATTAACAATACGTGAATCCGTGAACA 1017
QY 970 TCAATGTTCCAGATTGCGCTTCCAGTTACTGGCAGTGCCCTCCACAGATACGACACA 1029
DB 1018 TGTGTGTTCAAGATCCGACTCCGCGCTATTTGGCTGTGCCGCTCCAGACACTGCTCA 1077
QY 1030 ACAAGCCAAAATGATTGATGAAGATACACTTCAGATGTTGTTAATAGGATTTAACAA 1089
DB 1078 ACAAGTTAAAAAGGTCCAGCAGAGAACTCTTAATGATGTTAATGAGGTTTGACAA 1137
QY 1090 GAACCATGTGTGAATCACTGTGACGACAGACTTCAAAATGAGGCAACTGTTGCATATTA 1149
DB 1138 GAATCAGCTAATGAATCTCTGCAAAACAGATTGCAGAATGAGGCAACAGTTGCCATATTA 1197
QY 1150 TTTACTATTGACAATCGGTTTAGAGCAACTAGTGCTATCTTGGGCGAGATTATCAAGA 1209
DB 1198 TTTACTCTTGACAATAGGCTTCGTACAACCAAGTGGTTATCTTGATCTGAGTTTCAAGA 1257
QY 1210 ATCAATGACAGAAATTTAAATCAGCTGGCGCTCATCTGAATCATCTAAGTTCTGTACGAG 1269
DB 1258 ATCTATGACTCATCTTGTCTCA--AGTAATCGCTGAACAACACCACTTCAGCAACTGA 1314
QY 1270 GAATATGTTCCAGAGACAGTATCCTCATAGCAGTGTGGCGCATATATCTCTGT 1329
DB 1315 ACTTCGTACGATGGGTTTTCAGAAATCTCCAGGTTCTGGCTTGAGGCGAGATTTTGACGC 1374
QY 1330 TGAAGAAAATGGCGCTTGAGCTTCAGTCTTGCGGCCACCCCTCGTAATAATGTTGTA 1389
DB 1375 TGAAGGAAATGGGCGCTTGCTTCAGTCTTCAGACACATCCACGAGAAATTAATAGTGA 1434
QY 1390 GGTCTTAAAGCACTTCAAGAAATTAACGTCAGATGGAAGAAAGATGGGCACTACAACGT 1449

DB 1435 AGTGCTTAAAGCTCTGCAAGAACTGAATGTTTACTGGAATAAGATTGGACACTACAACT 1494
QY 1450 GAAATGAGATGTTGCCAGGTTTCTGAAGTTAATGACAGCTTAGATGCCAGCAAG 1509
DB 1495 GAAATGACATGAGAGTCCGTGGCTGCTTGAGAGT-----ATGATGCATAACAGTGATAG 1548
QY 1510 CTTTCTTGTTGACTCTACCATCATGATTAATGATGATGCTTAATGGAGGCTACCTACTGT 1569
DB 1549 CTTCAGTGCGGAGTCTGCTAATATGAAACTGATGTTTTCATGAGAAATCAACCCCGAC 1608
QY 1570 GATCAAGTTGAATTCAGCTTTAACAAGACGAGAGACGACAAAGTAACCTTAGATATGCA 1629
DB 1609 AGTGAAGTTGAGATTGAGCTTTACAAACGAGGATGAGAAAGTAACCTTCTTGACCTGCA 1668
QY 1630 GAGAGTTACTGACCTCAGCTGCTCTTCTTGAATCTTGTGCGGCTTCTTACCAAGCT 1689
DB 1669 AAGGTGAGTGATCAGATCATCTTCTTCTTGAGCTGTGTTCGCGCTTCTTAACCTAGCT 1728
QY 1690 TAGGTTCTAT 1700
DB 1729 GAGAGTTCTT 1739

RESULT 5
ACCC0744
ID ACC00744 standard; cDNA; 2107 BP.
XX
AC ACC00744;
XX
DT 16-MAY-2003 (first entry)
XX
DE Zea mays oil trait related cdna sequence SEQ ID NO:237.
XX
KW plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW LIP5-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CKC-like transcription factor; antisense inhibition; co-suppression;
KW transgenic plant; gene; ss.
XX
OS Zea mays.
XX
PN WO2003002751-A2.
XX
PD 09-JAN-2003.
XX
PF 27-JUN-2002; 2002MO-US020152.
XX
PR 29-JUN-2001; 2001US-0301913P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI (PION-) PIONEER HI-BRED INT INC.
XX
PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT,
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B,
PI Tarczynski MC;
XX
DR MPI; 2003-201509/19.
DR P-PSDB; ABR40709.
XX
PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
PS Claim 18; Page 274-275; 542pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP5-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or

PR 29-JUN-2001; 2001US-0301913P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczynski MC;
XX
DR WPI; 2003-201509/19.
DR P-PSDB; ABR40710.
XX
PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
PS Claim 18; Page 277-278; 542pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
CC
SQ Sequence 2052 BP; 563 A; 445 C; 481 G; 563 T; 0 U; 0 Other;
Query Match 40.7%; Score 793.4; DB 7; Length 2052;
Best Local Similarity 72.4%; Pred. No. 7.9e-201;
Matches 1079; Conservative 0; Mismatches 391; Indels 21; Gaps 3;
QY 210 CATTAAAGAACTACAACCTGGAGAAGAACTTAGTATCGGTACATTGGAAAAGTGAAGA 269
DB 244 CGTTGAGGAATTATCGGATTGGCAAGACTCTCGGAATTGGCTCATTCGGAAGTGA AAA 303
QY 270 TTGCAGAGCATAGCTTACTGACATAGGGTTGCTATAAGATCATCAACTGCCGCAAA 329
DB 304 TTGCGAGCATATCAGCACTGACACACAAGGTGGCAATCAAGATTCTCAACCGCGTAAAA 363
QY 330 TGAGAAATATGGAATGGAAGAGAAGCAAGAGAGATTCAAGATATTGAAGTTGTCA 389
DB 364 TCAGAGGCGATGAGATGGAAGAGAAAGTTAAAGAGATTAAAGATTGAAGTTATTTA 423
QY 390 TTCACCCCCCATATCATTCGGCTTATGAGGTATATACACACCCTACAGATATATGTG 449
DB 424 TGCATCCACATATTAATCCGCTCTATGAGGTTATAGACACACCGGCTGATATTATGTTG 483
QY 450 TGATGAATATTTGAAGTATGCGAGTATTTGATTACATTGTTGAGAAAGGAGATTAC 509
DB 484 TTATGAGTATGTTAAAGTGTGGGAATTATTGATTACATTGTTGAAGAAAGTAGGCTGC 543
QY 510 AGGAAGATGAAGCTCGTCGAATCTTCCAGCAGATCATATCTGCGTGAATACTGCCATA 569
DB 544 AAGGAAGAAGAGCTCGCGCTTCTTCCAAAGATTAATCCGCTGTGAATAATTGCCATA 603
QY 570 GAAACATGTTGTCCACCGTGACCTAAAGCCGGA AAACTGTACTTGAATCAAGTATA 629
DB 604 GAAACATGTTGTGTGATCTGTGATCTAAAGCCAGAAAACCTCTATTGGAATCAAAATGCA 663
QY 630 ATGTAAACTTGGCGATTGTTGCTGTGAGCAATGTCATGCATGATGGCCATTCTGAAGA 689
DB 664 ATGTTAAGATTGAGATTGTTGGCTTAAGTAATGTTATGCGGAGTGTGATTTCTGAAGA 723

QY 690 CTAGCTGGGAGTCCGAACATATGCTGCTCCAGAGGTAATATCTGTAACCTATATGCTG 749
DB 724 CAAGTTGTGTAGCCCAATATATGCTGCTCCAGAGGTAATATCTGTAACCTATATGCTG 783
QY 750 GACCTGAGCTCGATGTATGAGAGTTGTGGGGTGATTTCTTAATGCTCTTCTTGTGAAGT 809
DB 784 GACCTGAAAGTTGATGTGTGAGCTGTGGGGTTATTTATGCTCTTTTATGTGGTACTC 843
QY 810 TTCCATTTGATGATGAGAAATATTTCCCAATCTGTTCAAAAAAATTAAGGAGGATCTTACA 869
DB 844 TGCCATTTGATGACGAGAACATACCAAACTTTTAAAGAAATTAAGGAGGATGAAATATTA 903
QY 870 CACTTCCAAGTCATTGTGCTGCTTTGGCCAGGATTTGATCCCAAGATGCTTGTGTTG 929
DB 904 CCTTCCAGCCATTGTGCTGTCGAGCAAGGATTGATTCCAAAGAAATGCTAGTTGTCG 963
QY 930 AGCTTGAAGAAGATCACAATTAAGGAAATTGCGAGCATCAATGTTCCAGATTGCGC 989
DB 964 ATCTTGAAGCGGATCACCAATCGTGAATTCGGAACATGATGTTCAAAATTCCTTC 1023
QY 990 TTCCAGCTTACTTGGCAGTGCCTCCACAGATACGACACAAGCCAAAATGATGTATG 1049
DB 1024 TCCGCGCTATTGTAAGTGTGCTCTCCAGATAGTGCAGCAAGTCAAAAAGTGTGATG 1083
QY 1050 AAGATACACTTCGAGATGTTGTTAATATGGATTAAACAAGAACCATGTGTGAATCAC 1109
DB 1084 AGGAACCTCTCCGTGAGGTTTAAAGTATGGATATGACAGAACCTGTTGTGAATCAA 1143
QY 1110 TGTGACGAGACTTCAAAATGAGGCACTGTTCATATATTTAATATGGAATCGGT 1169
DB 1144 TCCAAAAAGGCTGCAAAATGAGGCACTGTTCATATTAATCTTGGACAAATAGGC 1203
QY 1170 TTAGAGCACTAGTGGCTATCTTGGGCGAGATTATCAAGAAATCAATGACAGAAATTAA 1229
DB 1204 TCCGTACAACCAAGTGGCTATCTTGAAGCTGAATGTCAAAGACTATGAGACTCCTCATTC 1263
QY 1230 ATCAGCTGGCGTCATCTGAATCATCTAGTCTGTGACAGGAATTAATGTTCCAGAAAGCA 1289
DB 1264 CAAACATCGCATCATATGAACAACCAAGTTACAGCAGTGGGAATAGACAGCAATATTTA 1323
QY 1290 GTGATCTCATAGCAGTGTGTCGCGCCATATATATCTGTTGAAGAAAGAAATGGCGCTTG 1349
DB 1324 TGGAGTCTC---CAGTTGGCTTGAGACCAACATCTTCCAGCTGAGAGAAATGGGCTCTTG 1380
QY 1350 GACTTCAGTCTGGGCCCCACCTCTGTAATATATGTTGAGTCTTAAAGCACTTCAAG 1409
DB 1381 GTCTTCACTCTCGAGCACATCCAAAAGAAATATATGTCGAAGTCTGTAAGCTCTGCAAG 1440
QY 1410 AATTAAACGTCAAGTGAAGAAATGGGCACTACAACGTGAATGCAAGATGTCGCCAG 1469
DB 1441 AATTAAATGTTTACTGAAAAAGATAGCTCACTATTAACATGAAGTGCAAGATGAGTCTTG 1500
QY 1470 GGTTCCTGAAGTTAATGACACGTTAGATGCCAGCAACAGCTTTCTGTGACTCTAACCA 1529
DB 1501 GCTTCTGCTCAAAATTCATAACAATCAATCACTCA-----GTGAGGGT 1545
QY 1530 TCATGATTAATGATGATGCTAATGGAGGCTACCTACTGTGAATCAAGTTGAATTCAGC 1589
DB 1546 CCATTGAACGTATAGCCTGAGTGAAGTTA---AGTTTAATTAAGTTGAATTCAGC 1602
QY 1590 TTTACAGACGAAGACGACAAATGTAATCTTATGATATGACAGAGTTACTGACCTGAGC 1649
DB 1603 TGTACAAAACAAGACGAGAAATATCTCTCGATTTGCAAAAGATCAGTGGCCACAGC 1662
QY 1650 TGCTTCTTCTGACTTCTGTGCGGCTTCTTACCAAGCTTAAGGCTTCTAT 1700
DB 1663 TCCTCTTCTGACTGTGTGCGGCTTCTTAACTCAACTGAGAGTTCTTT 1713
RESULT 7
AAAS2772
ID AAAS2772 standard; cDNA; 2123 BP.

XX AC AAA52772; .
XX DT 03-JAN-2001 (first entry)
XX DE Soybean putative catabolite repression protein SNF1 coding sequence #2.
XX KM Soybean; carbon catabolite repression; sucrose non-fermenting protein 1;
XX KW SNF1; plant growth; ss.
XX OS Glycine max.
XX FH Key Location/Qualifiers
FT CDS 123..1667
FT /*tag= a
FT /product= "SNF1"
XX PN WO200036115-A2.
XX PD 22-JUN-2000.
XX PF 15-DEC-1999; 99WO-US029824.
XX PR 16-DEC-1998; 98US-0112563P.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PI Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ,
PI Miao G;
XX DR WPI; 2000-431593/37.
XX DR P-PSDB; AAB03420.
XX PT New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
PT involved in carbon catabolite repression in plants and seeds, useful for
PT controlling carbon and nitrogen partitioning pathways during plant growth
PT and development.
XX PS Claim 2; Page 42-43; 59pp; English.
XX CC The present sequence is a putative sucrose non-fermenting protein SNF1
CC coding sequence from the soybean. The sequence was isolated by searching
CC a pod cDNA library for sequences similar to those known to encode SNF1 in
CC Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The
CC protein is involved in carbon catabolite repression, and so the gene and
CC partitioning pathways during plant growth and development. They can also
CC be used to alter the accumulation of carbohydrates, lipids and proteins
CC during plant growth
SQ Sequence 2123 BP; 593 A; 395 C; 477 G; 658 T; 0 U; 0 Other;
QY Query Match 40.2%; Score 782.6; DB 3; Length 2123;
QY Best Local Similarity 71.1%; Pred. No. 6.1e-198;
QY Matches 1072; Conservative 0; Mismatches 414; Indels 21; Gaps 2;
QY 213 TAAGAACTACAACTGGAGAAGAACTTAGGTATCGGTACATTTGAAAAGTGAAGATTG 272
DB 169 TACCAATATTAATTTGGAAAAACACTCGGATTGGATCTTTGGCAAGTGAATTTG 228
QY 273 CAGAGCATAGCTTACTGGACATAGGTTGCTATTAAGATCATCACTACGCCCAATGA 332
DB 229 CAGAACATGTGTTGACTGGCCATTAAGTTGGATCAAGATCCTTAACGACGCAAGATTA 288
QY 333 GAAATATGAAATGGAGAAGAAAGCAAGAGAATTCAGATATTGAAGTTGTTCAATTC 392
DB 289 AGAACATGAAATGGAAAGAAAAGTGAGAGAGAAATCAAAATTTTAAGATTGTTCAATGC 348
QY 393 ACCCCCATATCATTCGGCTTTATGAGGTCAATACACACCTACAGATATATATGTTGTA 452
DB 349 ATCCTCACATTAATTCGACTTTATGAAGTCAATGAAAACCTCAACTGACATATATGTTGTA 408
QY 453 TGAATATATGTAGTATGCGAGTTATTTGATTACATTTGTTGAGAAAGCAGATTACAGG 512

DB 409 TGGAGTATGTGAAGTCTGAGAGACTTTTCGATTACATAGTAGAAGGATGCTGCAGG 468
QY 513 AAGATGAAGTCTGTCGAATCTTCCAGACATCATATCTGGCGTCCGAATACTGCCATAGA 572
DB 469 AAGATGAAGTCTGTAATTTTTCAGACAGATAATCTCTGGGGTGCAGTACTGTACAGGA 528
QY 573 ACATGTTGTCACCGTGACCTAAAGCCGAAAACTTGTACTTGAATTCAAAGTATATG 632
DB 529 ATATGTTGTTCAATAGAGATTGAAGCTGAGAAATTACTTTGGAATCCAAATGTAATG 588
QY 633 TAAAACTTGGGATTTTGTCTGAGCAATGTCATGATGATGAGGCCATTTCTGAGACTA 692
DB 589 TCAAGATTGCTGATTTTGGCTTGAGCAACATCATGCGTATGCTACTTTTAAACAA 648
QY 693 GCTGTGGAGTCCGAAGTATGCTGCTCCAGAGTAATATCTGTAAACTATATGCTGAGC 752
DB 649 GTTGTGAAGCCCTAATCATATGACGCTCCTGAGGTTATCTCTGGGAAATTGTATGCTGAGC 708
QY 753 CTGAGTCTGATATGAGATTGTTGGGGTGAATCTTATGCTCTTTGTGAACTCTTC 812
DB 709 CTGAAGTGAATGCTGAGCTGTGGTAAATTTATATGCCCCCTTTTGTGGCACCCTTC 768
QY 813 CATTGATGATGAGAAATATTTCCCAATCTGTCAAAAAATTAAGGAGGTATCTACACAC 872
DB 769 CTTTGAATGAGAAATATTTCCAAATCTCTCAAGAAATAAGGTGGATTACACTC 828
QY 873 TTCCAAGTCTTGTCTGCTTGGCCAGGATTTGATCCACGAATGCTTGTGTGAGC 932
DB 829 TTCCAGTCTATCTATCACCCGGTGTAGAGATTGATACCAAGGATGCTGTGTTGACC 888
QY 933 CTATGAAGAGATCACATTTAGGAAATTCGGAGCATCAATGTTCCAGATTGCGCTTC 992
DB 889 CTATGAGGAGATGACCATATCCTGAGATCCGTCAACACCCCATGTTCCAAAGCTGACTTC 948
QY 993 CACGTACTTGGCAGTGCCTCCACCAATACGACACACACCAAGCCAAATGATTGATGAAG 1052
DB 949 CACGTATTATGCTGTGCCACACCAATACATGCAACAGGCCAAATAAGATTGATGAGG 1008
QY 1053 ATACACTTCAGATGTTGTTAATATGGGATTTAACAAGAACCATGCTGTCAATCACTGT 1112
DB 1009 AGATCCTTCAGAAAGTGTGAAATGGGATTTGACAGGAATCAATGTGAATCTCTTG 1068
QY 1113 GCAGCAGACTTCAAAATGAGGCAACTGTGCATATTATTACTAATTGAGCAATCGGTTTA 1172
DB 1069 GGAACAGGATACAAATGAGGGTACTGTGCATATACTATTGTTAATTGGAACAACGATTTTC 1128
QY 1173 GAGCAACTAGTGGCTATCTTGGGGCAGATTATCAAGAATCAATGACAGAAATTAAATC 1232
DB 1129 GTGTTTCCAGTGGCTATCTTGGAGCTGAGTTCAAGAGACCATGATTCGGTTTAATC 1188
QY 1233 AGTGGCGTCATCTGAATCATCTAGTTCTGTGTAAGAGGATTAATGTTCCAGGAAGCAGTG 1292
DB 1189 AAATGCATTCAGTGAACCTTCTTTCAGTTGTTGAAACCGCTTTCAGGCTACATGG 1248
QY 1293 ATCTCATAGCAGTGGTTTGGCGCATATTATCTGTTGAAAGAAAATGGCGCTTGAC 1352
DB 1249 AATATCCAGAGTAGATCGAGGCAACAGTTCCTGTTGAAAGAAAATGGCCCTTGCGC 1308
QY 1353 TTCAGTCTGGGCCCAACCTGCTGAATAATGTTGAGGTCTTAAAGCACTTCAAGAAT 1412
DB 1309 TTCAGTCTGAGCCCATCTCGTGAATAATGACTGAGGTTCTTAAAGCTTTGCAAGAAAT 1368
QY 1413 TAAACGTGATGGAAGAAGATGGCACTACAACGTGAATGCAATGATGGTCCAGGGT 1472
DB 1369 TAAATGTTGTTGGAAGAAGATGCTCACTACAACATGAAGTGAAGTGGTGTGCGCA 1428
QY 1473 TTCCTG-----AAGTTAATGACACGTTAGATGCCAGCAACAGCTTCTTG 1517
DB 1429 TTCCTGTCACCAACGAAGGAATGTTAACAATAATGTGCATAGTAATCACTTTGGAG 1488
QY 1518 GTGACTTCAACATCATGATATGATGATGCTAATGGGAGGCTAACCTACTGTGATCAAGT 1577

Db 1489 ATGATTCACAATATTGAGATGATGCTGTTTCT-----ACTTCAATGTGTCAGT 1542
Oy 1578 TTGAATTCACGCTTTTACAGACGAAAGCAGCAAGTACCTCTTAGATATGACAGAGTTA 1637
Db 1543 TTGAAGTGACGCTTTACAAACC CGGAGAAAGATATCTGCTTGATCTTCAAGGCTGC 1602
Oy 1638 CTGACCTCAGCTGCTCTCTCTGACTTCCTGCGGCTTCCTTACCAAGCTTAGGTTT 1697
Db 1603 AGGTCACAGTTTCTTTCTTGATCTATGCTGCTTCTTCCCTTGACAGCTTCGTGCC 1662
Oy 1698 TATAGTG 1704
Db 1663 TCTAGAG 1669
RESULT 8
ACC00749
ID ACC00749 standard; cDNA; 2123 BP.
XX
AC ACC00749;
XX
DT 16-MAY-2003 (first entry)
XX
DE Glycine max oil trait related cDNA sequence SEQ ID NO:247.
XX
KW Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CKC-like transcription factor; antisense inhibition; co-suppression;
KW transgenic plant; gene; ss.
XX
OS Glycine max.
XX
PN WO2003002751-A2.
XX
PD 09-JAN-2003.
XX
PF 27-JUN-2002; 2002WO-US020152.
XX
PR 29-JUN-2001; 2001US-0301913P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczynski MC;
XX
DR WPI; 2003-201509/19.
DR P-PSDB; ABR40714.
XX
PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
PS Claim 18; Page 286-287; 542pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present

CC invention
XX
SQ Sequence 2123 BP; 593 A; 395 C; 477 G; 658 T; 0 U; 0 Other;
Query Match 40.2%; Score 782.6; DB 7; Length 2123;
Best Local Similarity 71.1%; Pred. No. 6.1e-198;
Matches 1072; Conservative 0; Mismatches 414; Indels 21; Gaps 2;
Oy 213 TAAGAACTACAACCTGGAGAACTTAGTATCGGTACATTGGAAGAAGTGAAGATTG 272
Db 169 TACCAATTATAAATTGGAAAACACTCGGATTGGATCTTTGGCAAGTGAAGATTG 228
Oy 273 CAGAGCATAGCTTACTGACATAGGGTTGCTATTAAGATCATCACTGCCCAATGA 332
Db 229 CAGACATGTGTGACTGGCCATAGAGTTGCCATCAAGATCCTTAACCGACGCAAGATTA 288
Oy 333 GAAATATGGAATGGAAGAGAAAGCAAGAGAGAAATTCAAGATTTGAAGTTGTCATTTC 392
Db 289 AGAACAATGAAATGGAAGAAAAGTGAGAAAGAAATCAAAATTTTAAGATTGTTCAATGC 348
Oy 393 ACCCCATATCATTCGGCTTTATGAGGTCAATATACACACCTACAGATATATATGTTGA 452
Db 349 ATCTCATATATTTCGACTTTATGAAGTCATAGAACTCCAAGTACATATATATGTTGCA 408
Oy 453 TGAATATTGTAAGTATGCGAGTATTGATTACATTGTTGAGAAAGCAGATTACAGG 512
Db 409 TGAATATTGTAAGTATGCGAGTATTGATTACATTGTTGAGAAAGCAGATTACAGG 468
Oy 513 AAGATGAGCTCGTCAATCTTCCAGACAGATCATATCTGGCGTCAATACTGCCATAGAA 572
Db 469 AAGATGAGCTCGTCAATCTTCCAGACAGATCATATCTGGCGTCAATACTGCCATAGAA 528
Oy 573 ACATGTTGTCACCCGTACCTAAAGCCGGAAGAACTGTTACTGATTCCAAGTATAATG 632
Db 529 ATATGGTGTTCATAGAGATTGGAAGCTGAGAAATTTACTTTGGAAGTCCAAGTATAATG 588
Oy 633 TAAACCTTCCGAGTTTGGTCTGACCAATGTCATGATGATGAGCCATTTTCTGAAGACTA 692
Db 589 TCAAGATTGCTGATTTTGGCTTGACCAATCATGATGATGATGATGATGATGATGATGAT 648
Oy 693 GCTGTGGAGTCCGAACTATGCTGCTCCAGAGTAAATATCTGCTAACTATATGCTGAC 752
Db 649 GTTGTGAAGCCCTAATATGACGCTCCTGAGTTATCTGCGGAAATGATGATGATGATG 708
Oy 753 CTGAGTCGATGATGAGTGTGCGGATGATTTCTTATGCTCTTCTTGTGCACTCTTC 812
Db 709 CTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 768
Oy 813 CATTTGATGATGAGATATTTCCCAATCTGTTCAAAAAAATTAAGGAGTATCTACACAC 872
Db 769 CTTTGTGATGATGAAATATTTCCAAATCTCTCAAGAAATTAAGGAGTATCTACACAC 828
Oy 873 TTCCAAGTATTTGCTGCTTTGGCCAGGATTTGATCCCAAGATGCTTGTGTTGAGC 932
Db 829 TTCCCAATCTATCAACCCGCTGAGATTTGATACCAAGGATGCTTGTGTTGAGC 888
Oy 933 CTATGAAGAGATCACAATTAGGGAATTCGGAGCATCAATGCTTCCAGATTGCGCTTC 992
Db 889 CTATGAGAGAGATGACCAATACCTGAGATTCGTCACACACCAATGCTTCCAGCTGACCTTC 948
Oy 993 CACGTTACTGGCAGTGCCTCCACAGATACGACACAAACCAAGCAATGATGATGAG 1052
Db 949 CACGTTACTGGCAGTGCCTCCACAGATACGATCAATGCAACGAGCCCAAAAGATTGATGAGG 1008
Oy 1053 ATACACTTCAGATGTTGTTAATATGAGATTTTAAACAAGCAATGCTGTGATCACTGT 1112
Db 1009 AGATCCTTCAGAAAGTGTGAATGAGATTTGACAGAAATCAATGCTTGAATCTCTTG 1068
Oy 1113 GCACGAGACTTCAAAATGAGCACTGTGCATATATTTACTATTTGACCAATCGGTTTA 1172
Db 1069 GGAACAGGATCAAAATGAGGCTACTGTGCATATATTTGTTATTTGACCAACCGATTTTC 1128
Oy 1173 GAGCACTAGTGCTATCTTGGGGCAGATTATCAAGAATCAATGACAGGAATTTAAATC 1232

Db 1129 GTGTTCCAGTGGCTATCTTGAGCTGAGTTTCAAGAGACCATGATTCGGGTTTAAATC 1188
Qy 1233 AGCTGGCGTCATCTGAATCATCTAGTCTGGTACGAGGAATTATGTTCCAGSAGCAGTG 1292
Db 1189 AATGCAATCCAGTGAACCTGCTCTTCTGAGTTGGTGAACCGCTTCCAGGCTACATG 1248
Qy 1293 ATCCTCATAGCAGTGGTTTGGCGCCATATATCTGTGAAAGAAAATGGCGCTTGAC 1352
Db 1249 AATATCCAGAGTAGATGATCGAGCAACAGTTCCTGTTGAAAAGAAATGGCCCTTGCGC 1308
Qy 1353 TTCAGTCTCGGCGCCACCTCGTGAATAATGTTGAGTCTTAAAGCACTTCAAGAT 1412
Db 1309 TTCAGTCTCGAGCCCATCCCTCGTGAATAATGATGAGGTTCTTAAAGCTTGCAGAAT 1368
Qy 1413 TAAACGTCAATGAGAGAAGATGGGCACTACACGTGAATGCAGATGGTCCAGGGT 1472
Db 1369 TAAATGTTGTTGGAAGAAGATTGGTCACTACACATGAAGTGTAGGTGGTTCGCA 1428
Qy 1473 TTCCTG-----AAGTAAATGACGCTTAGATGCCAGCAACGCTTCTTG 1517
Db 1429 TTCCTGTCACCAAGGAAGATGTTAACAAATATGTGCATAGTAATCATTAATTGGAG 1488
Qy 1518 GTGACTTACCATCATGATGATATGATGATGATGAGGCTACCTACTGATCAAGT 1577
Db 1489 ATGATTCACACATTAATGAGATGATGCTGTTCT-----ACTTCAAAATGCTCAAGT 1542
Qy 1578 TTGAATTCACGCTTACAAAGACGAGACAGTACCTCTTAGATATGACAGAGTTA 1637
Db 1543 TTGAAGTCAAGCTTACAAAAACCGGAAGAAAGATATCTGCTGATCTTCAAGGTC 1602
Qy 1638 CTGACCTCAAGCTCTCTCTTCTGACTTCTGTGGCGCTTCTTACCAAGCTTAGGTTT 1697
Db 1603 AGGTCACAGTCTTCTTCTTCTGATCATGTGCTTCTTCTGACAGCTTGTGTCC 1662
Qy 1698 TATAGTG 1704
Db 1663 TCTAGAG 1669

RESULT 9
AAAF62011
ID AAF62011 standard; DNA; 1929 BP.
XX AAF62011;
AC AAF62011;
DT 02-MAY-2001 (first entry)
XX
DE Tomato LesNFI (sucrose nonfermenting yeast homologue) gene.
XX
KW Sucrose non-fermenting; SNF-4; SNF-1; tomato; sugar metabolism; seed;
KW source-sink; fruit; enhanced quality; sugar accumulation; LesNFI;
KW stress resistance; transgenic plant; germination stimulation; ds.
XX
OS Lycopersicon esculentum.
XX
PN WO200107570-A1.
XX
PD 01-FEB-2001.
XX
PF 21-JUL-2000; 2000WO-US019981.
XX
PR 21-JUL-1999; 99US-00359161.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Bradford KJ, Peetambar D, Yang H, Cooley M, Downie B, Gee OH;
XX
DR WPI; 2001-168545/17.
XX
PT New sucrose non-fermenting (SNFI) and SNF4 polynucleotides and expression
PT cassettes containing the polynucleotides for modulating source-sink
PT relationships in plants and enhancing yield or quality of harvested plant

PT products.
XX
PS Claim 19; Page 39; 43pp; English.
XX
CC This invention relates to polynucleotide sequences encoding plant sucrose
CC non-fermenting SNF-4 or SNF-1 polypeptides. Specifically included in the
CC invention are tomato LesNF-4 and LesNF-1 polynucleotide sequences. A
CC recombinant expression vector comprising SNF-4 or SNF-1 polynucleotide
CC sequences is useful for modulating sugar metabolism in a plant. The
CC recombinant expression cassette comprising the DNA sequence is useful for
CC modulating source-sink relationships in plants and therefore enhances
CC yield or quality of harvested plant products, such as fruit. SNF-4 and
CC SNF-1 DNA can be used to enhance sink activity or starch or lipid
CC accumulation in fruits. Also they can be used to enhance sugar
CC accumulation in seeds. The expression cassettes can also be used to
CC enhance responsiveness to stress conditions in plants. Enhanced
CC expression of SNF1 and SNF4 polynucleotides or polypeptides is used to
CC alter expression of sugar related genes or to enhance resistance to
CC stress. Inhibition of endogenous SNF1 or SNF4 genes modulates the
CC activity of enzymes associated with sugar metabolism. In seeds,
CC inhibition of SNF4 expression can be used to break dormancy and stimulate
CC germination. The present sequence represents the tomato LesNF-1 gene
XX
SQ Sequence 1929 BP; 546 A; 384 C; 442 G; 557 T; 0 U; 0 Other;
Query Match 40.1%; Score 780.8; DB 4; Length 1929;
Best Local Similarity 71.5%; Pred. No. 1.8e-197;
Matches 1074; Conservative 0; Mismatches 412; Indels 16; Gaps 3;
Qy 212 TTAAGAACTACAACCTCGGAAGACTTTAGTATCGGTACATTTGGAAGTGAAGATT 271
Db 78 TTACGGAAGCTATAAAGTCCGGAAGAACTTGCGATGTGATCGTTCGCAAGTTAAATA 137
Qy 272 GCAGAGCAATAGCTTACTGACATAGGGTGTCTATAAGATCATCACTGCCGCAATG 331
Db 138 GCTGAACATACGTTAACAAGGCGCACAAAGTTGCTGTCAAGATTCTTAATCGTCAAAAATC 197
Qy 332 AGAAATATGAAATGGAAGAGAAAGCAAGAGAAATTCAGATATTTGAAGTGTTCATT 391
Db 198 AGGAATATGACATGAGAGAGAAAGTCCGTAGAGAAATCAAAATATTGAGATTGTCATG 257
Qy 392 CACCCCAATATCTTCGGCTTTATGAGGTATATACACACCTACAGATATATATGTTG 451
Db 258 CATCTCATATATTATACGCTTTATGAGGTATAGAGACACCATCAGATATATATGTTG 317
Qy 452 ATGAATATTTGAATATGAGGAGTATTGATTACATTTGTTGAAGAAAGCAGATTACAG 511
Db 318 ATGAGATATGTAATCTGCGAGTATTGATTACATTTGTTGAAGAAAGCAGATTGCA 377
Qy 512 GAAGATGAAGCTCGTGAATCTTCCAGCAGATCATATCTGGCCGCAATATCTGCCATAGA 571
Db 378 GAGGATGAAGCTCGTGAATCTTTCAGCAGATTAATTTCTGGTGTGAGTACTGCCATAGA 437
Qy 572 AACATGTTGTCCACCGTGACCTTAAAGCCGGAAGAACTTGTACTGTATTCAAGTATAT 631
Db 438 AACATGTTGTTCATAGAGACCTTAAGCCTGAAGAACTTCTTGAACCTCAAAATGAAT 497
Qy 632 GTPAAACTGCGGATTTTGGTCTGAGCAATGTCAATGATGCGCATTTTCTGAAGACT 691
Db 498 GTGAAGATCGCAGATTTTGGTTGAGCAATATCATGCGGATGCTCATTTTCTGAAGACA 557
Qy 692 AGCTGTGAGAGTCCGAATATGCTCTCCAGAGGTAATATCTGTTAACTATATGCTGA 751
Db 558 AGTTGCGAAGCCCAACTATGCTGCCAGAGTTATATGAGTAAATGTATGCTGGC 617
Qy 752 CCTGAGTGCATGTATGAGTGTGGGGTGATTTCTTATGCTCTTCTTGTGAAGCTCTT 811
Db 618 CCTGAGTGCATGTATGAGTGTGGGGTGATTTCTTATGCTCTTCTGTCGACCCCTT 677
Qy 812 CCATTTGATGATGAGATATTTCCCAATCTGTTCAAAAAATTAAAGGAGTATCTACACA 871
Db 678 CCGTTTGAAGATGAAAAACATACCAATCTTTTAAAGAAATAAAGGAGTATATATCT 737

| | | | |
|----|------|--|------|
| QY | 872 | CTTCCAAGTCATTTGTCTCTTTGGCCAGGGATTTGATCCCAAGATGCTTGTGTGAG | 931 |
| Db | 738 | CTGCCAGCCATTTATCAGCTGTCGAGGGATTTGATCCGAGGATGCTTATAGTCAC | 797 |
| QY | 932 | CCTATGAAGAAATCACAATTAGGGAAATTCGGAGCATCAATGTTCCAGATTCCGCTT | 991 |
| Db | 798 | CCAATGAAGCGAATGACTAATTCCTGAGATTCCCTGCACCTTGTTCCAAGCTCATTTG | 857 |
| QY | 992 | CCACGTTACTTGGCAGTGCCTCCACAGATACGACACAACCAAAATGATTGATGAA | 1051 |
| Db | 858 | CCACGCTATTGGCCGTGCTCCACAGATACAAACCAACAAAGAAAGATCGATGAA | 917 |
| QY | 1052 | GATACACTTCGAGATGTTGTTAATATGGATTAAACAAGACCATGTGTGTAATCACTG | 1111 |
| Db | 918 | GAGATTCTTCAAGAGGTGGTTAAGATGGATTTCAGAGAACAACTTACTGAGTCTCTT | 977 |
| QY | 1112 | TGCAGCAGACTTCAAATGAGCCACTGTTGCATATTATTACTATTGGACAATCGGTTT | 1171 |
| Db | 978 | CGCAATAGAGTTCAAAATGAGGGCACTGTTGCATATCTATCTCTCCAGACAATCGCAT | 1037 |
| QY | 1172 | AGAGCAACTAGTGGCTATCTTGGGGCAGATTATCAAGAATCAATGACAGGAATTTAAT | 1231 |
| Db | 1038 | CGTGTTCACACTGGCTATCTTGGAGCTGAATTCAGAGATCCATGGAATATGTTACAC | 1097 |
| QY | 1232 | CAGCTGGCGTCATCTGAATCACTAGTCTGTGTACGAGAAATATGTTCCAGGAAGCACT | 1291 |
| Db | 1098 | CGGATCAATCTAATGAACCGCTGCTTCCCTGTGTGTCACGTTTCCAGGAATATG | 1157 |
| QY | 1292 | GATCCTCATAGCAGTGGTTTGGCGGCATATTATCCTGTGGAAGAAATGGCGCTTGA | 1351 |
| Db | 1158 | GATTATCAGCAAGCTGGTGCAG--ACAGTTCGCCATGGAAGAAATGGGCTCTTGCGC | 1214 |
| QY | 1352 | CTTCAGTCTCGGCCCAACCTCGTGAATAATATGTTGAGTCTTAAAGCACTTCAAGAA | 1411 |
| Db | 1215 | CTCCAGTCTCGAGCGCATCCACGTGAATAATGACTGAAGTTTGAAGCTCTGCAAGAA | 1274 |
| QY | 1412 | TTAAACGTCAAGTGAAGAGAATGGGCACCTACAACGTGAATGCAGATGTCGCCAGGG | 1471 |
| Db | 1275 | CTGAATGTATGTTGAA-AAAGTTGCTCAGTATTAATGAATGTCGATGGTTCCTAGC | 1333 |
| QY | 1472 | TTTCTGGAAGTTAATGACACGTTAGATGCCA-----GCAACAGCTTTCCTGGT | 1519 |
| Db | 1334 | TTACCTGGTCATCATGAAGGCACTGGGTGTTAATTCATGCATGGGAATCAAGTCTTTGGA | 1393 |
| QY | 1520 | GACTCTACCATCATGATATAATGATGCTAATGGAGGCTAATCTGTGATCAAGTTT | 1579 |
| Db | 1394 | GATGATTCAATCATGATGAATGATGGGGCCACAAGTTTAACAATGTGTCAAGTTT | 1453 |
| QY | 1580 | GAATTCAGCTTTTACAAGACGAAGACGAACAAGTACCTCTTATGATATGCAGAGATTACT | 1639 |
| Db | 1454 | GAAATTCAAGCTTTACAACCAAGGAGGAGAGAAAGTACTTGTCTGACCTTCAGAGACTTCAG | 1513 |
| QY | 1640 | GGACCTCAGCTGCTCTTCTTGAATCTCTGTGCGGCTTCTTACCAAGCTTAGGGTTCTA | 1699 |
| Db | 1514 | GGTCCACAATTCCTCTTCTGGAATCTGTGTGCTTTTCTTGTCAAGCTTCAGTACTT | 1573 |
| QY | 1700 | TA 1701 | |
| Db | 1574 | TA 1575 | |

| | |
|-----------|---|
| RESULT 10 | |
| ABZ12357 | |
| ID | ABZ12357 standard; DNA, 1539 BP. |
| XX | |
| AC | ABZ12357; |
| XX | |
| DT | 21-JAN-2003 (first entry) |
| XX | |
| DE | Arabidopsis thaliana stress regulated gene SEQ ID NO 162. |
| XX | |
| KW | Arabidopsis thaliana; plant; gene; stress; transgenic; ds |
| XX | |

OS Arabidopsis thaliana.
XX
XX WO200216655-A2.
PN
XX
XX 28-FEB-2002.
PD
XX
XX 24-AUG-2001; 2001WO-US026685.
PF
XX
XX 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX
XX (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
PA
XX
XX Harper JF, Kreps J, Wang X, Zhu T;
PI
XX
XX WPI; 2002-304127/34.
DR
XX
XX Identifying a stress condition to which a plant cell has been exposed and
PT producing plants with increased tolerance to these abiotic stresses.
PT
XX
XX Claim 144; SEQ ID NO 162; 577pp + Sequence listing; English.

CC The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 1539 BP; 439 A; 291 C; 369 G; 440 T; 0 U; 0 Other;

| | | | | |
|-----------------------|--------------|---------------------|-----------------|--------------|
| Query Match | 40.1%; | Score 780.2; | DB 6; | Length 1539; |
| Best Local Similarity | 70.2%; | Pred. No. 2.3e-197; | | |
| Matches 1046; | Conservative | 0; | Mismatches 443; | Indels 0; |
| | | | | Gaps 0; |

QY 212 TTAAGGAAGCTACAACTCTGGGAAGAACTTTAGGTAATCGGTACATTTGGAAAGAGTGAAGATT 271
 Db 49 TTACCGAATTACAACTGTGGTAAAACTCTTGGAAATTGGGCTCTTTGGGAAGGTGAAAAATA 108
 QY 272 GCAGAGCATTAAGCTTACTGGAACATAGGGTTGCTATAAAGATCATCAACTGCCGCCAAATG 331
 Db 109 GCAGAGCATGTTGTCA CAGGGCATTAAGGTTGTATCAAAATCCTTAATCGTCGTAAGATC 168
 QY 332 AGAATATGGAATGGAAGAGAAGCAAGAGAAATTCAGATATGAAATTGTTGTCATT 391
 Db 169 AAGAACATGGAGATGGAAGAGAAAGTGAGGAGGAGATTAAGATTTACGGTGTGTTATG 228
 QY 392 CACCCCATATCATTCGGCTTTATGAGGTCATATACACACCTACAGATATATATGTTGTG 451
 Db 229 CATCCTCATATTATTCCGACAGTATGAGGTAATAGAACCCAGAGTGACATTATGTTGTG 288
 QY 452 ATGGAATATTGTAAGTATGCGCAGATTATTGATTTACATTTGTTGAGAAAGCAGATTACAG 511
 Db 289 ATGAGTATGTCAAGTCTGAGAGAGCTCTTGATATATTTGTTGAGAAAGCAGATTACAA 348
 QY 512 GAAGATGAAGCTCGTCGAATCTTCCAGCAGATCATATCTGGCGTGAATACTGCCATAGA 571
 Db 349 GAAGATGAGGCTCGTAACTTTTCCAGCAGATATATCTGCTGTAGAGTACTGCCATCGT 408
 QY 572 AACATGTTGTCCACCGTGACCTAAAGCCGGAATACTGTTACTTGATTCAAGTATAAT 631
 Db 409 AATATGTTGTCCATAGAGACCTGAAGCCTGAGAAATTTACTATTGGATTGAGGCTGTAAT 468
 QY 632 GTAAAACTTGGCGAATTTTGGTCTGAGCAATGTCATGATGAGCCATTTTCTGAAGACT 691

Db 469 ATTAAGATTGCAGACTTTGGGTGAGTAAATGTTATGCGGATGGTCAATTTCTAAAGACG 528
QY 692 AGCTGTGGAGTCCGAACATATGCTGTCCAGAGGTAATATCTGGTAAACTATATGCTGGA 751
Db 529 AGTTGTGAAGCCCCAACACTACGCTGCTCCCGAGGTTATATCAGGTAATAATTATATGCTGGA 588
QY 752 CCTGAGGTCGATGTATGAGAGTGTGGGGTGAATCTTTATGCTCTTCTTTGTGGAACCTTT 811
Db 589 CCTGAAGTAGATGTATGAGAGTTGCGGAGTTATATTTGACGCTCTATATATGCGGTAACCTTT 648
QY 812 CCATTGTGATGAGAAATATTTCCCAATCTGTTCAAAAAAATTAAAGGAGGTAATCTACACA 871
Db 649 CTTTGTGATGAGAAACATTTCCCAACCTTTTCAAGAAAAATTAAAGGAGGTAATTTACACT 708
QY 872 CTTCCAAAGTCAATTTGCTGCTTTGGCCAGGATTGATCCCAAGATGCTGTTGTTGAG 931
Db 709 CTTCCAAAGTCAATTTATCATCTGAGGCTAGAGACTGATCCCAAGATGCTTATAGTTGAC 768
QY 932 CCTATGAAGAAATCACAATTAGGAAATTCGGAGCATCAATGTTCCAGATTGCGCCTT 991
Db 769 CCGTGAAACGAATCACCATCTCCAGATCCGTCAACACCGTTGGTTCCAGACTCATCTC 828
QY 992 CCACGTTACTTGGCAGTGCCTCCACAGATACGACACACAAGCCAAATGATGTAGAA 1051
Db 829 CCTCGTTATCTTGCTGTCTCTCCACCGGATACAGTAGACAGCGCTAAAGAATCAATGAG 888
QY 1052 GATACACTTCGAGATGTTGTTAATATGGGATTAAACAAGAACCATGTGTGTAATCACTG 1111
Db 889 GAGATAGTTCAAGAGTGGTTAAACATGGGATTGATAGAAACCAAGTTTGGAAATCTCTA 948
QY 1112 TGCAGCAGACTTCAAAAATGAGGCAACTGTTGCAATATATTACTATTTGCAATCGGTTT 1171
Db 949 CGCAACAGAACACAAAACGATGCTACTGTTCATTAATACTACTGTTATGGATTAACCGGTTT 1008
QY 1172 AGAGCAACTAGTGGCTATCTTGGGAGAGATTATCAAGAATCAATGAGACGAATTTAAAT 1231
Db 1009 CGTGTTCGAAGTGGTATCTAGAATCCGAGTTCAAGAGACAAACAGACAGTGGTTCCAAT 1068
QY 1232 CAGCTGGCGTCACTCTGAATCATCTAGTTCTGTTACGAGGAATATGTTCCAGGAAGCAGT 1291
Db 1069 CCTATGCCGACACCTGGAAGCGGGCGCTTCACTGTAGGCCACTGGATTCTGCACATGTG 1128
QY 1292 GATCCTCATAGCAGTGGTTTGGCGGCATATATCTCTGTGAAAGAAAATGGCGCTTGA 1351
Db 1129 GATCACTACGGGTTGGGAGCAAGATCACAAAGTCCCTGTTGATCGAAAATGGGCTCTTGA 1188
QY 1352 CTTCACTTCGGGCCCACTCGTGAATATATGTTGAGGCTTTAAAGCACTTCAAGAA 1411
Db 1189 CTTCACTTCATGCGCATCTCGTGAATCAATGAATGAAGTTTGAAGCTCTTCAAGAA 1248
QY 1412 TTAAACGTCAATGGAAGAAGATGGGCACTACAACTGAATGACAGTGGTGCCAGGG 1471
Db 1249 CTCAATGTGTGGAAGAAGATGTGTCACTACAAATGATGAATGAGGTTCCCTGCT 1308
QY 1472 TTTCTGAAGTTAATGACACGTTAGATGCCAGCAACAGCTTCTTGTTGACTCTACCATC 1531
Db 1309 TTAGCTGATGGTCAAGATACTATGTCAACAAATCAGCTGCACCTCAGAGATGAATCCAGC 1368
QY 1532 ATGATAATGATGATGCTAATGGAGGCTACTGTGATCAAGTTTGAATTCAGCTT 1591
Db 1369 ATCAATTGAGGATGATGCTGCCATGACTTCAACCACTGTCAATCAAAATTTGAATTCAGCTA 1428
QY 1592 TACAAGACGAAGACGACAAAGTACCTCTTGAATATGACAGAGATTACTGGAACCTCAGCTG 1651
Db 1429 TACAAGACCGGGAAGAGAAAGTACTTGCTGATATACAGAGATTAAAGCTCCGAGTTT 1488
QY 1652 CTCTTCCTTGAATCTGTGCGGCTTCTTACCAAGCTTAGGGTTCTAT 1700
Db 1489 CTCTTCTTGAATCTATGCGCGCTTCTTACAGAGCTTCTGTGATCT 1537

RESULT 11
AAC44825

ID AAC44825 standard; DNA; 1792 BP.
XX
AC AAC44825;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44271.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 04-MAY-1999; 99US-0132407P.
PR 05-MAY-1999; 99US-0132484P.
PR 06-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132863P.
PR 14-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.
PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.

| | | |
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| PR | 18-JUN-1999; | 99US-0139461P. |
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| PR | 18-JUN-1999; | 99US-0139750P. |
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| PR | 21-JUN-1999; | 99US-0139817P. |
| PR | 22-JUN-1999; | 99US-0140353P. |
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| PR | 24-JUN-1999; | 99US-0140695P. |
| PR | 28-JUN-1999; | 99US-0140823P. |
| PR | 30-JUN-1999; | 99US-0141287P. |
| PR | 01-JUL-1999; | 99US-0141842P. |
| PR | 01-JUL-1999; | 99US-0142154P. |
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| PR | 08-JUL-1999; | 99US-0142803P. |
| PR | 09-JUL-1999; | 99US-0142920P. |
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| PR | 14-JUL-1999; | 99US-0143542P. |
| PR | 15-JUL-1999; | 99US-0144005P. |
| PR | 16-JUL-1999; | 99US-0144085P. |
| PR | 16-JUL-1999; | 99US-0144325P. |
| PR | 19-JUL-1999; | 99US-0144331P. |
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| PR | 19-JUL-1999; | 99US-0144333P. |
| PR | 19-JUL-1999; | 99US-0144335P. |
| PR | 19-JUL-1999; | 99US-0144352P. |
| PR | 20-JUL-1999; | 99US-0144632P. |
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| PR | 21-JUL-1999; | 99US-0144814P. |
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| PR | 05-AUG-1999; | 99US-0147719P. |
| PR | 05-AUG-1999; | 99US-0147260P. |
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| PR | 06-AUG-1999; | 99US-0147416P. |
| PR | 09-AUG-1999; | 99US-0147493P. |
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| PR | 17-AUG-1999; | 99US-0149175P. |
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| PR | 30-AUG-1999; | 99US-0151080P. |
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| PR | 01-SEP-1999; | 99US-0151930P. |
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| PR | 10-SEP-1999; | 99US-0153070P. |
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| PR | 15-SEP-1999; | 99US-0154018P. |
| PR | 16-SEP-1999; | 99US-0154039P. |
| PR | 20-SEP-1999; | 99US-0154779P. |
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| PR | 04-OCT-1999; | 99US-0157117P. |
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| PR | 07-OCT-1999; | 99US-0158029P. |
| PR | 08-OCT-1999; | 99US-0158232P. |
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| PR | 13-OCT-1999; | 99US-0159294P. |
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| PR | 14-OCT-1999; | 99US-0159330P. |
| PR | 14-OCT-1999; | 99US-0159331P. |
| PR | 14-OCT-1999; | 99US-0159637P. |
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| PR | 21-OCT-1999; | 99US-0160741P. |
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| PR | 21-OCT-1999; | 99US-0160770P. |
| PR | 21-OCT-1999; | 99US-0160814P. |
| PR | 21-OCT-1999; | 99US-0160815P. |
| PR | 22-OCT-1999; | 99US-0160980P. |
| PR | 22-OCT-1999; | 99US-0160989P. |
| PR | 22-OCT-1999; | 99US-0160989P. |
| PR | 25-OCT-1999; | 99US-0161404P. |
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| PR | 25-OCT-1999; | 99US-0161406P. |
| PR | 26-OCT-1999; | 99US-0161359P. |
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| PR | 26-OCT-1999; | 99US-0161361P. |
| PR | 28-OCT-1999; | 99US-0161920P. |
| PR | 28-OCT-1999; | 99US-0161922P. |
| PR | 28-OCT-1999; | 99US-0161993P. |
| PR | 29-OCT-1999; | 99US-0162142P. |

| | | | | |
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| Query Match | 40.1%; | Score 780.2; | DB 3; | Length 1792; |
| Best Local Similarity | 70.2%; | Pred. No. 2.5e-197; | | |
| Matches 1046; | Conservative | 0; | Mismatches 443; | Indels 0; |
| | | | | Gaps 0; |

[illegible]

Db 482 CATCCTCATATTAATTCGGCAGTATGAGTAATAGAACCAAGAGTGAATTTATGTTGTG 541
Qy 452 ATGAATATATTGTAAGTATGCGAGTTATTTGATTACATTGTTGAGAAAGCAGATTACAG 511
Db 542 ATGAGTATGTCAGTCTGAGAGCTCTTGATTATATTGTTGAGAAAGCAGATTACAA 601
Qy 512 GAAGATGAAGCTCGTGAATCTTCCAGCAGATCATATCTGCGCTGAATTAATGCCATAGA 571
Db 602 GAAGATGAGGCTCGTAACCTTTTCCAGCAGATAATATCTGCTGTAAGTAATGCCATCGT 661
Qy 572 AACATGTTGTCACCCGTGACCTAAAGCCGGAATACTGTTACTTGAATTCAAAGTATAAT 631
Db 662 AATATGTTGTCATAGAGACCTGAAGCCTGAGAAATTTACTAATTGGAATTCGAGGTGTAAT 721
Qy 632 GTAAACCTGCGGATTTTGGTCTGAGCAATGTCATGATGCGCATTTTCTGAAGACT 691
Db 722 ATTAAGATTGCACTTTGGGTGAGTAATGTTATGCGGATGTCATTTCTAAAGACG 781
Qy 692 AGCTGTGAGTCCGAACCTATGCTGCTCCAGAGTAATATCTGTAATCTATATGCTGGA 751
Db 782 AGTGTGAGAGCCCAACTACGCTGCTCCGAGGTTATATCAGGTAATATATGCTGGA 841
Qy 752 CCTGAGTGCATGTAATGAGTGTGCGGTGAATCTTATGCTCTCTTGTGGAACCTTT 811
Db 842 CTGAAGTATGATGATGAGAGTTCGCGAGTTATATGTAAGCTCTATATGCGGTAATCTT 901
Qy 812 CCATTGATGATGAGAAATATTTCCCAATCTGTTCAAAAAATTAAAGGAGTAATCTACACA 871
Db 902 CTTTGTGATGATGAATAACATTTCCCAACCTTTTCAAGAAATTAAAGGTGGGATTTACACT 961
Qy 872 CTTCGAAGTATTTGCTGCTGCTTTGGCCAGGATTTGATCCCAAGATGCTGTTGTTGAG 931
Db 962 CTTCGAAGTATTTATCATCTGAGGCTAGAGACTGATCCCAAGAGTCTTATAGTTGAC 1021
Qy 932 CCTATGAAGAGATCACAATTAAGGAAATTCGGGAGCATCAATGTTCCAGATTGCGCTT 991
Db 1022 CCGTGAAAGCAATCACCATTCCTGAGATCCGTCAACACCGTTGGTCCAGACTCATCTC 1081
Qy 992 CCACGTTACTGGCAGTGCCTCCACAGATACGACACAACAAGCCAAATGATTGATGAA 1051
Db 1082 CCTCGTTATCTTGCTGCTCTCCACCGGATACAGTAGAGCAGGCTAAAGATCAATGAG 1141
Qy 1052 GATACACTTCGAGATGTTGTTAATATGGGATTTAAACAAGAACCATGTTGTGATCACTG 1111
Db 1142 GAGATAGTTCAAGAGAGTGTTAACATGGGATTTGATGAAACCAGGTTTGGAAATCTCTA 1201
Qy 1112 TGCAGCAGACTTCAAAATAGGCAACTGTTGCATATTATTACTATATGCAATCGGTTT 1171
Db 1202 CGCAACAGAACACAATAACGATGCTACTGTTAATTAATACTACCTGTTATGATTAACCGGTTT 1261
Qy 1172 AGAGCAACTAGTGCTTATCTTGGGCGAGATTAACAAGATCAATGACAGAAATTTAAAT 1231
Db 1262 CGTGTCCAAAGGCTTATCTAGAATCCGAGTTTCAAGAGACAACAGAGTGTTCAT 1321
Qy 1232 CAGCTGGCGTCACTGTAATCATCTAGTCTGCTGTAACGAGAAATTAATGTTCCAGGAAGCAGT 1291
Db 1322 CCTATGCCGACACCTGAAGCGGGCGCTTCACTGTAGGCCACTGGATTCCTGCACATGTG 1381
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Db 1382 GATCACTACGGGTTGGGAGCAAGATCACAGTCCCTGTTGATCGAAATGGGCTCTTGA 1441
Qy 1352 CTTCAAGTCTGGGCCCCACCTCGTGAATTAATGTTGAGGCTTTAAAGCACTTCAAGAA 1411
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Qy 1412 TTAAACGTCAATGGAAGAAGATGGGCACTAACAAGTGAATGCAAGTGGTCCCGAGGG 1471
Db 1502 CTCAATGTGTGTTGAAGAAGATGTGTCACTAACAACATGAATGTGATGGGTTCTGTGT 1561
Qy 1472 TTTCTGAAGTTAATGACAGCTTAGATGCCAGCAACAGCTTTCTTGTAATCTTACCATC 1531
Db 1562 TTAGCTGATGGTCAGAAATACTATGTGTCAACAAATCAGCTGCACTTCAGAGATGAATCCAGC 1621

Qy 1532 ATGATTAATGATGATGCTAATGGGAGGCTACCTACTGTGATCAAGTTTGAAATCCAGCTT 1591
Db 1622 ATCATTTGAGATGACTGTGCCATGACTTCAACCACTGTCTATCAATTTGAATTCAGCTA 1681
Qy 1592 TACAAGCAGAGGACGACAACTACTTATGATATGCAGAGAGTTAATCTGAGCTCAGCTG 1651
Db 1682 TACAAGCCCGGGAAGAGAGTACTTGCTGATATACAGAGTTAAACGGTCCGAGTTT 1741
Qy 1652 CTCTTCTGACTTCTGTGCGGCTTCTTACCAAGCTTAGGTTCTAT 1700
Db 1742 CTCTTCTGATCTATGCGCGCTTCTTACAGAGCTTCGTGATCT 1790

RESULT 12
AAL46639
ID AAL46639 standard, cDNA; 1825 BP.
XX
AC AAL46639;
XX
AC
XX
DT 05-AUG-2002 (first entry)
XX
DE A thaliana AKIN11 coding sequence.
XX
KM AKIN11; pathogen resistance; transgenic; plant; antibacterial; virucide;
KM fungicide; nematocide; gene; ss.
XX Arabidopsis thaliana.
OS
FH Key Location/Qualifiers
FT CDS 1..1539
FT /tag= a
FT /product= "AKIN11"
XX
PN WO200238780-A2.
XX
PD 16-MAY-2002.
XX
PF 07-NOV-2001; 2001WO-FR003457.
XX
PR 08-NOV-2000; 2000FR-00014354.
XX
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
PA (CNRS) CENT NAT RECH SCI.
XX
PI Roby D, Balague C, Godard F, Lummerzheim M;
XX
DR WPI; 2002-426954/45.
DR P-PSDB; AAO17663.
XX
PT Inducing or increasing resistance to pathogens in plants e.g. industrial
PT scale flowers and vegetables, by introducing a nucleic acid that encodes
PT the AKIN11 peptide.
XX
PS Claim 2; Page 67; 76pp; French.
XX
XX The present invention relates to the use of a nucleic acid that causes
CC the synthesis of the AKIN11 protein, to induce or increase the resistance
CC to pathogen attack in plants. The nucleic acid and its encoded protein
CC can be used to impart resistance to bacteria, viruses, fungi and
CC nematodes, especially necrotropic pathogens such as Xanthomonas
CC campestris, in large-scale crops, vegetables and flowers. Probes and
CC primers that hybridise with the AKIN11 gene can be used to detect
CC resistance against pathogens, and antisense sequences can be used to
CC modulate resistance. The present sequence is the AKIN11 cDNA of the
CC invention
XX
SQ Sequence 1825 BP; 525 A; 330 C; 409 G; 561 T; 0 U; 0 Other;

Query Match 40.0%; Score 778.6; DB 6; Length 1825;
Best Local Similarity 70.0%; Pred. No. 6.7e-197;
Matches 1048; Conservative 0; Mismatches 449; Indels 0; Gaps 0;

| | | | | | | | | | |
|----|------|-----------|--------------|--------------|----------------|------------|--------------|---------------|------|
| QY | 212 | TTAAGGAAC | TACCAACCTGGG | AAGAACTTTAGG | TATCGG | TACATTTGG | AAAAAGTG | AAGATT | 271 |
| | | | | | | | | | |
| Db | 49 | TTACCGAAT | TACCAAGCTTGG | TAAAACTCTTGG | AATTGGGCTTTTGG | GAAGGTG | AAAAATA | 108 | |
| QY | 272 | GCAGAGCAT | TAAAGCTTAC | TGACATAGG | GGTGTCTAT | TAAAGTCA | TCACTGCCG | CAATG | 331 |
| | | | | | | | | | |
| Db | 109 | GCAGAGCAT | GTGTGTAC | AGGCGCATAA | GGTGTCTATCA | AAATCCTTAA | TCGTGTA | GATC | 168 |
| QY | 332 | AGAAATATG | GAATGGAAG | AAAGCAAA | GAGAAATTC | AGATATTG | GAAGTGTG | CAAT | 391 |
| | | | | | | | | | |
| Db | 169 | AAGACATG | AGATGGA | AGAAAGT | AGAGGAG | GATTAAG | ATTCACG | GTGTTATG | 228 |
| QY | 392 | CACCCCAT | TATCATTTGG | GCTTATG | AGGTCATAT | ACACCTA | CAGATATAT | TATGTTG | 451 |
| | | | | | | | | | |
| Db | 229 | CATCCTCA | TATTAATTCGG | CAGTATG | AGGTAA | TAGAGAC | CCACAGT | GACATTTATG | 288 |
| QY | 452 | ATGGAATAT | TGTAAGTATG | GCAGCTTA | TTTGATTAC | ATTGTTG | AGAAAGC | AGATTAC | 511 |
| | | | | | | | | | |
| Db | 289 | ATGAGTAT | GTCAAGTCTG | GAGACTCTT | GATTATATTG | TGAGAAA | AGCAGATT | ACAA | 348 |
| QY | 512 | GAAGATGA | AGCTCGT | CGAATCTT | CCAGACAG | ATCATATC | TGGCGT | CGAATAC | 571 |
| | | | | | | | | | |
| Db | 349 | GAAGATGA | GAGCTCGT | AACTTTTCC | AGCAGAT | ATATCTG | GTGAG | ACTGCCAT | 408 |
| QY | 572 | AACATG | GTGTCCACC | GTGACCT | TAAAGCCG | AAAACTT | GTTACTG | ATTCAAG | 631 |
| | | | | | | | | | |
| Db | 409 | AATATG | GTGTCCAT | AGACCTGA | AGCTGAG | AATTTACT | ATTGATTC | GAGTGTAA | 468 |
| QY | 632 | GTTAAAC | CTTGCGATTTT | GGTCTG | AGCAATG | TCAATG | CAATG | CCATTTCTG | 691 |
| | | | | | | | | | |
| Db | 469 | ATTAA | GATTGCAG | ACTTTGGG | TGAGTAATG | TATCGG | GATGTCATTTCT | TAAGACG | 528 |
| QY | 692 | AGCTGTG | GAGAGTCCG | AACTATG | CTCTCC | AGAGGTAA | TATCTGTAA | CTATATG | 751 |
| | | | | | | | | | |
| Db | 529 | AGTTGTG | GAAGCCCC | CAACTAC | GTCTCTCC | GAGGTTAT | TATCAG | TAAATTATATG | 588 |
| QY | 752 | CCTGAGG | TGCATGTATG | AGTTGTGGG | GTGATCTTTAT | GCTCTCTT | GTGTGA | ACTCTT | 811 |
| | | | | | | | | | |
| Db | 589 | CTGAAG | TAGATGATG | AGTTGG | AGTTATAT | TGTACG | CTCTATTATG | CGGTACTCTT | 648 |
| QY | 812 | CCATTG | ATGATGAA | TATTTCC | AACTCTGTT | CAAAAAAT | TAAAGG | AGTATCT | 871 |
| | | | | | | | | | |
| Db | 649 | CCTTT | GATGATGA | AAAAACAT | TCCCACTTTT | CAAGAAAT | TAAAGG | GTGATTTAC | 708 |
| QY | 872 | CTTCCA | AGTCATTTGT | CTGCTTGG | CCAGGATTTG | ATCCCA | GAAATG | CTTGTGTTG | 931 |
| | | | | | | | | | |
| Db | 709 | CTTCCA | AGTCATTTAT | CACTGA | GGCTAG | AGACCTG | ATCCCA | GAGATGCTTATAG | 768 |
| QY | 932 | CCTATG | AGAAGATCA | CAATTAG | GGAATTCG | GAGCATCA | TGTTCC | AGATTCG | 991 |
| | | | | | | | | | |
| Db | 769 | CCGGT | GAAGCAATCA | CCATTC | CTGAGATCC | GTCA | CAACCG | TGTTC | 828 |
| QY | 992 | CCACG | TTACTTGG | CAGTGCC | TCCACAG | ATACGACA | CAACCAAG | CCAAATG | 1051 |
| | | | | | | | | | |
| Db | 829 | CTCTG | TATCTTGCTG | CTCTCC | ACCGATAC | AGTAG | AGCAGACT | TAAAGATCA | 888 |
| QY | 1052 | GATTA | CACTTCG | AGATGTTG | TAAATATG | GGAATTTAA | CAAGAAC | ATGTTG | 1111 |
| | | | | | | | | | |
| Db | 889 | GAGAT | AGTTCAAG | AGTGT | TAAATG | GGAATTTG | ATAGAA | CCAGTTT | 948 |
| QY | 1112 | TGCA | GCACTTCA | AAATGAG | CACTGTTG | CATATTAT | TTACTA | TTTGACA | 1171 |
| | | | | | | | | | |
| Db | 949 | CGCA | CAGAAC | ACAAACG | ATGCTACT | GTTCAT | ACTACCTG | TATTTG | 1008 |
| QY | 1172 | AGAG | CACTAGT | GGCTATCTT | GGGAGAT | TATCAAG | AATCAATG | ACAGAA | 1231 |
| | | | | | | | | | |
| Db | 1009 | CGTG | TCCAAAGT | GGCTATCT | AGATCCG | AGTTTCA | | | |

Db 1129 GATCACTACGGGTTGGAGACAGATCACAAGTCCCTGTGTATCGAAAAATGGCCTTTGGA 1188

Qy 1352 CTTCACTCTCGGCCCCACCCTCGTGAATAATGGTTGAGGCTTTAAAGCACTTCAAGAA 1411

Db 1189 CTTCACTCTCATGCGCATCTCTGTGAATCATGAATGAAGTTTGAAGCTTTCAAGAA 1248

Qy 1412 TTAAACGTGAGATGGAAGAAGATGGGCACTACAACGTGAATGCAGATGGTCCAGGG 1471

Db 1249 CTCATGTGTGTGGAGAAGATTGGTCACTACAACATGAATGTGATGGGTTCTGTGT 1308

Qy 1472 TTTCCCTGAAGTTAATGACACGTTAGATGCCAGCAACAGCTTCTTGTGACTCAACATC 1531

Db 1309 TTAGCTGATGTCAGAAATATCTATGTCACACATCAGCTGCACCTCAGAGATGAATCCAGC 1368

Qy 1532 ATGATATATGATGATGCTAATGGGAGGCTACCTACTGTGATCAAGTTTGAATTCCAGCTT 1591

Db 1369 ATCATTTGAGGATGACTGTGCCATGACTTCAACCACCTGTATCAAAATTGAACTTCAAGTA 1428

Qy 1592 TACAAGACGAAGACGACGACCAAGTACTTTAGATATGCAAGAGATTACTGGAACCTCAGCTG 1651

Db 1429 TACAAGACCCGGGGAAGAAGAGTACTTCTGTGATATACAGAGAGTTAACGGTCCGCAAGTTT 1488

Qy 1652 CTCTTCTTGAAGTTCTGTGCGGCTTCTTACCAAGCTTAGGGTTCTATATAGTGCTT 1708

Db 1489 CTCTTCTTGAAGTTATATGCGCGGCTTCTTACAGAGCTTCGTGTGATCTGAATGTTT 1545

| | |
|----|--|
| | RESULT 13 |
| ID | AAL46642 standard; cDNA; 1825 BP. |
| XX | |
| AC | AAL46642; |
| XX | |
| DT | 05-AUG-2002 (first entry) |
| XX | |
| DE | A thaliana AKIN1 mutant coding sequence. |
| XX | |
| KW | AKIN1; pathogen resistance; transgenic; plant; antibacterial; virucide; fungicide; nematocide; gene; mutant; ss. |
| KM | |
| XX | |
| OS | Arabidopsis thaliana. |
| XX | |
| FH | Key Location/Qualifiers |
| FT | CDS 1..1539 |
| FT | /tag= a |
| FT | /product= "AKIN1" |
| XX | |
| PN | WO200238780-A2. |
| XX | |
| PD | 16-MAY-2002. |
| XX | |
| PF | 07-NOV-2001; 2001MO-FR003457. |
| XX | |
| PR | 08-NOV-2000; 2000FR-00014354. |
| XX | |
| PA | (INRG) INRA INST NAT RECH AGRONOMIQUE. (CNRS) CENT NAT RECH SCI. |
| XX | |
| PI | Roby D, Balague C, Godard F, Lummerzhelm M; WPI; 2002-426954/45. P-PsDB; AA017664. |
| DR | |
| XX | |
| PT | Inducing or increasing resistance to pathogens in plants e.g. industrial scale flowers and vegetables, by introducing a nucleic acid that encodes the AKIN1 peptide. |
| XX | |
| PS | Example 4; Page 72; 76pp; French. |
| XX | |
| CC | The present invention relates to the use of a nucleic acid that causes the synthesis of the AKIN1 protein, to induce or increase the resistance to pathogen attack in plants. The nucleic acid and its encoded protein |

CC can be used to impart resistance to bacteria, viruses, fungi and
CC nematodes, especially necrotrophic pathogens such as Xanthomonas
CC campestris, in large-scale crops, vegetables and flowers. Probes and
CC primers that hybridise with the AKIN1 gene can be used to detect
CC resistance against pathogens, and antisense sequences can be used to
CC modulate resistance. The present sequence is a mutant version of the
CC AKIN1 cDNA of the invention

XX
SQ Sequence 1825 BP; 525 A; 329 C; 409 G; 562 T; 0 U; 0 Other;

Query Match 39.9%; Score 777; DB 6; Length 1825;

Best Local Similarity 69.9%; Pred. No. 1.8e-196;

Matches 1047; Conservative 0; Mismatches 450; Indels 0; Gaps 0;

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Oy 212 TTAAAGAACTACAACCTGGGAAGAACTTTAGGTATCGGTACATTGGAAAGTGAAGATT 271
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 49 TTACCGAATTACAAGCTTGTAAAACTCTTGAATTGGGTCTTTGGGAAGGTGAAAATA 108

Oy 272 GCAGAGCATAAAGCTTACTGACATAGGGTTGCTATAAAGATCATCAACTGCCCAATG 331
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 109 GCAGAGCATGTTGTCAAGGCATTAAGGTGTCTATCAAATCCTTAATGTCGTAAGATC 168

Oy 332 AGAATATGAAATGGAAGAGAAGCAAGAGAAATTCAGATATGGAAGTTGTCATT 391
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 169 AAGACATGAGATGGAAGAGAAGAGAGAGAGAGATTAAGATTCTACGGTTGTTATG 228

Oy 392 CACCCCATATCATTCGGCTTATGAGGTCAATATACACACCTACAGATATATGTTGTG 451
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 229 CATCCTCATATTAATTCGGCAGTATAGGTAATAGAGACCACGAGTGAACATTAATGTTG 288

Oy 452 ATGAATATTTGTAAGTATGCGGAGTATTTGATTACATTTGTTGAGAAAGCAGATTACAG 511
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Db 289 ATGAGTATGTCAAGTCTGAGAGCTCTTGTGATTATTTGTTGAGAAAGCAGATTACAA 348

Oy 512 GAAGATGAAGCTGTCGAATCTTCCAGCAGATCATATCTGCGTCGAATTACTGCCATAGA 571
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Db 349 GAAGATGAGGCTGCTAACTTTTCCAGCAGATAATATCTGTTAGAGTACTGCCATCGT 408

Oy 572 AACATGTTGTCACCGTGACCTAAAGCCGGAATACTGTTACTTGATCAAGTATAAT 631
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Db 409 AATATGTTGTCATAGAGACCTGAAGCCTGAAGATTACTATGATTCGAGGTGTAAT 468

Oy 632 GTAAACTTGGCATTTTGTGCTGAGCAATTCATGCATGATGCCATTTCTGAAGACT 691
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Db 469 ATTAAGATTGCAGACTTTGGGTGAGTAATGTTATCGGGATGTCATTTCTAAAGACG 528

Oy 692 AGCTGTGGAGTCCGAACATATGCTGCTCCAGAGGTAATATCTGTTAACTATATGCTGGA 751
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Db 529 AGTTGTGAAGCCCAACTACGCTGCTCCGAGGTTATATCAGGTAAATTATATGCTGGA 588

Oy 752 CCTGAGTGCATGTATGAGAGTGTGGGGTGATCTTTATGCTCTTCTTGTGAACCTCTT 811
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Db 589 CCTGAAGTATGATGATGAGAGTGGAGATTATGTAAGCTCTATTAATGCGTACTCTT 648

Oy 812 CCATTTGATGATGAGAATATTTCCCAATCTGTCAAAAAAATTAAAGAGGATATCTACACA 871
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Oy 872 CTTCCAAGTCAATTTGCTGCTTGGCCAGGATTTGATCCCAAGATGCTGTTGTTGAG 931
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Db 709 CTTCCAAGTCAATTTATCATCTGAGGCTAGAGACCTGATCCCAAGAGTCTTATAGTTGAC 768

Oy 932 CCTATGAAGAGAAATCACAATTAGGGAATTCGGAGCATCAATGTTCCAGATTGCGCTT 991
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Db 769 CCGGTGAAGCAATCAACCAATCTCTGAGATCGTCAACACCGTTGTTCCAGACTCATCTC 828

Oy 992 CCACGTTACTGGCAGTGCCTCCACACAGATACGACACAACAAGCCAAATGATGTAGAA 1051
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Oy 1052 GATACACCTTGAGATGTTGTTAATATGGGATTAAACAAGAACCATGTTGTGATCACTG 1111
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Oy 1112 TGCAGCAGACTTCAAAATGAGGCAACTGTTCATATTTACTATTGGACAATCGGTTT 1171
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Db 949 CGCAACAGAACACAAAACGATGCTACTGTACATACCTGTTATTGGATAACTGTTTC 1008

Oy 1172 AGAGCAACTAGTGCTATCTTGGGGCAGATTATCAAGAATCAATGACAGGAATTTAAT 1231
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Oy 1352 CTTCAGTCTCGGCGCCACCCTCGTGAATAATGTTGAGGTCTTAAAGCACTCAAGAA 1411
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Oy 1412 TTAACGTCAGATGGAAGAGATGGGCACTACAACGTTGAATGCGAGATGTCGCCAGGG 1471
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Db 1369 ATCATTTGAGATGACTGTGCCATGACTTCACCCACTGTCTATCAAAATTGAATTCAGCTA 1428

Oy 1592 TACAAGACGAAGCAGACAGCAATCTTATGATATGACAGAGTTAAGTCTGACCTCAGCTG 1651
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Db 1429 TACAAGCCCCGGGAAGAGAGTACTTCTGATATACAGAGGTTAAACGTCGCCAGTTT 1488

Oy 1652 CTCTTCTTGACTTCTGTGCGGCTTCTTACCAAGCTTAGGGTTCTATAGTGCTC 1708
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1489 CTCTTGTGATCTATGCGCGCTTCTTACAGAGCTTCGTGTGATCTGAATGTTT 1545

RESULT 14
AA171048
ID AA171048 standard; cDNA; 1539 BP.
XX
AC AA171048;
XX
DT 18-MAR-2002 (first entry)
XX
DE Arabidopsis SNF-1 protein kinase cDNA.
XX
KW SNF-1; protein kinase; transgenic plant; disease resistance; geminivirus;
KM stress resistance; crop protection; ss.
XX
OS Arabidopsis thaliana.
XX
FH
FH Key
FT CDS
FT 1.1531
FT /*tag= a
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FT /transl_except= (pos:223. .225, aa:Pro)
FT /transl_except= (pos:292. .294, aa:Arg)
FT /transl_except= (pos:610. .612, aa:Cys)
FT /transl_except= (pos:718. .720, aa:Lys)
FT /transl_except= (pos:751. .753, aa:Ala)
FT /transl_except= (pos:778. .780, aa:Ala)
FT /transl_except= (pos:922. .924, aa:Gly)
FT /transl_except= (pos:1108. .1110, aa:His)
FT /transl_except= (pos:1177. .1179, aa:Asn)
FT /transl_except= (pos:1183. .1185, aa:Lys)
FT /transl_except= (pos:1192. .1194, aa:Trp)
FT /transl_except= (pos:1198. .1200, aa:Lys)
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| | |
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| FT | /transl_except= (pos:1486. .1488, aa:Pro) |
| FT | /transl_except= (pos:1492. .1494, aa:Pro) |
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| FT | /*tag= b |
| FT | /note= "encodes Asp" |
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| FT | /*tag= c |
| FT | /note= "encodes Cys" |
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| XX | WO200111036-A1. |
| XX | |
| PD | 15-FEB-2001. |
| XX | |
| PF | 07-AUG-2000; 2000WO-US021624. |
| XX | |
| PR | 06-AUG-1999; 99US-0147613P. |
| XX | |
| PA | (OHIS) UNIV OHIO STATE RES FOUND. |
| XX | |
| PI | Bisaro D; |
| XX | |
| DR | WPI; 2002-113778/15. |
| DR | P-PSDB; AAM50578. |
| XX | |
| PT | Transforming plant cell useful to prepare plants with enhanced resistance |
| PT | to viral pathogen, by transforming cell with exogenous DNA fragment |
| PT | having polynucleotide encoding SNF-1 protein kinase or its catalytic |
| XX | domain. |
| PS | Example 1; Fig 1; 36pp; English. |

CC The presence sequence is that of cDNA encoding SNF-1 protein kinase (see
 CC AAM50578) of *Arabidopsis thaliana*. SNF-1 is a serine/threonine kinase
 CC that plays a key role in glucose sensing and signal transduction
 CC pathways. It also regulates enzymes involved in lipid metabolism. The SNF
 CC -1 cDNA was obtained in a yeast two-hybrid screen using a truncated
 CC tomato golden mosaic virus TRAP protein as bait and an *Arabidopsis* cDNA
 CC library as prey. The cDNA was recognised as encoding SNF-1 by virtue of
 CC its homology to yeast and tobacco SNF-1 and by its identity to previously
 CC cloned *Arabidopsis* SNF-1. A method of preparing plants with enhanced
 CC resistance to infection by plant pathogens involves transforming a plant
 CC cell with a SNF-1 transgene, i.e. a DNA construct encoding SNF-1 protein
 CC kinase or its catalytic domain. The DNA construct may include an
 CC inducible, constitutive or tissue-specific promoter, and the plant cell
 CC may be from a monocot or dicot. The transformed plant cell is used to
 CC generate a transgenic plant that shows enhanced resistance to plant
 CC pathogens, particularly viral pathogens (especially geminiviruses), and to
 CC abiotic stress. In an example, transgenic *Nicotiana benthamiana* plants
 CC overexpressing *Arabidopsis* SNF-1 kinase showed increased resistance to
 CC beet curly top virus compared with control plants
 CC
 XX
 SQ Sequence 1539 BP; 441 A; 289 C; 368 G; 439 T; 0 U; 2 Other;

| | | | | |
|----------------------------|--------|---------------------|-----------|--------------|
| Query Match | 39.9% | Score 776.6; | DB 6; | Length 1539; |
| Best Local Similarity | 70.0%; | Pred. No. 2.1e-196; | | |
| Matches 1043; Conservative | 0; | Mismatches 446; | Indels 0; | Gaps 0; |

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QY      212 TTAAGGACTACAACCTGGAGAACTTTAGGTATCGGTACATTGGAAAAGTGAAGATT 271
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Db      49  TTACCGAATTACAAGCTTGTGTAAAACTCTTGAATTGGGCTTTTGGGAAGGTGAATA 108
QY      272 GCAGAGCATTAAGCTTACTGACATAGGGTTCGTATAAAGATCATCAACTGCCGCAAAATG 331
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QY      332 AGAATATGGAATGGAAGAGAAGAAAGCAAGAGAGAATTCAAGATATTGAAGTTGTTCAAT 391
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Db      169 AAGAACATGAGATGGAAGAGAAGAAAGTAGAGGAGATTAAGATTCTACGGTTGTTATG 228
QY      392 CACCCCATATCATTCGGCTTTATGAGGTCAATACACACCTACAGATATATATGTTGTG 451
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| Qy | 452 | ATGGAATATTGTAAGTATGCGGAGTTATTGATTAATGTTGAGAAAGCAGATTACAG | 511 |
| Db | 289 | ATGAGTATGTCAGTCTGAGAGCTCTTGATTAATTGTTGAGAAAGCAGATTACAA | 348 |
| Qy | 512 | GAAGATGAAGCTCGTGAATCTTCCAGCAGATCATATCTGCGTGAATACTGCCATAGA | 571 |
| Db | 349 | GAAGATGAGCTCGTAACCTTTTCCAGCAGATTAATCTGGTGTAGAGTACTGCCATCGT | 408 |
| Qy | 572 | AACATGTTGTCCACCCTGACCTTAAAGCCGAAAATCTGTTACTTGATCAAAAGTATAAT | 631 |
| Db | 409 | AATATGTTGTCCATAGAGACCTGAAGCCTGAGAAATTTACTATTGGATTGAGGTGTAAT | 468 |
| Qy | 632 | GTAACCTTGCGGATTTTGGTCTGAGCAATGTCATGCATGATGGCCATTTCTGAAGACT | 691 |
| Db | 469 | ATTAGATTGAGANTTTGGGTGAGTAATGTATGCGGAGTGTCAATTTCTAAAGACG | 528 |
| Qy | 692 | AGCTGTGGAGTCCGAACTAAGCTGCTCCAGAGGTAATATCTGTAACATATATGCTGA | 751 |
| Db | 529 | AGTTGTGAGAGCCCACTACGCTGCTCCCGAGGTTATATCAGGTAATATATGCTGA | 588 |
| Qy | 752 | CCTGAGTTCGATGTATGAGATTGTGGGTGATTTCTTTATGCTCTTCTTGGGAAGCTTT | 811 |
| Db | 589 | CCTGAAGTAGATGTATGAGTTACGAGTTATATGTATACGCTCTATTTATGNGTACTCTT | 648 |
| Qy | 812 | CCATTTGATGATGAGAAATATCCCAATCTGTTCAAAAAATTAAAGGAGGTATCTACACA | 871 |
| Db | 649 | CCTTTTGATGATGAAAAACATTCCAACCTTTTCAAGAAAATTAAAGGTGGATTACACT | 708 |
| Qy | 872 | CTTCCAAGTCATTTGTCTGCTTTGGCCAGGAGATTGATCCACGAATGCTTGTGTTGAG | 931 |
| Db | 709 | CTTCCAAGTCATTTATCATCTGAGGCTAGAGACCTGATCCCAAGATGCTTATAGTTGAC | 768 |
| Qy | 932 | CCTATGAGAGAAATCACAAATTAGGGAATTCGGAGCATCAATGTTCCAGATTGCGCTT | 991 |
| Db | 769 | CCGCTGAACCAATCACCAATTCCTGAGATCCGCTCACACCGTTGGTTCCAGACTCATCTC | 828 |
| Qy | 992 | CCACGTTACTTGGCAGTGCCTCCACCAGATACGACACAACAAGCCAAAATGATTGATGA | 1051 |
| Db | 829 | CCTCGTTATCTTCTGCTCTCTCCACCGATACAGTAGAGCAGACTAAAAAAGATCAATGAG | 888 |
| Qy | 1052 | GATACACTTCAGAGATGTTGTTAATATGGGATTTAACAAGAACCATGTGTGTAATCACTG | 1111 |
| Db | 889 | GAGATAGTTCAAGAGTGTTAACATGGGATTTGATGAACCAAGCTTTGGAATCTCTA | 948 |
| Qy | 1112 | TGCAGCAGCTTCAAATGAGGCACTGTTGCATATTAATTACTATTGCAATCGGTTT | 1171 |
| Db | 949 | CGCAACAGAACACAAAACGATGCTACTGTTACATCTACCTGTTATTGATAACCGGTTT | 1008 |
| Qy | 1172 | AGAGCAACTAGTGGCTATCTTGGGGCAGATTATCAAGAAATCAATGACAGAAATTTAAT | 1231 |
| Db | 1009 | CGTGTTCAGAGTGGCTATCTAGAAATCCGAGTTTCAGSAGACAACAGACAGTGGCTCCAAT | 1068 |
| Qy | 1232 | CAGTGGCGTCATCTGAATCATCTAGTTCTGTGTAAGAGAAATTAATGTTCCAGGAACAGT | 1291 |
| Db | 1069 | CCTATGCGCACACCTGAAGCGGCGCTTCACTGTAGGCCAGTGATTCCTGCAATGTG | 1128 |
| Qy | 1292 | GATCCTCATAGCAGTGTGTTGGGCCATATTAATCCGTGTGAAAAGAAAATGGCGCTTGA | 1351 |
| Db | 1129 | GATCATCTACGGGTTGGAGCAGATCACAAAGTCCCTGTGTTGATCGAAAATGGGCTCTTGA | 1188 |
| Qy | 1352 | CTTCAAGTCTGGGGCCCAACCTGCTGTAATTAATGTTGAGGTCTTAAAAGCACTTCAAGAA | 1411 |
| Db | 1189 | CTTCAAGTCTGATCGCATCTCTGTGAATCATGAATGAAGTTTGAAGCTCTTCAAGAA | 1248 |
| Qy | 1412 | TTAAACGTGAGATGGAAGAAATGGGCACTACAACGTGAATGAGATGTTGCCAGGG | 1471 |
| Db | 1249 | CTCAATGTGTGTTGGAAGAAATGGTCACTACAACATGAATGTCGATGGGTTCTGTT | 1308 |
| Qy | 1472 | TTTCTGTAAGTAAATGACACGTTAGATGCCAGCAACAGCTTCTTGATGCTACCATC | 1531 |
| Db | 1309 | TTAGCTGATGTCAGAAATCTATGTTCAACAATCAGTCTGCACTTCAGAGATGAATCCAGC | 1368 |


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Db      1205 ATCAAGGGTAAGAAATGCGGCAACAGTTCCTGTGAGAGAAATGGGCCCTTGGGCTTC 1264
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Db      1265 AGTCTCGAGCCCAACCAAGTGAATATGACTGAGGCTCTTAAGCTCTACAAGAAATTAA 1324
QY      1416 ACGTCAGATGGAAGAAGATGGGCACTTACACGTGAATATGAGATGGTGCCCAAGGTTTC 1475
Db      1325 ATGTTTGTGGAAGAAGATTGACACATTAACATGAAGTGCAGATGGGTGCTGGCACTG 1384
QY      1476 CT-----GAAGTTAATGACACGTTAGATGCCAGCAACAGCTTTCTTGGTGA 1523
Db      1385 CTGTCATCATGAAGAAGATGATTAACTTCTCTGATAGTAATCATTACTTTGAAATG 1444
QY      1524 CTACCATCATGATTAATGATGATGCTTAATGGAGGCTTACCTACTGTGATCAAGTTGAAT 1583
Db      1445 ATTCGGGCAATTAATGAATAATGAAGCTGTTCTAAG--TCAAATGTGGTCAAGTTGAAG 1501
QY      1584 TCCAGCTTTACAGACGAAGACGACCAAGTACCTCTTAGATATGACAGAGTTACTGAC 1643
Db      1502 TGCAGCTTTACAAAACCTCGTAGAGAGAAATATCTGCTTGATCTTCAAAGGCTCCAGGGCC 1561
QY      1644 CTCAGCTGCTCTTCTTGACTTCTGTCGGGCTTCTTACCAAGCTTAGGGTCTATAGT 1703
Db      1562 CACAGTTTCTTTCTTGATCTGTGCGCTGCTTCTTTCACAGCTACGTGTTCTCTAGT 1621
QY      1704 G 1704
Db      1622 G 1622

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Search completed: July 9, 2004, 11:38:16
 Job time : 841 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 10:15:14 ; Search time 5184 Seconds
(without alignments)
11221.360 Million cell updates/sec

Title: US-09-857-522B-3

Perfect score: 1948
Sequence: 1 gtcgaccacgcgtccgac.....taaaaaaaaaaaaaaaaa 1948

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estcin:*
4: em_estmu:*
5: em_estcov:*
6: em_estpl:*
7: em_estro:*
8: em_hnc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hnc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
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21: em_gss_fun:*
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23: em_gss_mus:*
24: em_gss_pro:*
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26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1948 | 100.0 | 1948 | 11 | AY107942 Zea mays |
| 2 | 734 | 37.7 | 904 | 14 | CA272308 SCVPLB208 |
| 3 | 634.6 | 32.6 | 690 | 13 | CA076858 SCMCAM110 |
| 4 | 632.6 | 32.5 | 784 | 14 | CB620008 OSIEa040 |

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| 5 | 618.6 | 31.8 | 674 | 13 | CA077133 SCQCAM104 |
| 6 | 606.8 | 31.1 | 650 | 13 | CA125391 SCRRLR101 |
| 7 | 604.4 | 31.0 | 676 | 14 | CF574471 MCSA115H0 |
| 8 | 598.8 | 30.7 | 782 | 14 | CB659701 OSUNEc160 |
| 9 | 593 | 30.4 | 956 | 13 | CA149321 SCJLR2102 |
| 10 | 592.8 | 30.4 | 597 | 9 | AW091047 614070C04 |
| 11 | 589.2 | 30.2 | 863 | 12 | BI950083 HVSME1001 |
| 12 | 589 | 30.2 | 1391 | 11 | AY112453 Zea mays |
| 13 | 586.8 | 30.1 | 850 | 14 | CB632244 OSIEb10F |
| 14 | 584.2 | 30.0 | 794 | 13 | BQ805778 WHE3570_H |
| 15 | 578 | 29.7 | 829 | 14 | CB621531 OSIEa07H |
| 16 | 571.4 | 29.3 | 862 | 14 | CK195998 FGAS00444 |
| 17 | 565.4 | 29.0 | 704 | 14 | CF307150 HDA1--05- |
| 18 | 561.2 | 28.8 | 682 | 14 | CD223882 CCC1_30_C |
| 19 | 559.8 | 28.7 | 572 | 9 | AW018231 614070C04 |
| 20 | 558 | 28.6 | 736 | 14 | CD423640 SAI_24_D1 |
| 21 | 546 | 28.0 | 596 | 14 | CA271697 SCMLB208 |
| 22 | 545 | 28.0 | 733 | 14 | CD938346 OV.109M09 |
| 23 | 532.6 | 27.3 | 547 | 9 | AI740056 605070C04 |
| 24 | 531.2 | 27.3 | 659 | 14 | CD223772 CCC1_30_C |
| 25 | 525.8 | 27.0 | 641 | 12 | BJ292522 BJ292522 |
| 26 | 523.6 | 26.9 | 753 | 14 | CB669005 OSUNEe01C |
| 27 | 522.8 | 26.8 | 675 | 14 | CA256476 SCSGFL419 |
| 28 | 521.2 | 26.8 | 728 | 14 | CD938735 OV.110M12 |
| 29 | 515.6 | 26.5 | 699 | 14 | CD872331 AZO2.120G |
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| 41 | 478.2 | 24.5 | 743 | 14 | CA219136 SCRFAD111 |
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| 43 | 477 | 24.5 | 819 | 14 | CK199874 FGAS00838 |
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| 45 | 473.6 | 24.3 | 684 | 13 | CA072415 SCEPAM101 |

ALIGNMENTS

RESULT 1
AY107942 1948 bp mRNA linear HTC 16-OCT-2002
LOCUS
DEFINITION Zea mays PCO079657 mRNA sequence.
ACCESSION AY107942
VERSION AY107942.1 GI:21211020
KEYWORDS
SOURCE
ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1948)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA

COMMENT
If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZMDB: www.zmdb.iastate.edu.

FEATURES

source

location/Qualifiers

1..1948

/organism="Zea mays"

/mol_type="mRNA"

/db_xref="MaizeDB:634435"

/db_xref="taxon:4577"

/clone_lib="Maize Mapping Project/DuPont Cornsensus library"

/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 100.0%; Score 1948; DB 11; Length 1948;

Best Local Similarity 100.0%; Pred. No. 9.2e-287;

Matches 1948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTCGACCCACGCGTCGGAGCCAAAGCCGGGATACGCCCCCAAGTCCAAAAGCCCTCTCC 60
Db 1 GTCGACCCACGCGTCGGAGCCAAAGCCGGGATACGCCCCCAAGTCCAAAAGCCCTCTCC 60
QY 61 GCCCCGCTCTCCACTCGTAGGTGTTCTCCCGCTCTCCGCGGACACTGCTCGTCCGCG 120
Db 61 GCCCCGCTCTCCACTCGTAGGTGTTCTCCCGCTCTCCGCGGACACTGCTCGTCCGCGC 120
QY 121 GCAGGAAGTTGACCTGTGAGGGCCGCGCAACCCGGTAAGTAAGTGAAGTAAGTGAAGT 180
Db 121 GCAGGAAGTTGACCTGTGAGGGCCGCGCAACCCGGTAAGTAAGTGAAGTAAGTGAAGT 180
QY 181 AAGTAGTAAGGAGTGGGCACTTGAAGCATTAAGAACTACAACCTGGGAAGAACTTT 240
Db 181 AAGTAGTAAGGAGTGGGCACTTGAAGCATTAAGAACTACAACCTGGGAAGAACTTT 240
QY 181 AAGTAGTAAGGAGTGGGCACTTGAAGCATTAAGAACTACAACCTGGGAAGAACTTT 240
Db 181 AAGTAGTAAGGAGTGGGCACTTGAAGCATTAAGAACTACAACCTGGGAAGAACTTT 240
QY 241 AGGTATCGGTACATTTGGAAGTGAAGATTGCAGAGCATTAAGCTTAAGCTTACATAGG 300
Db 241 AGGTATCGGTACATTTGGAAGTGAAGATTGCAGAGCATTAAGCTTACATAGG 300
QY 301 TGCTATAAAGATCATCACTGCCGCCAAATGAGAAATATGGAATGGAAGAAAGCAAA 360
Db 301 TGCTATAAAGATCATCACTGCCGCCAAATGAGAAATATGGAATGGAAGAAAGCAAA 360
QY 361 GAGAGAATTCAAGATATTTGAAGTTGTTCAATCAACCCCATATCATTCGGCTTTATGAG 420
Db 361 GAGAGAATTCAAGATATTTGAAGTTGTTCAATCAACCCCATATCATTCGGCTTTATGAG 420
QY 421 CATATACACACCTACAGATATATGTTGATGGAATATTTGAAGTAAGTGAAGTAT 480
Db 421 CATATACACACCTACAGATATATGTTGATGGAATATTTGAAGTAAGTGAAGTAT 480
QY 481 TGATTACATTTGGAAGAGCAGATTACAGAAAGATGAAGCTCGTCAATCTTCCAGCA 540
Db 481 TGATTACATTTGGAAGAGCAGATTACAGAAAGATGAAGCTCGTCAATCTTCCAGCA 540
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Db 541 GATCATATCTGGCGTGAATACTGCCATAGAAACATGGTGTCCACCGTGAACCTAAAGCC 600
QY 601 GGAAGAACTTGTTACTGATTCAAGATATATGTAAGAACTTGCGGATTTGGTCTGAGCAA 660
Db 601 GGAAGAACTTGTTACTGATTCAAGATATATGTAAGAACTTGCGGATTTGGTCTGAGCAA 660
QY 661 TGTGATGATGATGAGCCATTTTCTGAAGACTAGCTGTGGAGTCCGAACATATGCTGCTCC 720
Db 661 TGTGATGATGATGAGCCATTTTCTGAAGACTAGCTGTGGAGTCCGAACATATGCTGCTCC 720
QY 721 AGAGTAATATCTGTAAGCTATATGCTGAGCTGAGTGAATGAGTGTGGGGT 780
Db 721 AGAGTAATATCTGTAAGCTATATGCTGAGCTGAGTGAATGAGTGTGGGGT 780

Db 721 AGAGTAATATCTGTAAGCTATATGCTGAGCTGAGTGAATGAGTGTGGGGT 780
QY 781 GATTCTTTATGCTCTTCTTTGGAACTCTTCCATTTGATGATGAGAAATATTTCCCAATCT 840
Db 781 GATTCTTTATGCTCTTCTTTGGAACTCTTCCATTTGATGATGAGAAATATTTCCCAATCT 840
QY 841 GTTCAAAAAAATTAAAGGAGGTATCTACACACTTCCAAAGTCATTTGTCTTGGCCAG 900
Db 841 GTTCAAAAAAATTAAAGGAGGTATCTACACACTTCCAAAGTCATTTGTCTTGGCCAG 900
QY 901 GGATTGATCCACGAATGCTGTGTTGAGCCTATGAGAGAAATCACAAATTAGGAAAT 960
Db 901 GGATTGATCCACGAATGCTGTGTTGAGCCTATGAGAGAAATCACAAATTAGGAAAT 960
QY 961 TCGGAGCATCAATGTTCCAGATTCCGCTTCCACGTTACTTGGCAGTGCCCTCCACCAGA 1020
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QY 1021 TACGACACAACAAGCCAAATGATGATGAAGATACATTGAGATGTTGTTAATATGCG 1080
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QY 1081 ATTTAACAAGAACCATGTGTGTAATCACTGTGACAGCAGACTTCAAAATGAGGCAACTGT 1140
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QY 1141 TGCAATTAATTTACTATTGAGCAATCGGTTAGAGCAACTAGTGCTATCTTGGGCGAGA 1200
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QY 1261 TGGTACGAGGAATTATGTTCCAGAGAGCAGTATCCTCATAGCAGTGCTTGGCGCCATA 1320
Db 1261 TGGTACGAGGAATTATGTTCCAGAGAGCAGTATCCTCATAGCAGTGCTTGGCGCCATA 1320
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Db 1321 TTATCTGTTGAAAAGAAAATGGGCGCTTGACCTCAGTCTTGGGCCCAACCTCGTGAAT 1380
QY 1381 AATGTTGAGGCTCTTAAAAGCACTTCAAGAATTAAACGTGATGGAAGAAATGGGCA 1440
Db 1381 AATGTTGAGGCTCTTAAAAGCACTTCAAGAATTAAACGTGATGGAAGAAATGGGCA 1440
QY 1441 CTACAAGTGAATGAGATGAGTGGCCAGGGTTCTGAAGTTAATGACACGTTAGATGC 1500
Db 1441 CTACAAGTGAATGAGATGAGTGGCCAGGGTTCTGAAGTTAATGACACGTTAGATGC 1500
QY 1501 CAGCAACAGCTTTCTTGGTACTCTACCATCATGATGAATATGATGCTAATGGAGGCT 1560
Db 1501 CAGCAACAGCTTTCTTGGTACTCTACCATCATGATGAATATGATGCTAATGGAGGCT 1560
QY 1561 ACCTACTGTGATCAAGTTTGAATTCAGCTTTACAAAGACGAAAGCAAGTACCTCTT 1620
Db 1561 ACCTACTGTGATCAAGTTTGAATTCAGCTTTACAAAGACGAAAGCAAGTACCTCTT 1620
QY 1621 AGATATGAGAGAGTTACTGACCTCAGCTGCTCTTCTGACTCTGCTGCGGCTTCTCT 1680
Db 1621 AGATATGAGAGAGTTACTGACCTCAGCTGCTCTTCTGACTCTGCTGCGGCTTCTCT 1680
QY 1681 TACCAAGCTTAGGGTTCTATAGTGTCTACCATGTGCAAAATTTCACTGTGTGATGAAT 1740
Db 1681 TACCAAGCTTAGGGTTCTATAGTGTCTACCATGTGCAAAATTTCACTGTGTGATGAAT 1740
QY 1741 AACCGAAGCATGTAATAAGAACTTGTCTCGTCTTTGACAACGAACATGTTGAG 1800
Db 1741 AACCGAAGCATGTAATAAGAACTTGTCTCGTCTTTGACAACGAACATGTTGAG 1800
QY 1801 TGACTGTCTTGTGTGAGCGCGTAAGGTCATGTATACTTAGGTTAGTACTATTTTCTGT 1860
Db 1801 TGACTGTCTTGTGTGAGCGCGTAAGGTCATGTATACTTAGGTTAGTACTATTTTCTGT 1860

| QY | 1861 | TCTTAATATTTTGTGCTGCTAGTAGTATAGTTCATTTTGAAGCTAAACGTTACGAATTA | 1920 |
|------------|--|---|-----------------|
| Db | 1861 | TCTTAATATTTTGTGCTGCTAGTAGTATAGTTCATTTTGAAGCTAAACGTTACGAATTA | 1920 |
| QY | 1921 | AAAAAGAGTAAAAAAAAAAAAAAAAAAAAA | 1948 |
| Db | 1921 | AAAAAGAGTAAAAAAAAAAAAAAAAAAAAA | 1948 |
| RESULT 2 | | | |
| LOCUS | CA272308 | 904 bp | mRNA |
| DEFINITION | SCVPLB2089A09.g LB2 Saccharum officinarum cDNA clone SCVPLB2089A09 | | EST 26-SEP-2003 |
| ACCESSION | CA272308 | | |
| VERSION | CA272308.1 | | GI:35983605 |
| KEYWORDS | EST. | | |
| SOURCE | Saccharum officinarum | | |
| ORGANISM | Saccharum officinarum | | |
| REFERENCE | | | |
| AUTHORS | Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. | | |
| TITLE | The libraries that made SUCEST | | |
| JOURNAL | Genet. Mol. Biol. 24 (1-4), 1-7 (2001) | | |
| COMMENT | Contact: Arruda P | | |

Email: parnuda@unicamp.br
 Clone distribution: [clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center \(BCCC\) at http://www.bcccenter.fcav.unesp.br](http://www.bcccenter.fcav.unesp.br)
 plates: 089 row: A column: 09
 Seq primer: T7 Promoter Primer.

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source | 1. .904 |

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/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCVPLB2089A09"
/lab_host="DH10B"
/clone_lib="LB2"
/note="Organ: lateral buds from plants adult plants
growing in greenhouse; Vector: pSport1; Site_1: SalI;
Site_2: NotI; An unidirectional cDNA library generated
from [lateral buds from plants adult plants growing in
greenhouse]. cDNA was prepared from polyA+ mRNA using
Superscript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://succest.lad.ic.unicamp.br/public"

```

ORIGIN

| | | | | |
|---------------------------|-------|---------------------|-----------|-------------|
| Query Match | 37.7% | Score 734; | DB 14; | Length 904; |
| Best Local Similarity | 91.2% | Pred. No. 3.4e-102; | | |
| Matches 812; Conservative | 0; | Mismatches 75; | Indels 3; | Gaps 3; |

| | | | |
|----|-----|---|-----|
| QY | 392 | CACCCCATATCATTCGGCTTTATGAGGTCATATACACACCCTACAGATATATATGTTGTG | 451 |
| | | | |
| Db | 4 | CACCCCATATCATTCGGCTTTATGAGGTCATATACACACCACAGATATATATGTTGTG | 63 |
| QY | 452 | ATGGAATATTTGTAAGTATGGCGAGTTATTTGATTACATTGTTGAGAAAGGCAGATTACAG | 511 |
| | | | |
| Db | 64 | ATGGAATATTTGAGAGTATGGCGAGTTGTTGATTACATTGTTGAGAAAGGCAGATTACTA | 123 |
| QY | 512 | GAGATGAAGCTCGTGAATCTTCCAGCAGATCATATCTGGCGTGAATACTGCCATAGA | 571 |

| | | | |
|----|------|---|------|
| Db | 124 | G A A G A T G A G G C T C G C C G C A T C T T C C A G C A G A T C A T A T C T G G T G C G A A T A C T G C A T A G A | 183 |
| QY | 572 | A A C A T G T T G T C C A C C G T G A C C T T A A G C C G A A A C T T G T A C T T G A T T C A A G T A T A T | 631 |
| Db | 184 | A A C A T G T T G T C C A C C G T G A C C T T A A G C C A G A A A C T T G T A C T T G A T T C A A G T A T A T | 243 |
| QY | 632 | G T A A A A C T T G C G G A T T T T G G T C T G A G C A A T G T C A T G C A T G A T G C C A T T T T C T G A A G A C T | 691 |
| Db | 244 | G T A A A A C T T G C T G A C T T T T G G T T T G A G C A A T G T C A T G C A T G A T G C C A T T T T T T G A A G A C C | 303 |
| QY | 692 | A G C T G T G G A G T C C G A A C T A T G C T G C T C C A G A G T A A T A T C T G T A A C T A T A T G C T G A | 751 |
| Db | 304 | A G C T G T G G A G T C C G A A C T A T G C T G C T C C A G A G T A A T A T C T G T A A C T A T A T G C T G A | 363 |
| QY | 752 | C C T G A G G T C G A T G T A T G A G A G T T G T G G G G T A T T C T T A T G C T C T T T T G T G A A C T C T T | 811 |
| Db | 364 | C C T G A G G T C G A T G T A T G A G A G T T G T G A G A T G A T C C T T A T G C T C T T T T G T G A A C T C T T | 423 |
| QY | 812 | C C A T T T G A T G A T G A G A A T A T T C C C A A T C T G T T C A A A A A A A T T A A G G A G A G T A T C T A C A | 871 |
| Db | 424 | C C A T T T G A T G A T G A G A A T A T T C C C A A C C T G T T C A A A A A A A T T A A G G A G A G T A T C T A C A | 483 |
| QY | 872 | C T T C C A A G T C A T T T G T C T G C T T T T G G C C A G G A T T G A T C C C A G A A T G C T T G T T G A G | 931 |
| Db | 484 | C T T C C A A G T C A T T A T C T G C T T T G G C T A G G A T T G A T C C C A G A A T G C T T G T T G T C G A G | 543 |
| QY | 932 | C C T A T G A G A G A A T C A C A A T T A G G G A A T T C G G A C A T C A A T G S T T C C A G A T T C G C C T T | 991 |
| Db | 544 | C C T A T G A G A G A A T C A C A A T T C G G G A A T T C G G A G A C A T C A A T G S T T C C A G A C T C G C C T T | 603 |
| QY | 992 | C C A C G T T A C T T G G C A G T G C C T C C A C C A G A T A C G A C A C A C A A G C C A A A A T G A T T G A T G A A | 1051 |
| Db | 604 | T C T C G T T A C T T G G C A G T G C C T T C A C C A G A C A C G A C A C A A G C C A A A A T G A T T G A T G A A | 663 |
| QY | 1052 | G A T A C A C T T C G A G A T G T T G T A A T A T A T G G A T T T A A C A A G A A C C A A T G T G T G A A T C A C T G | 1111 |
| Db | 664 | G A T A C A C T T C G A G A T G - T G S T A A T A T G G A T T A A C - A G A A C C A T G T G A A A T C - C T G | 720 |
| QY | 1112 | T G C A G C A G A C T T C A A A A T G A G G C A A C T G T T G C A T A T T A T T A C T A T T G A C A A T C G G T T T | 1171 |
| Db | 721 | T G C A C C A A A C T T A A A A A T G A G G C A A C T G T G C A T A T T A T T A C T A T T G A C A A T T G G T T A | 780 |
| QY | 1172 | A G A G C A A C T A G T G G C T A C T T T G G G C A G A T T A T C A A G A A T C A A T G C A C A G A A T T A A T | 1231 |
| Db | 781 | A A A G C A A C T A G T G G C T T T T T T G G G C C G A A T T T C A A A A A T C A A G G G C C A G A A T T T T A A A | 840 |
| QY | 1232 | C A G C T G G C G T C A T C T G A A T C A T C T A G T T C T G T A C G A G A A T T A T G T T C C | 1281 |
| Db | 841 | T T A C T G G C G G G G C C A A A T A A T T A A T T T T T T G G C C A A G A A A T T T T T T T C | 890 |

RESULT 3
CA076858

| LOCUS | CA076858 | 690 bp | mRNA | linear | EST 23-SEP-2003 |
|------------|---|--------|------|--------|-----------------|
| DEFINITION | SCMCAM1105D1.1.g AML Saccharum officinarum cDNA clone SCMCAM1105D1.5', mRNA sequence. | | | | |

VERSION CA076858.1 GI:34929119

SOURCE

ORGANISM

Saccharum officinarum
Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum.

REFERENCE 1 (bases 1 to 690)

AUTHORS Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

TITLE The libraries that made SUCEST

JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

COMMENT

Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil

| | | | |
|----|------|---|------|
| Db | 181 | GAAGATGAGGCTGCCCGAATCTTCCAGACGATATATCTGGGGTAGAATACTGCCACAGA | 240 |
| Qy | 572 | AACATGTTGTCACCGTGACCTAAAGCCGGAAAACTTGTACTTGAATCAAGTATAT | 631 |
| Db | 241 | AACATGGTGGTTCATCGTATCTGAAGCCAGAAAACTGTACTGATTCAAAGTATAT | 300 |
| Qy | 632 | GTAACCTTGGCGATTTTGTCTGAGCAATGTCATGATGGCCATTTTCTGAAGACT | 691 |
| Db | 301 | GTAAGCTTGGTGAATTTGGTTGAGTAACGTCATGATGGCCATTTTGAAGACA | 360 |
| Qy | 692 | AGCTGTGGAGTCCGAACCTATGCTGCCAGAGTAATATCTGTAACCTATATGCTGA | 751 |
| Db | 361 | AGCTGTGGAGTCCAAACTATGCTGCCAGAGTATCTGTAAATTATATGCTGA | 420 |
| Qy | 752 | CCTGAGTGCATGTATGAGAGTGTGGGGTGAATCTTATGCTCTCTTGTGAACTCT | 811 |
| Db | 421 | CCTGAGGTTGATGTATGAGAGCTGTGAGTGAATCTTATGCTCTCTTGTGAACTCT | 480 |
| Qy | 812 | CCATTGATGATGAGAAATATTTCCCAATCTGTTCAAAAAATTAAAGGAGTATCTACA | 871 |
| Db | 481 | CCATTGATGATGAGAAATATTTCCCAACCTATTCAAAAAGATAAGGGTATATATACT | 540 |
| Qy | 872 | CTTCCAAAGTCATTTGTCTGCTTTGGCCAGGATTGATCCCAAGATGCTGTGTGAG | 931 |
| Db | 541 | CTCCCAAGTCATTTATCTGCTCTGCGCAGAGATTGATCCCAAGATGCTGTGTGAT | 600 |
| Qy | 932 | CCTATGAAGAAATCACAATTAGGAAATTCGGAGCATCAATGGTTCCAGATTGCGCTT | 991 |
| Db | 601 | CCAATGAAGAAATCACAATTCTGAAATTGAGAGCATCAGTGGTTCCAGATTGCGCTT | 660 |
| Qy | 992 | CCACGTTACTTGGCAGTGCCTCCACCAGATACGACACACAAGCCAAATGATTGATGA | 1051 |
| Db | 661 | CCTCGTACTTACGAGTGCCTCCACCAGACACACAGCAAGCCAAATGATTGATGA | 720 |
| Qy | 1052 | GATACACTTTCGAGATGTTTATATGCGATTAAACAAGAACATGTGTGTAATCACTG | 1111 |
| Db | 721 | GATACCTTTCAGATGTCTGTAACCTTGGGTTATGAAAAAGACCATGTGTGTAATCTCTG | 780 |
| Qy | 1112 | TGCA 1115 | |
| Db | 781 | CGCA 784 | |

RESULT 5
CA077133 674 bp mRNA linear EST 23-SEP-2003
LOCUS SCQAM1048C02.g AML Saccharum officinarum cDNA clone SCQAM1048C02
DEFINITION 5', mRNA sequence.
ACCESSION CA077133
VERSION CA077133.1 GI:34929405
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 674)
REFERENCE
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: paruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 048 row: C column: 02
Seq primer: T7 Promoter Primer.

| FEATURES | location/Qualifiers |
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| source | 1. .674 /organism="Saccharum officinarum" /mol_type="mRNA" /db_xref="taxon:4547" /clone="SCQAM1048C02" /lab_host="DH10B" /clone_lib="AM1" /note="Organ: Apical meristem and tissues surrounding of mature plants; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [apical meristem and tissues surrounding of mature plants]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public " |

| | | | |
|----|------|---|------|
| Qy | 899 | AGGATTTGATCCACGAATGCTGTGTGAGCCTATGAAGAGAAATCAATTAGGAA | 958 |
| Db | 1 | AGGATTTGATCCACGAATGCTGTGTGAGCCTATGAAGAGAAATCAATTGCGAA | 60 |
| Qy | 959 | ATTGGGAGATCAATGTTCCAGATTGCGCTTCCAGCTTACTTGGCAGTGCCTCCACCA | 1018 |
| Db | 61 | ATTGGGAGATCAATGTTCCAGACTCGCTTCTCTTACTTGGCAGTGCCTCCACCA | 120 |
| Qy | 1019 | GATACGACAAACAAGCCAAATGATTGATGAAGATACACTTCCAGATGTTGTAATATG | 1078 |
| Db | 121 | GACACGACACAGCAAGCCAAATGATTGATGAAGATACACTTCCAGATGTTGTAATATG | 180 |
| Qy | 1079 | GGATTTAACAAGAACCATGTGTGTGAATCACTGTGCAGCAGACTTCAAAATGAGCAACT | 1138 |
| Db | 181 | GGATTTAACAAGAACCATGTGTGTGAATCACTGTGCAGCAGACTTCAAAATGAGCAACT | 240 |
| Qy | 1139 | GTTGCATATTATTACTATTGGACAATCGGTTAGAGCAACTAGTGCTATCTTGGGGCA | 1198 |
| Db | 241 | GTTGCATATTATTACTATTGGACAATCGGTTAGAGCAACTAGTGCTATCTTGGGGCA | 300 |
| Qy | 1199 | GATTATCAAGAAATCAATGAGCAGAAATTAATCAGCTGCGCTCATCTGAATCATCTAGT | 1258 |
| Db | 301 | GATTATCAAGAAATCAATGAGCAGAAATTAATCAGCTGCGCTCATCTGAATCATCTAGT | 360 |
| Qy | 1259 | TCTGTACGAGAAATATATGTTCCAGAACAGTGAATCCTCATAGCAGTGTGCGGCCA | 1318 |
| Db | 361 | TCTGTACGAGAAATATATGTTCCAGAACAGTGAATCCTCATAGCAGTGTGCGGCCA | 420 |
| Qy | 1319 | TATTATCTGTGAAAAAATGGGCGCTTGGAATCACTGCTGCGGCCCACTCGTGAA | 1378 |
| Db | 421 | CATTATCTGTGAAAAAATGGGCGCTTGGAATCACTGCTGCGGCCCACTCGTGAA | 480 |
| Qy | 1379 | ATAATGTTGAGGCTTTAAAGCACTTCAAGAAATTAACGTCAGATGGAAGAAATGGG | 1438 |
| Db | 481 | ATAATGTTGAGGCTTTAAAGCACTTAAAGAAATTAACGTCAGATGGAAGAAATGGG | 540 |
| Qy | 1439 | CACTACAACGTGAATGAGATGTCGCCAGAGTTTCTGAAGTTAATGACACGTTAGAT | 1498 |
| Db | 541 | CACTACAACGTGAATGAGATGTCGCCAGAGTTTCTGAAGTTAATGACACGTTAGAT | 600 |
| Qy | 1499 | GCCAGCAACGCTTCTTGTGACTCTAACCATCATGATGAATAATGATGCTAATGGG | 1555 |
| Db | 601 | GCCAGCAACGCTTCTTGTGACTCTAACCATCATGATGAATAATGATGCTAATGGG | 657 |

RESULT 6
CA125391 650 bp mRNA linear EST 24-SEP-2003
LOCUS CA125391

DEFINITION SCRLR1016D04.9 LRI Saccharum officinarum cDNA clone SCRLR1016D04
5' mRNA sequence.

ACCESSION CA125391
VERSION CA125391.1 GI:35003253
KEYWORDS EST.

SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.

REFERENCE 1 (bases 1 to 650)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

JOURNAL Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: paruda@unicamp.br

COMMENT Clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 016 row: D column: 04
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. 650
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/clone="SCRLR1016D04"
/lab_host="DH10B"
/clone_lib="LRI"
/note="Organ: Leaf roll from field grown adult plants
(large insert library); Vector: pSport1; Site 1: SalI;
Site 2: NotI; An undirectional cDNA library generated
from [leaf roll from field grown adult plants (large
insert library)]. cDNA was prepared from polyA+ mRNA
using Superscript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN

Query Match 31.1%; Score 606.8; DB 13; Length 650;
Best Local Similarity 95.8%; Pred. No. 8.6e-83;
Matches 623; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

QY 901 GGATTGATCCAGCAATGCTTGTGTGAGCCTATGAGAGAAATCAATTAGGAAT 960
|||||
DB 1 GGATTGATCCAGCAATGCTTGTGTGAGCCTATGAGAGAAATCAATTAGGAAT 60
|||||

QY 961 TCGGAGCATCAATGCTTCCAGATTCGCTTCCACGTTACTTGGAGTGCTCCACCAGA 1020
|||||
DB 61 TCGGAGCATCAATGCTTCCAGATTCGCTTCCACGTTACTTGGAGTGCTCCACCAGA 120
|||||

QY 1021 TAGCACACAAGCCAAATGATGATGAGATACACTTCGAGATGTTGTTAATATGGG 1080
|||||
DB 121 CACGACACAGCAAGCCAAATGATGATGAGATACACTTCGAGATGTTGTTAATATGGG 180
|||||

QY 1081 ATTTAACAAGAACATGTGTGTGATCACTGTGACGACGACTTCAAAATGAGGCAACTGT 1140
|||||
DB 181 ATTTAACAAGAACATGTGTGTGATCACTGTGACGACGACTTCAAAATGAGGCAACTGT 240
|||||

QY 1141 TGCATATTTACTATTGACCAATCGTTTGAAGCAACTAGTGGCTATCTTGGGCGAGA 1200
|||||
DB 241 TGCATATTTACTATTGACCAATCGTTTGAAGCAACTAGTGGCTATCTTGGGCGAGA 300
|||||

QY 1201 TTATCAAGATCAATGACAGGAATTTAAATCAGCTGGCGTCATCTGAATCATCTAGTTC 1260
|||||

DB 301 TTATCAAGATCAATGACAGGAATTAAATCAGCTGGCGTCTCCGAATCATCTAGTTC 360
|||||

QY 1261 TGGTACGAGGAATTATGTTCCAGGAAGCAGTATCTCTATAGCAGTGTGGCGCCATA 1320
|||||

DB 361 TGGTACGAGGAATTATGTTCCAGGAAGCAGTATCTCTATAGCAGGTTGGCGCCACA 420
|||||

QY 1321 TTATCTGTGAAAAGAAAATGGCGCTTGAGCTTCACTTCGCGGCCACCCTCGTGAAT 1380
|||||

DB 421 TTATCTGTGAAAAGAAAATGGCGCTTGAGCTTCACTTCGCGGCCACCCTCGTGAAT 480
|||||

QY 1381 AATGTTGAGGTCTTAAAAGCACTTCAAGATTTAAACGTGAGTGAAGAAGATGGCA 1440
|||||

DB 481 AATGTTGAGGTCTTAAAAGCACTTAAAGATTTAAATGCTGAGCTGAAGAAGATGGCA 540
|||||

QY 1441 CTACACGTGAATGACAGATGTGCCAGGGTTTCCGTAAGTTAATGACACGTTAGATGC 1500
|||||

DB 541 CTACACATGAATGACAGATGTGCCAAGGTTTCCGTAAGTTAATGACATGATGATGC 600
|||||

QY 1501 CAGCAACAGCTTCTTGTGACTCTACCATCATGATGATATGATGCTA 1550
|||||

DB 601 CAACACAGCTTCTTGTGACTCTACCATCATGATGATGATGCTA 650
|||||

RESULT 7 676 bp mRNA linear EST 24-SEP-2003
CF574471
LOCUS MCSA15H01 Maturing Sugarcane Stem Lambda ZIPILOX Library (MCS)
DEFINITION Saccharum sp. cDNA clone MCSA107E09 5' similar to protein kinase,
mRNA sequence.

ACCESSION CF574471
VERSION CF574471.1 GI:35205797
KEYWORDS EST.
SOURCE Saccharum sp.
ORGANISM Saccharum sp.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.

REFERENCE 1 (bases 1 to 676)
Casu, R.E., Dimmock, C.M., Chapman, S.C., Grof, C.P.L., McIntyre, C.L.,
Bonnett, G.D. and Manners, J.M.
Identification of differentially expressed transcripts from
maturing stem of sugarcane by in silico analysis of stem expressed
sequence tags and gene expression profiling
Unpublished (2003)

JOURNAL Contact: Rosanne E. Casu
Commonwealth Scientific and Industrial Research Organisation
Division of Plant Industry
Long Pocket Laboratories, 120 Meiers Rd, Indooroopilly, QLD, 4068,
Australia
Tel: 61 7 3214 2364
Fax: 61 7 3214 2881
Email: Rosanne.Casu@csiro.au

TITLE Bases 1-17 (GTCGACCCACGCTCCG): Sali adapter
Seq primer: T7 sequencing primer
High quality sequence stop: 676.

COMMENT location/Qualifiers
1. 676
/organism="Saccharum sp."
/mol_type="mRNA"
/cultivar="Q117"
/db_xref="taxon:15819"
/clone="MCSA107E09"
/dev_stage="12 months post-planting"
/lab_host="Y1090(ZL)"
/clone_lib="Maturing Sugarcane Stem Lambda ZIPILOX library
(MCS)"
/note="Organ: internodes 6-11; Vector: Lambda ZIPILOX;
Site 1: SalI; Site 2: NotI; mRNA was prepared from
internodes 6-11 of the sugarcane variety Q117. cDNA was
synthesised from a NotI-oligodT primer/adaptor using the
manufacturers protocols (Life Technologies) and then
ligated to a Sali adapter to facilitate directional
cloning. The cDNA was cloned into the Sali and NotI sites

FEATURES
source

Db 629 TATGCTGACCTGAGGTTGATGATGAGCTGTGAGTGATCCCTTATGCTCTCTTGT 688
QY 803 GGAACCTCTTCCATTGTGATGAGAAATATTCCTCATCTGTTCAAAAAATTAGGAGGT 862
Db 689 GGTACTCTTCCATTGTGATGAGAAATATTCCTCATCTATTCAAAAAGATAAAGGTTGT 748
QY 863 ATCTACACACTTCCAAGTCATTTGCTGCTTTGG 896
Db 749 ATATATACTCTCCCAAGTCATTTATCTGCTCTGG 782

RESULT 9
CA149321 956 bp mRNA linear EST 24-SEP-2003
LOCUS SCJLRZ1025G04.g RZ1 Saccharum officinarum cDNA clone SCJLRZ1025G04
DEFINITION 5', mRNA sequence.
ACCESSION CA149321
VERSION CA149321.1 GI:35051253
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum

REFERENCE
AUTHORS Vetore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: patruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 025 row: G column: 04
Seq primer: T7 Promoter Primer.

FEATURES

source

1. .956
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCJLRZ1025G04"
/lab_host="DH10B"
/clone_lib="RZ1"
/note="Organ: Shoot-root transition zone from young plants
(large insert library); Vector: pSport1; Site 1: SalI;
Site 2: NotI; An unidirectional cDNA library generated
from [Shoot-root transition zone from young plants (large
insert library)]. cDNA was prepared from polyA+ mRNA
using Superscript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 30.4%; Score 593; DB 13; Length 956;
Best local Similarity 96.1%; Pred. No. 8.7e-81;
Matches 608; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1076 ATGGATTTAACAGAACCATGTGTGTGATCACTGTGCAGCAGACTTCAAAATGAGGCA 1135
Db 1 ATGGGATTTAACAGAACCATGTGTGTGATCACTGTGCAGCAGACTTCAAAATGAGGCA 60
QY 1136 ACTGTGCATATTAATTACTATTGGACAACTCGTTTAGAGCAACTAGTGCCTAATCTTGGG 1195
Db 61 ACTGTGCATATTAATTACTATTGGACAACTCGTTTAGAGCAACTAGTGCCTAATCTTGGG 120

QY 1196 GCAGATTATCAAGATCAATGACAGGAATTTAAATCAGCTGGCGTCATCTGAATCATCT 1255
Db 121 GCAGATTGTCAAGATCAATGACAGGAATTTAAATCAGCTGGCGTCGTCGAATCATCT 180
QY 1256 AGTTCTGTACGAGGAATATGTTCAGGAAGCAGTGATCTCATAGCAGTGTTCGGG 1315
Db 181 AGTTCTGTACGAGGAATATGTTCAGGAAGCAGTGATCTCATAGCAGTGTTCGGG 240
QY 1316 CCATATTATCCTGTTGAAAGAAATGGCGCTTGACTTCAGTCTCGGGCCACCCTCGT 1375
Db 241 CCATATTATCCTGTTGAAAGAAATGGCGCTTGACTTCAGTCTCGGGCCACCCTCGT 300
QY 1376 GAAATATGCTTGAGGTCTTAAAGCACTTCAAGAATTAAAGTCAGATGGAAGAAGAT 1435
Db 301 GAAATATGATTTGAGGTCTTAAAGCACTTCAAGAATTAAAGTCAGATGGAAGAAGAT 360
QY 1436 GGGCACTACAAACGTGAATGCGATGCTGCCAGGGTTTCTGAAAGTTAATGACACGTTA 1495
Db 361 GGGCACTACAAACATGAATGCGATGCTGCCAGGGTTTCTGAAAGTTAATGACATGTTA 420
QY 1496 GATGCCAGCAACAGCTTTCTTGTGTAAGTCTTACCATCATGATGATGATGCTAATGGG 1555
Db 421 GATGCCAGCAACAGCTTTCTTGTGTAAGTCTTACCATCATGATGATGATGATGATGGG 480
QY 1556 AGGCTACTACTGTGATCAAGTTTGAATTCAGCTTTACAGACGAAGGACGACAAGTAC 1615
Db 481 AGGCTACTACTGTGATCAAGTTTGAATTCAGCTTTACAGACGAAGGACGACAAGTAC 540
QY 1616 CTCTAGATATGACAGAGATTACTGACCTCAGCTGCTTCTTGAATCTTGTGCGGCC 1675
Db 541 CTCTAGATATGACAGAGATTACTGACCTCAGCTGCTTCTTGAATCTTGTGCGGCC 600
QY 1676 TTCCTTACCAAGCTTAGGGTTCTATAGTGCTCT 1708
Db 601 TTCCTTACCAAGCTTAGGGTTCTATAGAGCTCT 633

RESULT 10

AW091047 597 bp mRNA linear EST 18-OCT-1999
LOCUS 614070C04.y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,
DEFINITION mRNA sequence.
ACCESSION AW091047
VERSION AW091047.1 GI:6056642
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 597)

Walbot,V.
Maize ESTs from various cDNA libraries sequenced at Stanford
University
JOURNAL Unpublished (1999)
COMMENT Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614070 row: C column: 04.

FEATURES
source
1. .597
/organism="Zea mays"
/mol_type="mRNA"
/cultiivar="W23"
/db_xref="taxon:4577"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XL0LR"
/clone_lib="614 - root cDNA library from Walbot Lab"

/note="Organ: root; Vector: pBluescriptII SK+; Site 1: EcoRI; Site_2: XhoI; 3-4 days old root tissue from Walbot Lab (LM)"

ORIGIN

Query Match 30.4%; Score 592.8; DB 9; Length 597;
Best Local Similarity 99.7%; Pred. No. 1.2e-80;
Matches 594; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1172 AGAGCAACTAGTGGCTATCTTGGGCGAGATTATCAGAATCAATGACAGAAATTTAAAT 1231
|||||
Db 2 AGAGCAACTAGTGGCTATCTTGGGCGAGATTATCAGAATCAATGACAGAAATTTAAAT 61

QY 1232 CAGCTGGCCTCATCTGAATCATCTAGTTCTGTGTAAGGAATTATGTTCCAGAAAGCAGT 1291
|||||
Db 62 CAGCTGGCCTCATCTGAATCATCTAGTTCTGTGTAAGGAATTATGTTCCAGAAAGCAGT 121

QY 1292 GATCCTCATAGCAGTGTGTTTGGCGCCATATTATCTGTGAAGAAATGGCGCTTGA 1351
|||||
Db 122 GATCCTCATAGCAGTGTGTTTGGCGCCATATTATCTGTGAAGAAATGGCGCTTGA 181

QY 1352 CTTCAGTCTCGGGCCCACTCTCGTGAATATATGTTGAGGCTTAAAGCACTTCAAGAA 1411
|||||
Db 182 CTTCAGTCTCGGGCCCACTCTCGTGAATATATGTTGAGGCTTAAAGCACTTCAAGAA 241

QY 1412 TTAAACGTACAGTGAAGAAGATGGGCACACTACAAGTGAATGACAGATGGTCCAGGG 1471
|||||
Db 242 TTAAACGTACAGTGAAGAAGATGGGCACACTACAAGTGAATGACAGATGGTCCAGGG 301

QY 1472 TTTCCTGAAGTTAATGACACGTTAGATGCAGACAGCTTTCTGTGACTCTACCATC 1531
|||||
Db 302 TTTCCTGAAGTTAATGACACGTTAGATGCAGACAGCTTTCTGTGACTCTACCATC 361

QY 1532 ATGATAATGATGATGCTAATGGGAGGCTACTGCTGATCAAGTTGAATTCAGCTT 1591
|||||
Db 362 ATGATAATGATGATGCTAATGGGAGGCTACTGCTGATCAAGTTGAATTCAGCTT 421

QY 1592 TACAAGACGAAGACGACAACTCTTATGATGACAGAGTTACTGCACTCAGCTG 1651
|||||
Db 422 TACAAGACGAAGACGACAACTCTTATGATGACAGAGTTACTGCACTCAGCTG 481

QY 1652 CTCTCTTGACTTCTGTGCGGCTTCTTACCAAGCTTAGGGTTCTATAGTGTCTACC 1711
|||||
Db 482 CTCTCTTGACTTCTGTGCGGCTTCTTACCAAGCTTAGGGTTCTATAGTGTCTACC 541

QY 1712 ATGTGCAAAATTTCACTGTGTGATGAATAACGAAAGCATGTAATAGAACCTT 1767
|||||
Db 542 ATGTGCAAAATTTCACTGTGTGATGAATAACGAAAGCATGTAATAGAACCTT 597

RESULT 11
BI950083 863 bp mRNA linear EST 19-OCT-2001
LOCUS HVSME1001BH14f Hordeum vulgare spike EST library HVCDNA0012
DEFINITION (Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
HVSME1001BH14f, mRNA sequence.

ACCESSION BI950083
VERSION BI950083.1 GI:16291889
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 863)
AUTHORS Wing,R., Muehlbauer,G.J., Close,T.J., Kleinhofs,A., Wise,R.,
Heinen,S., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M.,
Rambo,T., Simmons,J., Fenton,R.D., Malatrasi,M., Choi,D.W.,
Oates,R. and Main,D.

TITLE Development of a genetically and physically anchored EST resource
for barley genomics: Fusarium infected Morex spike cDNA library
JOURNAL Unpublished (2001)
COMMENT Contact: wing RA

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 601
Seq primer: AATTAAACCTCACTAAAGCG
High quality sequence stop: 729.
Location/Qualifiers

FEATURES
source

1. .863
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Morex"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="HVSME1001BH14f"
/tissue_type="Spike"
/lab_host="TJ121"
/clone_lib="Hordeum vulgare spike EST library HVCDNA0012 (Fusarium infected)"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Plants were grown at the University of Minnesota in the GJ Muehlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html)"

ORIGIN

Query Match 30.2%; Score 589.2; DB 12; Length 863;
Best Local Similarity 86.4%; Pred. No. 3.5e-80;
Matches 673; Conservative 0; Mismatches 104; Indels 2; Gaps 2;

QY 185 AGTAAAGGAGTGGCATTCTGAAGCATTAAGAACTACAACTGGGAAGAACTTTAGT 244
|||||
Db 5 ACTAGAGGAGCGGGCATTCTGAAGCGTTAAAGAACTACAACTGGGCAGAACATTAGT 64

QY 245 ATCGGTACATTTGAAAAAGTGAAGATTGCAGAGCATTAAGCTTACTGACATAGGGTTGCT 304
|||||
Db 65 ATAGGCACATTTGAAAAAGTGAAGATTGCAGAACATTAAGCATTAAGGACAAAGTTGCT 124

QY 305 ATAAAGATCATCAACTGCCGCAATGAGAAATATGAAATGGAAGAAAGCAAAAGAGA 364
|||||
Db 125 ATAAAGATTTGAACCGTGTCAATGAGAACTATGAACATGGAAGAAAGCAAAAGAGA 184

QY 365 GAATTCAGATATTGAAGTTGTTCATTCACCCCATATCATTCGGCTTTATGAGGTGATA 424
|||||
Db 185 GAGATCAAGATATTGAGGTGTTCATTCACCCCTCATATCATTCGGCTTTATGAGGTGATT 244

QY 425 TACACACCTACAGATATATATGTTGTGATGGAATATTGTAATATGCGAGTTATTGAT 484
|||||
Db 245 TACACACCTACAGATATATATGTTGTGATGGAATATTGCAAGTATGGGAGCTATTGAC 304

| | | | |
|----|-----|---|-----|
| Qy | 485 | TACATTGTGAGAAAGCGCAGATTACAGAGATGAAGCTCGTCCGAACTCTCCAGCAGATC | 544 |
| Db | 305 | TGCATTGTGAGAAAGGCGGTTACAGAGATGAGGCTCGTCCGAACTCTCCAGCAGATT | 364 |
| Qy | 545 | ATATCTGGCGTCGAATACTGCCATAGAAACATGGTTGTCCACCGTGAACCTAAAGCCGGAA | 604 |
| Db | 365 | ATATCTGGTGTGAATACTGCCACAGAAACATGGTTGTTCATCGTGAATCTAAAGCCAGAA | 424 |
| Qy | 605 | AACCTGTACTGATTCAAAGTATAATGTAATACTGCGGATTTGGTCTGAGCAATGTC | 664 |
| Db | 425 | AACCTGTACTGATTCCAATATATGTAACCTGCCGACTTGGATTAAGTATGTC | 484 |
| Qy | 665 | ATGCATGATGGCCATTTTCTGAAGACTAGCTGTGGAGTCCGAACTATGCTCTCCAGAG | 724 |
| Db | 485 | ATGCATGATGGCCATTTTCTGAAGACTAGCTGTGGAGTCCGAACTATGCTCTCCAGAG | 544 |
| Qy | 725 | GTAATATCTGTAAACTATATGCTGGACCTGAGGTCGATGTATGAGTTGTGGGTGATT | 784 |
| Db | 545 | GTTATCTCAGTAAATTGTACGCTGACCTGAGGTTGATGTTTGAGCTGTGGGTGATA | 604 |
| Qy | 785 | CTTTATGCTCTTCTTTGTGGAACCTTTCATTTGATGATGAGAAATATTCCTCAATCTGTT | 844 |
| Db | 605 | CTTTATGCTCTTCTTTGGGCACCTTCCATNTGATGATGACAAATTAATTCCAACCTGTT | 664 |
| Qy | 845 | AAAAAATTAAGGAGGTATCTACACACTTCCAACTTGTCTGCTTGGCCAGGAT | 904 |
| Db | 665 | AAAAAGATAAGGAGGCATCTATATCCTTCCAGTCATTATCTGCTTGCAGAGGAT | 724 |
| Qy | 905 | TTGATCCCAAGATGCTGTGTGTGAGCCATGAAGAGATCACAATTAAGGAATTGC | 963 |
| Db | 725 | TTGATCCCAAG-ATGCTTGTGTGTGATTTCTATGAAGAG-ATACCAATTCGTGAATTGC | 781 |

RESULT 12
AY112453 1391 bp mRNA linear HTC 17-OCT-2002
LOCUS Zea mays CL7115_1 mRNA sequence.
DEFINITION AY112453
ACCESSION AY112453
VERSION AY112453.1 GI:21217043
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1391)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1391)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES
source
1. 1391
Location/Qualifiers
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="Maizedb:632803"
/db_xref="taxon:4577"
/clone_lib="Maize Mapping Project/Dupont Consensus Library"
/note="this sequence is part of a project of EST assemblies resulting from the application of public

| | | | |
|---------------------------|------|---|-----------------------------------|
| ORIGIN | | contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project" | |
| Query Match | | 30.2%; | Score 589; DB 11; Length 1391; |
| Best Local Similarity | | 60.6%; | Pred. No. 2.8e-80; |
| Matches 785; Conservative | | 0; | Mismatches 507; Indels 3; Gaps 1; |
| Qy | 190 | AGGAGTGGGCATTTCTGAAGCATTAAGAACTACAACCTGGGAAGAACTTAGGTATCGG | 249 |
| Db | 98 | AGCGGAGAGAGATGCCAACCCCTTGAGCGGTTACAGAAATGGCAAAACCCCTGGAAATCG | 157 |
| Qy | 250 | TACATTGGAAGAAAGTGAAGATTGCAGAGCATTAAGCTTACTGGACATAGGTTGCTAATAA | 309 |
| Db | 158 | GTCGTTCCGTTAAAGTGAAGATCCGGGAACATATATTGACTGCTCATAAGGTGGCATCA | 217 |
| Qy | 310 | GATCATCAACTGCCGCCCAATGAGAAATATGAAATGGAAGAGAAAGCAAGAGAGAAAT | 369 |
| Db | 218 | GATTTCTCAATCCGAAGAGATCAGAAGCATGATTAANNNNNNNNNNNNNNNNNNNNNN | 277 |
| Qy | 370 | CAAGATATGAAGTGTTCATTCACCCCATATCATTCGGCTTATGAGTCATATACAC | 429 |
| Db | 278 | NAAGATTAAGATTAATTATGCAATCCTCATATCAGCCCTTATGAGTGATAGATAC | 337 |
| Qy | 430 | ACCTACAGATATATATGTTGTGAATGAAATATTGTAAGTATGCGAGTTATTGATTAACAT | 489 |
| Db | 338 | ACCTGATATATCTGTGTGTTATGAGATGTTAAATCTGGAGAGTTGTTGATTAACAT | 397 |
| Qy | 490 | TGTTGAGAAAGCAGATTACAGAGAGATGAAGCTCGTGAATCTTCCAGCAGATCATATC | 549 |
| Db | 398 | CGTTGAGAGGAGGAGGCTACACGAGAGAGAGAGCCGACACNNNNNNNCAGCAGATCATATC | 457 |
| Qy | 550 | TGGCGTGAATTACTGCCATAGAAACATGCTGTCCACCCTGAACCTTAAAGCCGGAACCT | 609 |
| Db | 458 | TGGTGTGAATTAATTCGCATAGCAATGCTGTCCACCGTCAATTTTAAAGCCAGAGAACT | 517 |
| Qy | 610 | GTTACTTGATTCAAAGTATATGTAATACTTGGGATTTGGTCTGAGCAATGTCATGCA | 669 |
| Db | 518 | TCTTTGGATTCAAATGCAATGTTAAGATTGCCGATTTGGCTTAAATATTAATGCG | 577 |
| Qy | 670 | TGATGCCATTTTCTGAAGACTAGCTGTGGAGTCCGAACATATGCTCTCCAGAGGTAAT | 729 |
| Db | 578 | TGATGTCACTTCTTAAGACGAGTGTGTAGCCCAATTAAGCACACCTGAGGTAT | 637 |
| Qy | 730 | ATCTGTAACCTATATGCTGAGCTGAGCTGAGTGTATGAGTGTGGGTGATTTCTTTA | 789 |
| Db | 638 | ATCTGTAACCTATATGCTGAGCTGAGTGTATGACATCTGAGCTGTGANNNNNNNNNN | 697 |
| Qy | 790 | TGCTCTTCTTTGTGGAACCTTCCATTTGATGATGAGAAATTTCCCAATCTGTTCAAAA | 849 |
| Db | 698 | NNNNNNNNNNNTGGCACTCTCCCATTTGACGATGAGAAATTTCCAAACCTTTNNNNNN | 757 |
| Qy | 850 | AATTAAGGAGGTATCTACACACTTCCAAGTCATTTGCTTCTTGGCCAGGATTTGAT | 909 |
| Db | 758 | NNNNNNNNNNNNNTATACCTTCTTCAATTTGTCACCTTCAAGGAGGACTTGAT | 817 |
| Qy | 910 | CCCAGATGCTGTGTGTTGAGCCTATGAAGAGATCACAATTAAGGAAATTCGGGAGCA | 969 |
| Db | 818 | TCCTAGATGCTGTTGNNN | 877 |
| Qy | 970 | TCAATGTTCCAGATTCCGCTTCCAGTACTTGCCAGTGCCTCCACGATACGACACA | 1029 |
| Db | 878 | TGTGTGTTCAAAATCCGACTTCGCGCTATTGTGCTGTACGCTCCAGACACTGCTCA | 937 |
| Qy | 1030 | ACAAGCCAAATGATTTGATGAAGATACACTTCGAGATGTTGTTAATATGGATTAAACA | 1089 |
| Db | 938 | ACAAGTTAAGAAGCTGACGAGAGAAACCTTAATGATGTTAAGATGGGTTTGACAA | 997 |
| Qy | 1090 | GAAACATGTGTGAATCATCTGTGACGACGACTTCAAAATGAGCAACTGTGCATATTA | 1149 |
| Db | 998 | GAATCAGCTAATTGAATCTGTGACACAAGATTGCAGAATGAGCAACAGTTGCCATATTA | 1057 |

| | | | |
|----|------|--|------|
| QY | 1150 | TTTACTATTGGACAATCGGTTTAGAGCAACTAGTGGCTATCTTGGGGCAGATTATCAAGA | 1209 |
| Db | 1058 | TTTACTCATGGACAAATAGGCTTCGTACAACCAGTGTTATCTTGGATCTGAAGTTCAAGA | 1117 |
| QY | 1210 | ATCAATGGACAGGAATTTAAATCAGCTGGCGTCATCTGAATCATCTAGTCTGGTACGAG | 1269 |
| Db | 1118 | ATCTATGACTCATCTTTCTCTCA---AGTAATCGCTGAACAACCAACTTCAGCAACTGA | 1174 |
| QY | 1270 | GAAATATGTTCAGGAAGCAGTATCCTCATAGCAGTGGTTTTGCCGCATATTATCTGT | 1329 |
| Db | 1175 | ACTTCGCAGCATGGGTTTTCAGAATCTCCAGGTTCTGGCTTGAGGCAGCATTTTGCAGC | 1234 |
| QY | 1330 | TGAAGAAAATGGGCGCTTGGACTTCAGTCTCGGGCCACCCCTGTGAATAATGGTTGA | 1389 |
| Db | 1235 | TGAAGGAATATGGGCCCTTGGTCTTCAGTCTCGAGCACATCCANNNNNNNNNNNNNNNN | 1294 |
| QY | 1390 | GGTCTTAAAGCACTTCAAGATTAAAGTCAGATGGAAGAGAATGGGCACTACAAGT | 1449 |
| Db | 1295 | NN | 1354 |
| QY | 1450 | GAAATGCAGATGGTGCCCAGGGTTTCTCTGAAGTTA | 1484 |
| Db | 1355 | NNNNNNGCAGATGAGTCCCTGGCTGCCTTGAGAGTA | 1389 |

| RESULT 13 | CB632244 | LOCUS | DEFINITION |
|-----------|---------------------|--------|---|
| | CB632244 | 850 bp | mRNA |
| | OS1EB10F22.f | OS1EB | Oryza sativa (indica cultivar-group) cDNA |
| | clone OS1EB10F22 5' | | mRNA sequence. |

| | | |
|-----------|--------------------------------------|-------------|
| ACCESSION | CB632244 | |
| VERSION | CB632244.1 | GI:29627233 |
| KEYWORDS | EST. | |
| SOURCE | Oryza sativa (indica cultivar-group) | |
| ORGANISM | Oryza sativa (indica cultivar-group) | |

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

| REFERENCE AUTHORS | TITLE | JOURNAL |
|----------------------|--|--|
| I (bases 1 to 850) | Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. | large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea unpublished (2003) |

JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing

Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>
PCR Primers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: F column: 22
Seq primer: gta aaa cga cgg cca gtg.

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| Source | 1. .850 |

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ORIGIN

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| Query Match | 30.1%; | Score 586.8; | DB 14; | Length 850; |
| Best Local Similarity | 86.4%; | Pred. No. 8.1e-80; | | |
| Matches .648; Conservative | 0; | Mismatches 102; | Indels 0; | Gaps 0; |

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| QY | 143 | GGCCGGCGGAACCCGGTAAAGTAAGAGTGAAAAATGAGTGAAGTACTGTAAGGAGTGGGCAT | 202 |
| Db | 100 | GGGCGGGGAGCTCCGGCGTCTCAGGGAAAAATGGATGGAAATGCTMAAGCGGTGGGCAT | 159 |
| QY | 203 | TCTGAAGCATTAAAGAACTACAACTGGGAAAGAACTTTAGGTATCGGTACATTGGAAAA | 262 |
| Db | 160 | TCTGAGGCACGTGAAGAACTACAACTTTGGAAGAAGCTTTAGGTATTTGGCTCATTTGAAAA | 219 |
| QY | 263 | GTAAGATTGCAGAGCATAACTTACTGGACATAGGGTTGCTATAAGATCATCAACTGC | 322 |
| Db | 220 | GTAAGATTGCAGAGCATAACTTACAGACACAGAGTTGCTATTAAGATCTCGAACCGC | 279 |
| QY | 323 | CGCCAAATGAGAAATATGGAATGGAAGAGAAAGCAAGAGAGAGAAATTCAGATATTGAAG | 382 |
| Db | 280 | CGCCAAATGAGAAATATGGAATGGAAGAGAAAGCAAGAGAGAGAAATCAAGATACTGAGA | 339 |
| QY | 383 | TTGTTCAATTCACCCCATATCATTCGGCTTTATGAGGTCAATATACACCTACAGATATA | 442 |
| Db | 340 | TTGTTCAATTCATCCCATATCATTCGCTTTATGAGGTATATATACATCTCCTACGATATA | 399 |
| QY | 443 | TATGTTGTGATGAATATTTGAAGTATGCGAGTTATTTGATTACATTGTTGAGAAAGGC | 502 |
| Db | 400 | TATGTTGTGATGAGTACTGCAAGTTTGAGAGAACTGTTGATTACATTGTTGAGAAAGGC | 459 |
| QY | 503 | AGATTACAGGAAGATGAAGCTGCTCGAATCTTCCAGCAGATCATATCTGGCGTCCAATAC | 562 |
| Db | 460 | AGTTGCAAGGAAGATGAGGCTCGCCGAATCTTCCAGCAGATTATATCTGGGGTAGAATAC | 519 |
| QY | 563 | TGCCATAGAAACATGCTTGTCCACCGTGACCTAAAGCCGGAAAACTTGTTACTTGATTCA | 622 |
| Db | 520 | TGCCACAGAAACATGCTTGTTCATCTGTATCTGAAGCCAGAAAACTTGCTACTGCAATTCA | 579 |
| QY | 623 | AAGTATATATGTAAAACTTGCGGATTTTGCTCTGAGCAATGTATGATGATGAGCCATT | 682 |
| Db | 580 | AAGTATATATGTAAAGCTTGCTGACTTTGTTGAGTAAACGTATGATGATGAGCCATT | 639 |
| QY | 683 | CTGAAGACTAGCTGTGGGAGTCCGAACATATGCTGCTCCAGAGGTAAATATCTGTAACCTA | 742 |
| Db | 640 | TTGAAGACAAGCTGTGGGAGTCCAAACATATGCTGCTCCAGAGGTGATCTCTGTATATTA | 699 |
| QY | 743 | TATGCTGAGCTGAGGTGATGATGAGTGTGTGGGTGATTTCTTATGCTCTTCTTTGT | 802 |
| Db | 700 | TATGCTGAGCTGAGGTGATGATGAGTGTGTGAGCTGAGGAGTGATCTTATGCTCTCCTTGT | 759 |
| QY | 803 | GGAACCTCTTCATTGATGATGAGATATTTCCCAATCTGTTCAAAAAATTAAGGAGGT | 862 |
| Db | 760 | GGAACCTCTTCATAATGATGATGAGATATTTCCCAACCTATTTCAAAAAATTAAGGAGGT | 819 |
| QY | 863 | ATCTACACACTTCCAAGTCAATTTGTCTGCT | 892 |
| Db | 820 | ATATATACTCTCCCGAGTCAATTAATCTGCT | 849 |

RESULT 14
BQ805778

| LOCUS | 794 bp | mRNA | linear | EST 31-JUL-2002 |
|------------|---|------|--------|-----------------|
| DEFINITION | WHE3570 H07 P14Z5 wheat developing grains cDNA library Triticum aestivum cDNA clone WHE3570 H07 P14, mRNA sequence. | | | |

| | | |
|-----------|------------|-------------|
| ACCESSION | BQ805778 | |
| VERSION | BQ805778.1 | GI:22029987 |

| KEYWORDS | EST. |
|----------|---------------------------------|
| SOURCE | Triticum aestivum (bread wheat) |
| ORGANISM | Triticum aestivum |

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.

REFERENCE
AUTHORS
1 (bases 1 to 794)
Altenbach, S., Anderson, O. D., Chao, S., Chin, A., Close, T. J.

Cronin, K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J.

AUTHORS

TITLE Rausch,C.J., Wilson,C. and Woo,J.
The structure and function of the expressed portion of the wheat
genomes - Developing grains cDNA library
JOURNAL Unpublished (2002)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818

FEATURES
Source Email: oandersn@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.
Location/Qualifiers
1. 794

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/lab_host="E. coli SOLR"
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/note="Vector: Lambda ZAP II, excised phagemid; Site_1:
ECORI; Plants were grown under six following different
environmental regimes in greenhouse, Environment 1)
24oc/17oc day/night, well-watered, with post-anthesis
fertilizer, Environment 2) 24oc/17oc day/night,
well-watered, without post-anthesis fertilizer,
Environment 3) 37oc/17oc day/night, well-watered, with
post-anthesis fertilizer, Environment 4) 37oc/17oc
day/night, well-watered, without post-anthesis fertilizer,
Environment 5) 37oc/17oc day/night plus drought, with
post-anthesis fertilizer, Environment 6) 37oc/17oc
day/night plus drought, without post-anthesis fertilizer,
developing wheat grains from the following were excised
and frozen in liquid nitrogen, Environment 1 at 3, 5, 7,
8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment
2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44
DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28,
32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20,
24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12,
16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10,
12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by
S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A
cDNA library was made using poly (A) RNA, and the cDNA
clones were in vivo excised to give phuescript SK(-)
phagemids in the TJ Close lab (Chin, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (others)."

ORIGIN
Query Match 30.0%; Score 584.2; DB 13; Length 794;
Best Local Similarity 84.7%; Pred. No. 2.1e-79;
Matches 655; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

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DB 22 TTAATTCACCCCTCATATCATCCGGTTATGAGTCATTGAGACACCTAAGCATATATT 81
OY 446 GTTGTGATGGAATATTTGAAGTATGGCGATTTGATTACATTGTTGAGAAAGGAGCA 505
DB 82 GTTGTGATGGAATATTTGAGAAATGTTGATTGATTACATTGTTGAGAAAGGAGCGG 141
OY 506 TTACAGGAAGATGAAGCTGTCGAATCTTCCAGCAGATCATATCTGGCGTGAATACTGC 565
DB 142 TTACAGGAAGATGAAGCTGTCGAATCTTCCAGCAGATTTATCTGTTGTAATACTGC 201
OY 566 CATAGAAACATGTTGTCACCGTGACCTAAAGCCGGAACCTGTTACTTGATTCAAG 625

DB 202 CACAGAAACATGTTGTTTCATCGTGATCTAAAGCCAGAAACTGTACTTGATTCTAA 261
OY 626 TATATGTAATAAATTGCGGATTGTTGCTGAGCAATGTCATGATGGCCATTCTCG 685
DB 262 TATATGTAATAAATTGTTGACTTTGGGTTAAGTAATGATGATGGCCATTCTTG 321
OY 686 AAGACTGCTGTTGGAGTCCGAATATGCTGCTCCAGAGGTAATATCTGTTAACTATAT 745
DB 322 AAGACTGCTGCGGAGTCTAAACTATGCTGCACAGAGCTTATCTCAGTAACCTGTAC 381
OY 746 GCTGACCTGAGGTCGATGATGAGTGTGGGTTGATCTTATGCTCTTGTGGA 805
DB 382 GCTGACCTGAGGTTGATGCTGAGCTGTGAGTATGCTTATGCTCTTGTGCGC 441
OY 806 ACTCTTCATTGATGATGAGATATTCCTCAATCTGTTCAAAAAAATTAAGGAGGTATC 865
DB 442 AGAGTTCCATTGAGGATGACAAATATTCCTCAACCTGATCAAAAAAGTAAGGAGGTTTC 501
OY 866 TACACACTTCCAAAGTCATTGTTGCTGCTTTGGCCAGGATTGATCCACGAATGCTGTT 925
DB 502 TATATCTTCCAAAGTTATTATTCGATCTTGCATGATGATTGATCCCAAGATACTTATT 561
OY 926 GTTGAAGCTTGAAGAGATCACAATTAGGAAATTCGGGACATCAATGTTCCAGATT 985
DB 562 GTTGAAGCTTGAAGAGATCACAATTGTTGAATTCGGGACCAACCATGTTTCAGAA 621
OY 986 CGCCTTCACGTTACTTGGCAGTCTCCACAGATACGACACAAGCCAAATGATT 1045
DB 622 CGCCTTCCTCGTACCTGCGAGTCTCCGCAACAGCCACAGCAAGCCAAATGATT 681
OY 1046 GATGAAGATACACTTCGAGATGTTGTTATATGGAATTAACAAGAACCATGTTGTGA 1105
DB 682 GATAAAGATACACTTCAGACATGTTGATCTGGATATGATAAAGATCATGTGGTGA 741
OY 1106 TCACCTGTCAGCAGACTTCAAAATGAGGCACTGTGTCATATTATTACTATT 1158
DB 742 TCACCTGTCAGATAGCGTGCAGAAATGAGGCAACTGTGTCATATTACTGCTCTT 794

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LOCUS OSIIBa07H13.f OSIIa Oryza sativa (indica cultivar-group) cDNA
DEFINITION clone OSIIBa07H13 5', mRNA sequence.
ACCESSION CB621531
VERSION CB621531.1 GI:29616519
KEYWORDS EST.
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
REFERENCE Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
AUTHORS Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE large-scale identification of ESTs involved in the interaction
COMMENT between rice and Magnaporthe grisea
Unpublished (2003)
JOURNAL Contact: Rod Wing
ARIZONA CONTACT: Rod Wing
UNIVERSITY OF ARIZONA Arizona Genomics Institute
BIOLOGICAL SCIENCES West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR PRIMERS
FORWARD: gta aaa cga cga cga gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: H column: 13
Seq primer: gta aaa cga cga cga gtc.
FEATURES
Source Location/Qualifiers
1. 829


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XhoI; Lesion Mimic SPL 11"
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Db      100 GGGCCGGGAGCTCCAGCGCTGCTCAGTGAATAATGATGGAATGCTAAAGCGGTGGGCAT 159  
  
QY      203 TCTGAAGCATTAAAGAACTACAACCTGGGAGAACTTTAGGTATCGGTACATTGGAAAA 262  
      |||||  
Db      160 TCTGAGGCACTGAAGAACTACAATCTTGAAGAACTTTAGGTATGGCTCAATTGGAAAA 219  
  
QY      263 GTGAAGATTGACAGACATAAGCTTACTGTGACATAGGTTGCTATTAAGATCACTCACTGC 322  
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QY      323 CGCCAAATGAGAAATATGAAATGGAAGAGAAAGCAAGAGAAATTCAGATATTGAAG 382  
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Db      280 CGCCAAATGAGAAATATGAAATGAGAGAGAAAGCAAGAGAAATCAAGATACTGAGA 339  
  
QY      383 TTGTTCAATTCACCCCATATCATTCGGCTTTATGAGGTCAATATACACACCTACAGATATA 442  
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QY      443 TATGTTGTGATGGAATATTGTAAGTATGGCGAGTTATTGATTACATTGTTGAGAAAGGC 502  
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QY      503 AGATTACAGGAAGATGAAGCTCGTGAATCTTCCAGCAGATCATATCTGGCGTGAATAC 562  
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Db      460 AGTTGACGAGAGATGAGGCTCGCCGAATCTTCCAGCAGATTATATCTGGGTTAGAATAC 519  
  
QY      563 TGCCATAGAAACATGTTGTCCACCCTGACCTAAAGCCGAAAACTGTTACTTGATTCA 622  
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Db      520 TGCCACAGAAACATGTTGTTCATCGTATCTGAGCCAGAAACTGTCTACTGGAATTCA 579  
  
QY      623 AAGTATATGTAAACTTGGGATTTTGTCTGAGCAATGTCAATGATGATGGCCATTTT 682  
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QY      743 TATGCTGACCTGAGGTCGATGTATGAGAGTTGGGGTGATCTTTATGCTCTCTTTGT 802  
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Db      700 TATGCTGACCTGAGGTCGATGTATGAGAGTCGAGTGATCCTTATGCTCTCTTTGT 759  
  
QY      803 GGAACCTCTTCATTGATGATGAGAAATATCCCAATCTGTTCAAAAAAATTAAAGGAGGT 862  
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Db      760 GGTACTCTTCATTGATGATGAGAAATATCCCACTATTCAAAAAAGATAAGGTGT 819  
  
QY      863 ATCTACACAC 872  
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 9, 2004, 11:12:59 ; Search time 917 Seconds
(without alignments)
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Perfect score: 1948
Sequence: 1 gtcgaccacgcgcgcgcgac.....taaaaaaaaaaaaaaa 1948

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3183909 seqs, 2436941669 residues

Total number of hits satisfying chosen parameters: 6367818

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1948 | 100.0 | 1948 | 13 | US-10-183-687-235, App Sequence 235, App |
| 2 | 1907 | 97.9 | 1926 | 13 | US-10-425-114-5805, App Sequence 5805, App |
| 3 | 1222.4 | 62.8 | 1300 | 13 | US-10-425-114-5415, App Sequence 5415, App |
| 4 | 1195.6 | 61.4 | 1899 | 13 | US-10-183-687-255, App Sequence 255, App |
| 5 | 1188.4 | 61.0 | 2119 | 13 | US-10-425-114-22369, App Sequence 22369, App |
| 6 | 1188.4 | 61.0 | 2607 | 17 | US-10-437-963-49666, App Sequence 49666, App |
| 7 | 848.8 | 43.6 | 2484 | 17 | US-10-437-963-49667, App Sequence 49667, App |
| 8 | 817.4 | 42.0 | 2224 | 17 | US-10-437-963-80980, App Sequence 80980, App |
| 9 | 814.6 | 41.8 | 1991 | 13 | US-10-425-114-35131, App Sequence 35131, App |
| 10 | 807.6 | 41.5 | 1778 | 13 | US-10-425-114-2148, App Sequence 2148, App |
| 11 | 804.2 | 41.3 | 2107 | 13 | US-10-183-687-237, App Sequence 237, App |
| 12 | 793.4 | 40.7 | 2052 | 13 | US-10-183-687-239, App Sequence 239, App |
| 13 | 793.2 | 40.7 | 1742 | 13 | US-10-425-114-4365, App Sequence 4365, App |
| 14 | 782.6 | 40.2 | 2123 | 13 | US-10-183-687-247, App Sequence 247, App |

| | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |
|--|--------------------|--------------------|-------------------|---------------------|---------------------|-------------------|-------------------|---------------------|---------------------|-------------------|-------------------|---------------------|-------------------|--------------------|---------------------|---------------------|---------------------|---------------------|-------------------|---------------------|---------------------|------------------|-------------------|---------------------|-------------------|---------------------|-------------------|-------------------|---------------------|-----------------|-----------------|
| | 780.2 | 780.2 | 763 | 755.4 | 755.4 | 744.4 | 639 | 582.4 | 522 | 304 | 297.8 | 297.8 | 296.8 | 248.8 | 237.8 | 232.4 | 229.2 | 229.2 | 229.2 | 229.2 | 229.2 | 229.2 | 229.2 | 227.6 | 224.4 | 224.4 | 222.2 | 219.4 | 219 | 219 | |
| | 40.1 | 40.1 | 39.2 | 38.8 | 38.8 | 38.2 | 32.8 | 29.9 | 26.8 | 15.6 | 15.3 | 15.3 | 15.2 | 12.8 | 12.2 | 11.9 | 11.8 | 11.8 | 11.8 | 11.8 | 11.8 | 11.8 | 11.7 | 11.5 | 11.5 | 11.5 | 11.4 | 11.3 | 11.2 | 11.2 | |
| | 1539 | 1539 | 2543 | 1539 | 1539 | 1539 | 1626 | 1277 | 2291 | 3079 | 1902 | 1902 | 986 | 725 | 1264 | 1548 | 1753 | 1803 | 1869 | 2173 | 2730 | 4719 | 2899 | 1607 | 1886 | 2010 | 1707 | 2572 | 1771 | 2086 | |
| | 9 | 11 | 13 | 11 | 11 | 13 | 16 | 13 | 13 | 9 | 16 | 16 | 9 | 16 | 16 | 17 | 13 | 13 | 13 | 13 | 13 | 16 | 16 | 13 | 13 | 13 | 13 | 16 | 13 | 15 | |
| | US-09-938-842A-162 | US-09-938-842A-162 | US-10-183-687-251 | US-09-938-842A-2657 | US-09-938-842A-2657 | US-10-183-687-257 | US-10-260-238-491 | US-10-424-599-37563 | US-10-424-599-37563 | US-09-834-975-974 | US-09-801-368-337 | US-10-369-493-25383 | US-09-770-445-263 | US-10-260-238-3050 | US-10-369-493-27551 | US-10-437-963-90028 | US-10-425-114-10423 | US-10-425-114-11678 | US-10-183-687-253 | US-10-424-599-83546 | US-10-424-599-83552 | US-10-258-106-25 | US-10-120-988-112 | US-10-425-114-24231 | US-10-425-114-281 | US-10-425-114-24620 | US-10-183-687-233 | US-10-191-803-134 | US-10-425-114-30848 | US-10-161-565-4 | US-09-919-585-4 |
| | Sequence 162, App | Sequence 162, App | Sequence 251, App | Sequence 2657, App | Sequence 2657, App | Sequence 257, App | Sequence 491, App | Sequence 38233, App | Sequence 37563, App | Sequence 974, App | Sequence 337, App | Sequence 25383, App | Sequence 263, App | Sequence 3050, App | Sequence 27551, App | Sequence 90028, App | Sequence 10423, App | Sequence 11678, App | Sequence 253, App | Sequence 83546, App | Sequence 83552, App | Sequence 25, App | Sequence 112, App | Sequence 24231, App | Sequence 281, App | Sequence 24620, App | Sequence 233, App | Sequence 134, App | Sequence 30848, App | Sequence 4, App | |

ALIGNMENTS

RESULT 1
US-10-183-687-235
; Sequence 235, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Caboon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B1458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; PRIOR APPLICATION NUMBER: 2002-06-27
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 235
; LENGTH: 1948
; TYPE: DNA
; ORGANISM: Zea mays
; US-10-183-687-235

Query Match 100.0%; Score 1948; DB 13; Length 1948;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1948; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCCACGCGTCCGAGCCAAAGCCGGCATACGCCCCCAAGTCCAAAAGCCCTCTCC 60
Db 1 GTGACCCACGCGTCCGAGCCAAAGCCGGCATACGCCCCCAAGTCCAAAAGCCCTCTCC 60
QY 61 GCGCCGCTCTCCCACTCGTAGGTGTTCTCCCGTCTCCGCGGCACTCGCTCGTCCGCGC 120
Db 61 GCGCCGCTCTCCCACTCGTAGGTGTTCTCCCGTCTCCGCGGCACTCGCTCGTCCGCGC 120
QY 121 GCAGGAGGTTGACCTGTGAGGGGCGGCGAACCCGGTAAGTAAGTGAATGATGG 180
Db 121 GCAGGAGGTTGACCTGTGAGGGGCGGCGAACCCGGTAAGTAAGTGAATGATGG 180
QY 181 AAGTAGTAAAGGAGTGGGCACTTGAAGCATTAAGGAACCTACACCTGGGAAGACTTT 240
Db 181 AAGTAGTAAAGGAGTGGGCACTTGAAGCATTAAGGAACCTACACCTGGGAAGACTTT 240
QY 241 AGGTATCGGTACATTTGAAAAAGTGAAGATTGACAGACATTAAGCTTACGACATAGGGT 300
Db 241 AGGTATCGGTACATTTGAAAAAGTGAAGATTGACAGACATTAAGCTTACGACATAGGGT 300
QY 301 TGCTATAAGATCATCAACTGCCGCAATGAGAAATATGAAATGAAAGAGAAAGCAAA 360
Db 301 TGCTATAAGATCATCAACTGCCGCAATGAGAAATATGAAATGAAAGAGAAAGCAAA 360
QY 361 GAGAGATCAAGATATTTGAAGTGTTCATCAACCCCATATCATTCGGCTTATGAGGT 420
Db 361 GAGAGATCAAGATATTTGAAGTGTTCATCAACCCCATATCATTCGGCTTATGAGGT 420
QY 421 CATATACACACCTACAGATATATGTGTGATGGAATATTTGAATGCGGAGTTATT 480
Db 421 CATATACACACCTACAGATATATGTGTGATGGAATATTTGAATGCGGAGTTATT 480
QY 481 TGATTACATGTTGAGAAAGGCGAGATTACAGAAAGATGAAGCTCGTGAATCTTCCAGCA 540
Db 481 TGATTACATGTTGAGAAAGGCGAGATTACAGAAAGATGAAGCTCGTGAATCTTCCAGCA 540
QY 541 GATCATATCGCGCTGCAATACTGCCATGAAACATGTTGCCACCGTGAACCTAAAGCC 600
Db 541 GATCATATCGCGCTGCAATACTGCCATGAAACATGTTGCCACCGTGAACCTAAAGCC 600
QY 601 GGAACCTGTACTTGAATCAAGTAAATGTAATACTGCGATTTGGTCTGAGCAA 660
Db 601 GGAACCTGTACTTGAATCAAGTAAATGTAATACTGCGATTTGGTCTGAGCAA 660
QY 661 TGTGATGATGATGCGCATTTTCTGAAGACTAGCTGTGGAGTCCGAACATATGCTGCTCC 720
Db 661 TGTGATGATGATGCGCATTTTCTGAAGACTAGCTGTGGAGTCCGAACATATGCTGCTCC 720
QY 721 AGAGTAATATCTGTAACATACTATGCTGACCTGAGTGCATGTAAGAGTTGTGGGT 780
Db 721 AGAGTAATATCTGTAACATACTATGCTGACCTGAGTGCATGTAAGAGTTGTGGGT 780
QY 781 GATTCTTTATGCTCTTCTTTGGAAGTCTTCCATTGATGATGAGAAATATCCCAATCT 840
Db 781 GATTCTTTATGCTCTTCTTTGGAAGTCTTCCATTGATGATGAGAAATATCCCAATCT 840
QY 841 GTTCAAAAAAATTAAAGGAGGTATCTACACACTTCCAGTCAATTGCTGCTTGGCCAG 900
Db 841 GTTCAAAAAAATTAAAGGAGGTATCTACACACTTCCAGTCAATTGCTGCTTGGCCAG 900
QY 901 GGATTGATCCCAAGATGCTGTTGTTGAGCCTATGAAGAGAAATCAAAATTAGGGAAT 960
Db 901 GGATTGATCCCAAGATGCTGTTGTTGAGCCTATGAAGAGAAATCAAAATTAGGGAAT 960
QY 961 TCGGAGCATCAATGCTTCCAGATTGCGCTTCCACGTTACTTGGCAGTGCCTCCACCAGA 1020
Db 961 TCGGAGCATCAATGCTTCCAGATTGCGCTTCCACGTTACTTGGCAGTGCCTCCACCAGA 1020
QY 1021 TACGACACAAAGCCAAATGATTGATGAGATACACTTCGAGATGTTGTTAATATGGG 1080
Db 1021 TACGACACAAAGCCAAATGATTGATGAGATACACTTCGAGATGTTGTTAATATGGG 1080
QY 1081 ATTTAACAAGAACATGTGTGTAATCACTGTGACAGCAGACTTCAAAATGAGGCAACTGT 1140

Db 1081 ATTTAACAAGAACATGTGTGTAATCACTGTGACAGCAGACTTCAAAATGAGGCAACTGT 1140
QY 1141 TGCATATTTATTACTATTGGACAATCGGTTTAGAGCACTAGTGGCTATCTTGGGGCAGA 1200
Db 1141 TGCATATTTATTACTATTGGACAATCGGTTTAGAGCACTAGTGGCTATCTTGGGGCAGA 1200
QY 1201 TTATCAAGAAATCAATGACAGGAATTTAAATCAGCTGGGCTCATCTGAATCATCTAGTTC 1260
Db 1201 TTATCAAGAAATCAATGACAGGAATTTAAATCAGCTGGGCTCATCTGAATCATCTAGTTC 1260
QY 1261 TGGTACGAGGAATTATGTTCCAGGAAGCAGTATCCTCATAGCAGTGTGTTGGCCATA 1320
Db 1261 TGGTACGAGGAATTATGTTCCAGGAAGCAGTATCCTCATAGCAGTGTGTTGGCCATA 1320
QY 1321 TTATCCTGTTGAAAAAGAAATGGGCGCTTGACTTCAGTCTCGGGCCACCCCTCGTGAAT 1380
Db 1321 TTATCCTGTTGAAAAAGAAATGGGCGCTTGACTTCAGTCTCGGGCCACCCCTCGTGAAT 1380
QY 1381 AATGTTGAGGCTTTAAAGCACTTCAAGATTTAAACGTACAGATGGAAGAAGATGGGCA 1440
Db 1381 AATGTTGAGGCTTTAAAGCACTTCAAGATTTAAACGTACAGATGGAAGAAGATGGGCA 1440
QY 1441 CTACAAAGTGAATGCAGATGGTGGCCAGGGTTTCCGTGAAGTTAATGACACGTTAGATGC 1500
Db 1441 CTACAAAGTGAATGCAGATGGTGGCCAGGGTTTCCGTGAAGTTAATGACACGTTAGATGC 1500
QY 1501 CAGCAACAGCTTCTTGTTGACTCTACCATCATGATATGATGATGCTAATGGAGGCT 1560
Db 1501 CAGCAACAGCTTCTTGTTGACTCTACCATCATGATATGATGATGCTAATGGAGGCT 1560
QY 1561 ACCTACTGTATCAAGTTGAAATTCAGCTTTCAAGCAGAAAGCAGCAAGTACTCTT 1620
Db 1561 ACCTACTGTATCAAGTTGAAATTCAGCTTTCAAGCAGAAAGCAGCAAGTACTCTT 1620
QY 1621 AGATATGACAGAGTACTGGAAGCTCAGCTGCTCTCTGACTTCTGCGGCTTCTCT 1680
Db 1621 AGATATGACAGAGTACTGGAAGCTCAGCTGCTCTCTGACTTCTGCGGCTTCTCT 1680
QY 1681 TACCAAGCTTAGGTTCTATAGTGTCTACCATGTGCAAAATTTCACTGTGATGAAAT 1740
Db 1681 TACCAAGCTTAGGTTCTATAGTGTCTACCATGTGCAAAATTTCACTGTGATGAAAT 1740
QY 1741 AACCGAAAGCATGTAAATAGGAACCTTGTCTGCTTTTGGACAACGACATGTTGAG 1800
Db 1741 AACCGAAAGCATGTAAATAGGAACCTTGTCTGCTTTTGGACAACGACATGTTGAG 1800
QY 1801 TGACTGGTCTTGTGTGAGCGCGTAAAGGTCATGTATACTTAAGTTAGTACTATTTTGGT 1860
Db 1801 TGACTGGTCTTGTGTGAGCGCGTAAAGGTCATGTATACTTAAGTTAGTACTATTTTGGT 1860
QY 1861 TCTTAATATTTGTCGTCTGCTAGTATGTTCAATTTTGAACCTAAACGTTACGAATTA 1920
Db 1861 TCTTAATATTTGTCGTCTGCTAGTATGTTCAATTTTGAACCTAAACGTTACGAATTA 1920
QY 1921 AAAAAAGTAAAAAAGAAAAA 1948
Db 1921 AAAAAAGTAAAAAAGAAAAA 1948

RESULT 2
US-10-425-114-5805
; Sequence 5805, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5805
LENGTH: 1926
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: 700473306_FLI
US-10-425-114-5805

Query Match 97.9%; Score 1907; DB 13; Length 1926;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1910; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 18 GACCAAGCCGGCATAGCGCCCCCAAGTCCAAAAGCCCTCTCCGCCCGCTCTCCCACTC 77
DB 1 GACCAAGCCGGCATAGCGCCCCCAAGTCCAAAAGCCCTCTCCGCCCGCTCTCCCACTC 60
QY 78 GTAGGTGTTCTCCCGTCTCCGCCGCACTCGCTCGTCCGCGCAGAGAAGTTGACCTG 137
DB 61 GTAGGTGTTCTCCCGTCTCCGCCGCACTCGCTCGTCCGCGCAGAGAAGTTGACCTG 120
QY 138 TCGAGGCGCGCGCAACCCGGTAAGTAAGATGAATAATGATGGAAGTAAGGAGTG 197
DB 121 TCGGGGGCCGCGAGCCCGTAAGTAAGATGAATAATGATGGAAGTAAGGAGTG 180
QY 198 GGCATTCTGAAGCATTAAGGAACCTACAACCTGGGAAGAACTTAAAGTATCGGTACATTTG 257
DB 181 GGCATTCTGAAGCATTAAGGAACCTACAACCTGGGAAGAACTTAAAGTATCGGTACATTTG 240
QY 258 GAAAAGTGAAGATTGACAGACATTAAGCTTACTGACATAGGGTGTCTATAAAGATCATCA 317
DB 241 GAAAAGTGAAGATTGACAGACATTAAGCTTACTGACATAGGGTGTCTATAAAGATCATCA 300
QY 318 ACTGCCGCCAAATGAGAAATATGAAATGGAAGAGAAAAGAGAGAAATCAAGATAT 377
DB 301 ACTGCCGCCAAATGAGAAATATGAAATGGAAGAGAAAAGAGAGAAATCAAGATAT 360
QY 378 TGAAGTTGTTCAATCAACCCCATATCATTCGGCTTATGAGGTCATATACACCTACAG 437
DB 361 TGAAGTTGTTCAATCAACCCCATATCATTCGGCTTATGAGGTCATATACACCTACAG 420
QY 438 ATATATATGTTGTGATGGAATATTGTAAGTATGCGAGTTATTGATTACATTGTTGAGA 497
DB 421 ATATATATGTTGTGATGGAATATTGTAAGTATGCGAGTTATTGATTACATTGTTGAGA 480
QY 498 AAGGCAGATTACAGGAAGATGAAGCTCGTGAATCTTCCAGCAGATCATATCTGGCGTCG 557
DB 481 AAGGCAGATTACAGGAAGATGAAGCTCGTGAATCTTCCAGCAGATCATATCTGGCGTCG 540
QY 558 AATAGTCCCATAGAAAATGTTGTGCCACCGTGAACCTTAAAGCCGGAACCTGTTACTTG 617
DB 541 AATAGTCCCATAGAAAATGTTGTGCCACCGTGAACCTTAAAGCCGGAACCTGTTACTTG 600
QY 618 ATTCAAAGTATAATGTAAAACTTGCAGATTTTGTCTGAGCAATGTCAATGATGATGCC 677
DB 601 ATTCAAAGTATAATGTAAAACTTGCAGATTTTGTCTGAGCAATGTCAATGATGATGCC 660
QY 678 ATTTCTGAAGACTGAGCTGTGGAGTCCGAACCTATGCTGCTCCAGAGTAATATCTGTA 737
DB 661 ATTTCTGAAGACTGAGCTGTGGAGTCCGAACCTATGCTGCTCCAGAGTAATATCTGTA 720
QY 738 AACTATATGCTGAGCTGAGGTGATGATGAGTTGTGGGTGATTTTATGCTCTTC 797
DB 721 AACTATATGCTGAGCTGAGGTGATGATGAGTTGTGGGTGATTTTATGCTCTTC 780
QY 798 TTTGTGGAACCTTTCCATTGATGATGAGAAATATCCCAATCTGTTCAAAAAAATTAAAG 857
DB 781 TTTGTGGAACCTTTCCATTGATGATGAGAAATATCCCAATCTGTTCAAAAAAATTAAAG 840
QY 858 GAGGTATCTACACTTCCAAAGTCATTGTCTGCTTTGGCCAGGAGATTGATCCACGAA 917

DB 841 GAGGTATCTACACTTCCAAAGTCATTGTCTGCTTTGGCCAGGATTTGATCCACGAA 900
QY 918 TGCTTGTGTTGAGCCCTATGAAGAGAAATCAAAATTAGGAAATTCGGGACATCAATGCT 977
DB 901 TGCTTGTGTTGAGCCCTATGAAGAGAAATCAAAATTAGGAAATTCGGGACATCAATGCT 960
QY 978 TCCAGATTGCGCTTCCACGTTACTTGGCAGTGCCTCCACAGATACACAACAAGCCA 1037
DB 961 TCCAGATTGCGCTTCCACGTTACTTGGCAGTGCCTCCACAGATACACAACAAGCCA 1020
QY 1038 AAATGATTGATGAAGATACACTTCGAGATGTTGTTAATATGGAATTTAAACAAGACCATG 1097
DB 1021 AAATGATTGATGAAGATACACTTCGAGATGTTGTTAATATGGAATTTAAACAAGACCATG 1080
QY 1098 TGTGTGAATCACTGTGCAGCAGACTTCAAAATGAGGCAACTGTTCATATTTACTAT 1157
DB 1081 TGTGTGAATCACTGTGCAGCAGACTTCAAAATGAGGCAACTGTTCATATTTACTAT 1140
QY 1158 TGGCAATCGGTTTAAAGCAACTAGTGGCTATCTTGGGGCAGATTATCAAGAATCAATGG 1217
DB 1141 TGGCAATCGGTTTAAAGCAACTAGTGGCTATCTTGGGGCAGATTATCAAGAATCAATGG 1200
QY 1218 ACAGAAATTTAAATCAAGCTGCGCTCATCTGAATCATCTAGTTCTGGTAAGGAATTAAG 1277
DB 1201 ACAGAAATTTAAATCAAGCTGCGCTCATCTGAATCATCTAGTTCTGGTAAGGAATTAAG 1260
QY 1278 TTCCAGGAAGCAGTGATCCTCATAGCAGTGTGTCGGCCATATTAATCCTGTGAAGAA 1337
DB 1261 TTCCAGGAAGCAGTGATCCTCATAGCAGTGTGTCGGCCATATTAATCCTGTGAAGAA 1320
QY 1338 AATGGCGGCTGGAATTCAGTCTCGGCCCAACCTCGTGAATTAATGTTGAGGCTTAA 1397
DB 1321 AATGGCGGCTGGAATTCAGTCTCGGCCCAACCTCGTGAATTAATGTTGAGGCTTAA 1380
QY 1398 AAGCACTTCAGAAATTTAAACGTCAGATGGAAGAAGATGGGCATACAACTGAATGCA 1457
DB 1381 AAGCACTTCAGAAATTTAAACGTCAGATGGAAGAAGATGGGCATACAACTGAATGCA 1440
QY 1458 GATGTCGCCAGGGTTTCTGGAAGTTAATGACACGTTAGATGCCAGAACAGCTTCTTG 1517
DB 1441 GATGTCGCCAGGGTTTCTGGAAGTTAATGACACGTTAGATGCCAGAACAGCTTCTTG 1500
QY 1518 GTGACTTACCATCATGATGAATGATGCTAATGGAGGCTAATCTGTGATCAAGT 1577
DB 1501 GTGACTTACCATCATGATGAATGATGCTAATGGAGGCTAATCTGTGATCAAGT 1560
QY 1578 TTGAATTCAGCTTTTACAAGACGAAGACGAACAAGTACCTTTAGATATGACAGAGATTA 1637
DB 1561 TTGAATTCAGCTTTTACAAGACGAAGACGAACAAGTACCTTTAGATATGACAGAGATTA 1620
QY 1638 CTGACCTCAGCTGCTCTTCTGACTTCTGTCGGGCTTCCCTTACCAAGCTTAGGGTTC 1697
DB 1621 CTGACCTCAGCTGCTCTTCTGACTTCTGTCGGGCTTCCCTTACCAAGCTTAGGGTTC 1680
QY 1698 TATAGTGTCTAACCATGTGCAAAATTTTCACTGTGTGATGAATTAACGAAAGCATGTAA 1757
DB 1681 TATAGTGTCTAACCATGTGCAAAATTTTCACTGTGTGATGAATTAACGAAAGCATGTAA 1740
QY 1758 TAGGAACCTGTTCTGCTCTTTTGAACAAGAACATGTTGAGTGAAGTCTGCTTGTGTTG 1817
DB 1741 TAGGAACCTGTTCTGCTCTTTTGAACAAGAACATGTTGAGTGAAGTCTGCTTGTGTTG 1800
QY 1818 AGCGGTAAGGTCATGTATATCTTAAGTTAGTACTATTTTCTTAAATATTTGTCGT 1877
DB 1801 AGCGGTAAGGTCATGTATCTTAAGTTAGTACTATTTTCTTAAATATTTGTCGT 1860
QY 1878 CTGCTAGTATAGTTTCAATTTTGAAGTAAACGTTACGAATAAAAAAGAGTAA 1932
DB 1861 CTGCTAGTATAGTTTCAATTTTGAAGTAAACGTTACGAATAAAAAAGAGTATA 1915

RESULT 3

US-10-425-114-5415
; Sequence 5415, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5415
; LENGTH: 1300
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700454849_FU1
US-10-425-114-5415

Query Match 62.8%; Score 1222.4; DB 13; Length 1300;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1223; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 709 CTATGCTGCTCCAGAGTATATCTGTAACTATATGCTGACCTGAGCTGATGATG 768
DB 1 CTATGCTGCTCCAGAGTATATCTGTAACTATATGCTGACCTGAGCTGATGATG 60
QY 769 GAGTGTGGGGGATCTTTATGCTCTCTTTGTGGAACCTCTCCATTGTGATGAGAA 828
DB 61 GAGTGTGGGGGATCTTTATGCTCTCTTTGTGGAACCTCTCCATTGTGATGAGAA 120
QY 829 TATTTCCCAATCTGTTCAAAAAATTAAAGGAGTATCTACACACTTCCAACTTTGTC 888
DB 121 TATTTCCCAATCTGTTCAAAAAATTAAAGGAGTATCTACACACTTCCAACTTTGTC 180
QY 889 TGCTTTGGCCAGGATTTGATCCCAAGATGCTGTTGTGAGCCTATGAAGAATCAC 948
DB 181 TGCTTTGGCCAGGATTTGATCCCAAGATGCTGTTGTGAGCCTATGAAGAATCAC 240
QY 949 AATTAGGAAATTCGGGAGCATCAATGTTCCAGATTCGCCCTCCACTTATCTGGCAGT 1008
DB 241 AATTAGGAAATTCGGGAGCATCAATGTTCCAGATTCGCCCTCCACTTATCTGGCAGT 300
QY 1009 GCCTCCACGATAGCACACAAGCCAAATGATTGATGAAGATACCTTCGAGATGT 1068
DB 301 GCCTCCACGATAGCACACAAGCCAAATGATTGATGAAGATACCTTCGAGATGT 360
QY 1069 TGTATATATGGATTTTAACAAGAACCATGTGTGAATCACTGTGCAGAGACTTCAAAA 1128
DB 361 TGTATATATGGATTTTAACAAGAACCATGTGTGAATCACTGTGCAGAGACTTCAAAA 420
QY 1129 TGAGGCAACTGTTGCATATTATTACTATTGGACAATCGGTTTAAAGCACTAGTGCTA 1188
DB 421 TGAGGCAACTGTTGCATATTATTACTATTGGACAATCGGTTTAAAGCACTAGTGCTA 480
QY 1189 TCTTTGGGGCAGATTATCAAGAATCAATGACAGGAATTTAAATCAGTGGCGTCATCTGA 1248
DB 481 TCTTTGGGGCAGATTATCAAGAATCAATGACAGGAATTTAAATCAGTGGCGTCATCTGA 540
QY 1249 ATCATCTAGTTCTGTACGAGGAATTAATTCAGGAAGCAGTGAATCCTCATAGCAGTGG 1308
DB 541 ATCATCTAGTTCTGTGTACGAGGAATTAATTCAGGAAGCAGTGAATCCTCATAGCAGTGG 600
QY 1309 TTTGCGGCCATATATATCTCTGTGAAGAATAATGGCGCTTGACCTTCAGTCTCGGCCCA 1368
DB 601 TTTGCGGCCATATATATCTCTGTGAAGAATAATGGCGCTTGACCTTCAGTCTCGGCCCA 660
QY 1369 CCCTCGTGAATAATGCTTGAGGTCTTAAAGCACTTCAAGATTTAAAGCTCAGATGAA 1428

DB 661 CCTCGTGAATAATGCTTGAGGTCTTAAAGCACTTCAAGAATTTAAAGCTCAGATGAA 720
QY 1429 GAAGATGGGCACTACAAAGTGAATGACAGATGAGTGCCCGAGGTTTCTGAAGTTAATGA 1488
DB 721 GAAGATGGGCACTACAAAGTGAATGACAGATGAGTGCCCGAGGTTTCTGAAGTTAATGA 780
QY 1489 CACGTTAGATGCCAGCAACAGCTTTCTTGTGACTCTTACCATCATGATGATGATGC 1548
DB 781 CACGTTAGATGCCAGCAACAGCTTTCTTGTGACTCTTACCATCATGATGATGATGC 840
QY 1549 TAATGGAGGCTACCTACTGTGATCAAGTTGAATTCCAGCTTTTACAAGACGAAGACGA 1608
DB 841 TAATGGAGGCTACCTACTGTGATCAAGTTGAATTCCAGCTTTTACAAGACGAAGACGA 900
QY 1609 CAACTACTCTTAGATATGACAGAGTTACTGACCTCAGCTGCTCTTCTGACTTCTG 1668
DB 901 CAACTACTCTTAGATATGACAGAGTTACTGACCTCAGCTGCTCTTCTGACTTCTG 960
QY 1669 TGCGGCTTCTTACCAGCTTAGGGTTCTATAGTGGTCAACATGTGCAAAATTTCACT 1728
DB 961 TGCGGCTTCTTACCAGCTTAGGGTTCTATAGTGGTCAACATGTGCAAAATTTCACT 1020
QY 1729 GTGCTGATGAATAACCGAAGCATGTAAATAGGAACCTTGTCTGCTTTTGACAAACG 1788
DB 1021 GTGCTGATGAATAACCGAAGCATGTAAATAGGAACCTTGTCTGCTTTTGACAAACG 1080
QY 1789 AACATGTTTGAAGTACTGCTGTTGTGTGAGCGCGTAAAGGTCATGATACCTTAGGTTAG 1848
DB 1081 AACATGTTTGAAGTACTGCTGTTGTGTGAGCGCGTAAAGGTCATGATACCTTAGGTTAG 1140
QY 1849 TACTATTTTCTGTTCTTAAATATTTGCTGCTGCTAGTATGATGTTTATTTGAAGTAA 1908
DB 1141 TACTATTTTCTGTTCTTAAATATTTGCTGCTGCTAGTATGATGTTTATTTGAAGTAA 1200
QY 1909 CGTTACGAATTAATAAAGAGTAA 1932
DB 1201 CGTTACGAATTAATAAAGAGTAA 1224

RESULT 4
US-10-183-687-255
; Sequence 255, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harwell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: BBI458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 255
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-183-687-255

| Query Match | Best Local Similarity | Score | DB | Length | Mismatches | Conservative | Mismatches | Indels | Gaps |
|-------------|--|--|------|--------|------------|--------------|------------|--------|------|
| 61.4%; | 85.8%; | 1195.6; | 13; | 1899; | 0; | 0; | 219; | 0; | 0; |
| Db | | | | | | | | | |
| 166 | AGTAAATGATGGAAGTAAAGGAGTGGCATTCGAACTTAAGAACTACA | 225 | | | | | | | |
| 60 | AGTAAATGGAAGGAACTAGAGAGGTGGCATTCGACCTTAAGAACTACA | 119 | | | | | | | |
| Qy | 226 | CCTGGAGAAGCTTTAGGTATCGGTACATTTGAAAAGTGAAGATTGCAGAGCATAGCT | 285 | | | | | | |
| Db | 120 | TGTGGCGAGAACATTAGGTATGACATTTGAAAAGTGAAGATTGCAGAGCATAGCA | 179 | | | | | | |
| Qy | 286 | TACTGACATAGGGTTGCTATTAAGATCATCACTGCCGCCAAATGAGAAATATGAAAT | 345 | | | | | | |
| Db | 180 | TACAGGGCATTAAGTTGCTATTAAGATTTGAAACCGTCGTCAAATGAGAACTATGAAAT | 239 | | | | | | |
| Qy | 346 | GGAAGAGAAAAGCAAGAGAGAAATTCAGATATTGAAGTTGTTCAATCAACCCCATATCAT | 405 | | | | | | |
| Db | 240 | GAAGAGAAAAGCAAGAGAGATCAAGATATTGAGGTGTTCAATCAACCCCATATCAT | 299 | | | | | | |
| Qy | 406 | TCGGCTTTATGAGGTCAATATACACCTACAGATATATATGTTGATGGAATATTTGTA | 465 | | | | | | |
| Db | 300 | CCGGCTTTATGAGGTCAATATACACCTACAGATATATATGTTGATGGAATATTTGCA | 359 | | | | | | |
| Qy | 466 | GTATGGCAGTTATTGATTACATTGTTGAGAAAGCAGATTACAGAAAGATGAAGCTCG | 525 | | | | | | |
| Db | 360 | GTAATGTTAGCTATTGCACTGCACTGTTGAGAAAGGCGGTTACAGAAAGATGAGGCTCG | 419 | | | | | | |
| Qy | 526 | TCGAATCTTCCAGCAGATCATATCTGGCGTCGAATACCTGCCATAGAAACATGTTGTCCA | 585 | | | | | | |
| Db | 420 | TCGAATCTTCCAGCAGATCATATCTGGCGTTGAATACCTGCCATAGAAACATGTTGTCCA | 479 | | | | | | |
| Qy | 586 | CCGTGAACCTAAAGCCGGAACCTTTGTTACTTGATTCGAAGTAAATGTAAACCTTGGCA | 645 | | | | | | |
| Db | 480 | TCGTGATCTAAAGCCAGAGAACCTGTTACTTGATTCGAATTAATGTAAACCTTGGCA | 539 | | | | | | |
| Qy | 646 | TTTTGCTCTGAGCAATGTCATGATGAGCCATTTCTGAAGCTAGCTGTGGAGTCC | 705 | | | | | | |
| Db | 540 | CTTGGGTTAAGTAATGTCATGATGAGCCATTTCTGAAGCTAGCTGTGGAGTCC | 599 | | | | | | |
| Qy | 706 | GAACTATGCTGCTCCAGAGTAAATCTGTTAACTATATGCTGGAACCTGAGTGCATGT | 765 | | | | | | |
| Db | 600 | AAACTATGCTGCACAGAGTTATCTCAGTAAATATATACGCTGGAACCTGAGTTGATGT | 659 | | | | | | |
| Qy | 766 | ATGAGTTGTGGGTGATTCTTATGCTCTTCTTTGTGAACCTTCCATTGTGATGA | 825 | | | | | | |
| Db | 660 | TTGAGCTGCGGGGTGATACTTATGCTCTTCTTTGTGGCACTTCCATTGTGATGA | 719 | | | | | | |
| Qy | 826 | GAATATTTCCCAATCTGTTCAAAAAATTAAGGAGGTATCTACACTTCCAAGTCATT | 885 | | | | | | |
| Db | 720 | CAATATTTCCCAACTGTTCAAAAAATTAAGGAGGATCTATATCTTCCAAGTCATT | 779 | | | | | | |
| Qy | 886 | GTTCTGCTTTGGCCAGGATTTGATCCCAAGATGCTTGTGTTGAAGCTATGAAGAGAA | 945 | | | | | | |
| Db | 780 | ATCTGCTCTTGCAAGGATTTGATCCCAAGATGCTTGTGTTGAATCCTATGAAGAGAA | 839 | | | | | | |
| Qy | 946 | CACAATTAGGGAATTCGGAGCATCAATGTTCCAGATTGCTTCCACGTTACTTGGC | 1005 | | | | | | |
| Db | 840 | CACAATTGCGGAATTCGAGAACCCATGTTTCAGAAATGCTTCCCTGCTACCTGCG | 899 | | | | | | |
| Qy | 1006 | AGTCCCTCCACCAGATACGACACAACAAGCCAAATGATTTGAAGATACACTTCGAG | 1065 | | | | | | |
| Db | 900 | AGTCCCTCCACCAGACACGCGCAGCAAGCCAAATGATTTGAAGATACACTTAAGA | 959 | | | | | | |
| Qy | 1066 | TGTTGTTAATATGGATTAAACAAGAACCATGTGTGTAATCACTGTGCAGCAGACTTCA | 1125 | | | | | | |
| Db | 960 | GATTTGCAACCTGGATATGATTAAGAACCATGTGTGTAATCATTTGTCAATAGGCTCA | 1019 | | | | | | |
| Qy | 1126 | AAATGAGGCAACTGTTGCATATTTACTATTTGAGCAATCGGTTTGAAGCACTAGTGG | 1185 | | | | | | |
| Db | 1020 | AAATGAGGCAACTGTTGCATATTTACTATTTGAGCAATCGGTTCCGGGCCACTAGTGG | 1079 | | | | | | |
| Qy | 1186 | CTATCTTGGGCGAGATTATCAAGAAATCAATGAGCAGGAATTTAATCAGCTGGCGTATC | 1245 | | | | | | |

Db 1080 CTATTTGGGGGCTGACTATCTACAATCAATGGGTAGAGAGTTTAATCAGTTTACTTCATT 1139

Qy 1246 TGAATCATCTAGTCTGTGTAGCAGGAATTATGTTCCAGAAGCAGTGATCTCATAGCAG 1305

Db 1140 GGAATCAGCAAGCCCAAGTACCAGGCGAGTATCTTCCAGCAAGCAATGATTTCTCAAGCCAG 1199

Qy 1306 TGGTTTGGCGGCCATATTAATCCTGTTGAAAGAAAAATGGGCGCTTGAGCTTCAGTCTCGGGC 1365

Db 1200 TGGCTTGGCGGCCATATTAATCCCGTTGAAAGAAAAATGGGCTCTTGGGCTCCAGTCTCGAGC 1259

Qy 1366 CCACCCCTCGTGAATAATAGTTGAGGTCTTAAGACACTTCAAGAATTAAAGTCAGATG 1425

Db 1260 TCAACCTCGTAGATAATGATCGAGGTTCTAAAGGCACTTCAAGAATTAAATGCTGCTG 1319

Qy 1426 GAAGAAGAATGGGCACTACAACGTGAATGCAATGCTGCCCCAGGGTTTCTGAAGTTAA 1485

Db 1320 GAAGAAGAATGGACACTACACATGAATGCAAGTGGTGCCCTGGGTTTCTCAGGTCAG 1379

Qy 1486 TGACACGTTAGATGCGCAGCAACAGCTTCTTGGTGACTCTACCATCATGATAATGATGA 1545

Db 1380 TGATATGTTAGATGCCAACCAACAGCTTGTGATGACTCTACCATCATGATAACGGCGA 1439

Qy 1546 TGCTAATGGAGGCTACCTACTGTGATCAAGTTTGAATTCAGCTTTACAAGACGAAGA 1605

Db 1440 TGCTAATGGAGGCTACCTGCGGTGATCAAGTTTGAATTCAGCTTTACAAGACCAAGA 1499

Qy 1606 CGACAAGTACCTTTAGATATGCAGAGAGTTACTGGAACCTCAGCTGCTCTTCTGACTT 1665

Db 1500 TGACAAGTACCTGCTAGATATGCAGAGAGTTACTGGAACCTCAGCTCCTCTCTGATTT 1559

Qy 1666 CTGTGCGGCTTCTCTTAACCAAGCTTAGGGTTCTAATAGTGCTACC 1711

Db 1560 TTGCGCGGCTTCTCTTAACCAACCTTAGGGTTCTAATAGTATGTGCC 1605

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RESULT 5
US-10-425-114-22369
; Sequence 22369, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21 (53131)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 22369
; LENGTH: 2119
; TYPE: DNA
; ORGANISM: Oryza sativa niponbare
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3477-009-G7_FLI
US-10-425-114-22369

```

| Query Match | 61.0%; | Score 1188.4; | DB 13; | Length 2119; |
|-----------------------|--------------|--|-----------------|--------------|
| Best Local Similarity | 85.4%; | Pred. No. 0; | | |
| Matches 1337; | Conservative | 0; | Mismatches 226; | Indels 3; |
| | | | Gaps | 1; |
| QY | 143 | GGCCGGCAACCCGGTAAGTAAGATGAAATGATGGAAGTAGTAAGGAGTGGGCAT | 202 | |
| | | | | |
| Db | 100 | GGGGGGGAGCTCCGGCGTGCTCAGTGAATGATGGAATGCTAAGCGCGTGGGCAT | 159 | |
| QY | 203 | TCTGAAGCATTAAGAACTACAACCTGGGAGAACTTTAGGTATCGGTACATTTGGAAAA | 262 | |
| | | | | |
| Db | 160 | TCTGAGGCACGTGAAGAACTACAATCTTTGGAGAACTTTAGGTATTTGGCTCATTTGGAAAA | 219 | |

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QY 263 GTGAAGATTGCAGACATTAAGCTTACTGGAACATAGGGTTGCTTATAAGATCATCAACTGC 322
    |||
DB 220 GTGAAGATTGCAGACATTAAGCTTACAGGACACAGAGTTGCTATTAAGATCCTGAACCGC 279
QY 323 CGCCAAATGAGAAATATGGAATGGAAGAAAGCAAGAGAAATCAAGATATTGAAG 382
    |||
DB 280 CGCCAAATGAGAAATATGGAATGAGAGAAAGCAAGAGAAATCAAGATATTGAAG 339
QY 383 TTGTTCAATTCACCCCATATCATTCGGCTTATGAGTCAATATACACCTACAGATATA 442
    |||
DB 340 TTGTTCAATTCACCCCATATCATTCGGCTTATGAGTCAATATACACCTACAGATATA 399
QY 443 TATGTTGTGATGGAATATTTGTAAGTATGCGCAGTTATTGATTACATTGTGAGAAAGGC 502
    |||
DB 400 TATGTTGTGATGAGTACTGCAAGTTTGAGAACTGTTGATTACATTGTGAGAAAGGC 459
QY 503 AGATTACAGAGATGAAGCTCGTGAATCTTCAGACAGATCATATCTGGCGTGAATAC 562
    |||
DB 460 AGTTGACAGAGATGAGGCTCGCCGAATCTTCAGACAGATTATCTGGGGTTGAATAC 519
QY 563 TGCCATAGAAACATGTTGTCCACCGTGACCTAAAGCCGAAACCTTGTTACTTGATTCA 622
    |||
DB 520 TGCCACAGAAACATGTTGTTCATCTGATCTGAAGCCAGAAACCTTGCTAGATTCA 579
QY 623 AAGTATATGTAAACTTGCGGATTTTGGTCTGAGCAATGTCAATGATGGCCATTTT 682
    |||
DB 580 AAGTATATGTAAAGCTTGCTGACTTTGGTTGAGTAACGTCAATGATGGCCATTTT 639
QY 683 CTGAAGACTAGCTGTGGGAGTCCGAACATATGCTCTCCAGAGGTAAATCTGTAAACTA 742
    |||
DB 640 TTGAAGACAAAGCTGTGGGAGTCCAACTATGCTCTCCAGAGGTGATCTGTAAATTA 699
QY 743 TATGCTGACCTGAGGCTCGATGTATGAGTTGGGGTGATCTTTATGCTCTTCTTGT 802
    |||
DB 700 TATGCTGACCTGAGGCTGATGTATGAGTTGGAGTGTGATCTTTATGCTCTTCTTGT 759
QY 803 GGAACCTCTTCATTGATGATGAGAAATATCCCAATCTGTTCAAAAAATTAAAGGAGGT 862
    |||
DB 760 GGTACTCTTCATTGATGATGAGAAATATCCCAACTATTCAAAAAGTAAGGAGGT 819
QY 863 ATCTACACACTTCCAAAGTCAATTTGTCTGCTTGGCCAGGATTTGATCCCAAGATGCTT 922
    |||
DB 820 ATATATACTCTCCCAAGTCAATTTATCTGCTGTGGCCAGAGATTTGATCCCAAGATGCTT 879
QY 923 GTTGTGAGCCTTAAGAAGAAATCACAATTAGGAAATTCCGAGCAATCAATGTTCCAG 982
    |||
DB 880 GTTGTGATCCCAATGAAGAAATCACAATTCGTAATTCGAGAGCATCAATGTTCCAG 939
QY 983 ATTGCGCTTCCACGTTACTTGGCAGTGCCTCCACAGATACGACACACAAGCCAAATG 1042
    |||
DB 940 ATTGCGCTTCCACGTTACTTGGCAGTGCCTCCACAGACACAGACACAAGCCAAATG 999
QY 1043 ATGATGAAGATACACTTGAGATGTTGTTAATATGGATTAAACAAGAACCATGTGTGT 1102
    |||
DB 1000 ATGATGAAGATACCTTCAAGATGTCGTAAACTTGGGTTATGAAAGACCATGTGTGT 1059
QY 1103 GAATCACTGTGCAGACACTTCAAAATGAGGCACTGTGCATATATTACTATTGAGAC 1162
    |||
DB 1060 GAATCTCTGGCAATAGACTGCAGAAATGAGGCACTGTGCATATATTACTCTTGAC 1119
QY 1163 AATCGTTTAGACAATACTAGTGGCTATCTTGGGCGAGATTATCAAGAAATCAATGACAGG 1222
    |||
DB 1120 AATCGATTCGAGCTACAGTGGCTATTTGGGAGCAAGACTATCAAGAAATCTTTGAGAGG 1179
QY 1223 AATTAAATCAGCTGGCGTCACTGAATCATCTAGTCTGTGAGAGAAATTAATGTTCCA 1282
    |||
DB 1180 AATTAAATCAGCTTTGCTTCACTGGAATCAGCAAGTTCAAAATACAAAGCAATTAATCTTCCA 1239
QY 1283 GGAAGCAGTATCTCATAGCAGTGTGTTGGCGCATATTATCTGTGAAAGAAATG 1342
    |||
DB 1240 GGAAGCAGTATCTCATAGCAGTGTGTTGGCGCATATTATCTGTGAAAGAAATG 1299
QY 1343 GCGCTTGACTTCACTCTCGGGCCACCCCTGTAATAATGTTGAGGCTTTAAAGCA 1402
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DB 1300 GCTCTGGACTTCAGTCAAGCTCAACCTCGCGAGATATGATGAGGCTCTAAAGGCA 1359
QY 1403 CTTCAAGATTTAAACGTACAGATGGAAGAATGGGCACTTCAACGTGAATGACAGATGG 1462
    |||
DB 1360 CTTCAAGACTTTAAATGTCTCTCGAAGAAGATGGACAGTACATGAATGACAGATGG 1419
QY 1463 TGCCAGGCTTCTGAGTTAATGACACGTTAGATGCGCAGCAACAGCTTCTTGTTGAC 1522
    |||
DB 1420 AGCGTTGGG--ACTCAGGCCACTGATATGTTAGATGTTAACAACAGCTTGTGATGAC 1476
QY 1523 TCTACCATCATGGAATATGATGATGCTAATGAGGAGGCTACTACTGTGATCAAGTTGAA 1582
    |||
DB 1477 TCAATCAATGATGATTAACGGTGAATGAATGGAGGCTACTGCTGATCAAGTTGAA 1536
QY 1583 TTCCAGCTTTAACAAGACGAAGGACGAACATACCTTTAGATATGACAGAGATTACTGA 1642
    |||
DB 1537 ATCCAGCTTTAACAAGACGAAGGAGAGATATCTGCTGATATGACAGAGATTAGGGG 1596
QY 1643 CCTCAGCTGCTCTCTCTTGAATCTGTGCGGCTTCCCTTACCAAGCTTAGGTTCTATAG 1702
    |||
DB 1597 CCTCAGCTCTTCTTCTGAGCTTCTGAGCTTCTGTGACAGACTTCTTACCAAGCTGAGGTTCTATAG 1656
QY 1703 TGGTCT 1708
    |||
DB 1657 TACCTT 1662
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RESULT 6
US-10-437-963-49666/c
; Sequence 49666, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 49666
; LENGTH: 2607
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52228C.1
US-10-437-963-49666

Query Match      61.0%; Score 1188.4; DB 17; Length 2607;
Best Local Similarity 85.4%; Pred. No. 0;
Matches 1337; Conservative 0; Mismatches 226; Indels 3; Gaps 1;

QY 143 GGGCGGGCAACCCGGTAAGTAAGTGAAGAAATGATGAGTAAGTAAGGAGTGGGCAT 202
    |||
DB 2063 GGGCGGGGAGCTCCGGCTGCTCAGTGAAGAAATGATGAGTAAGTAAGGCGGTGGCAT 2004
QY 203 TCTGAAGCAATTAAGAACTTCAACCTGGGAAGAACTTTAGTATCGGTACATTGGAAAA 262
    |||
DB 2003 TCTGAGGCACTGAAGAACTTCAACCTTTGGAAGAACTTTAGTATGCTCATTTGAAAA 1944
QY 263 GTGAAGATTGCAGAGCATTAAGCTTATGACATAGGGTTGCTAATAAGATCATCAACTGC 322
    |||
DB 1943 GTGAAGATTGCAGAGCATTAAGCTTATGACACAGAGTTGCTAATAAGATCCTGAACCGC 1884
QY 323 CGCCAAATGAGAAATATGGAATGGAAGAAAGCAAGAGAAATTCAGATATTGAAG 382
    |||
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Db 1883 CGCCAAATGAGAAATATGAAATGAGAGAAAGCAAAAGAGAAATCAAGATCTGAGA 1824

Qy 383 TTGTTTCATTCACCCCATATCATTCGGCTTATAGAGTCATATACACCTACAGATATA 442

Db 1823 TTGTTTCATTCACCCCATATCATTCGGCTTATAGAGTCATATACACCTACAGATATA 1764

Qy 443 TATGTTGATGGAATATTTAGTATGGCGAGTTATTTGATTACATTTGGAAGAGC 502

Db 1763 TATGTTGATGGAATATTTAGTATGGCGAGTTATTTGATTACATTTGGAAGAGC 1704

Qy 503 AGATTACAGAGATGAGAGCTCGTGAATCTTCCAGCAGATCATATCTGGCGTCGAATAC 562

Db 1703 AGTTGACAGAGATGAGAGCTCGCGGAATCTTCCAGCAGATCATATCTGGCGTCGAATAC 1644

Qy 563 TGCCATAGAAACATGGTGTTCACCCGTGACCTAAAGCCGAAACTTGTACTGATTCGA 622

Db 1643 TGCCACAGAAACATGGTGTTCATCGTATCGAAGCCAGAAACTTGTACTGATTCGA 1584

Qy 623 AAGTATATGTAATACTGCGGATTTGGTCTGAGCAATGTCATGATGCGCATTTT 682

Db 1583 AAGTATATGTAATACTTGTCTGACTTTGGTTGAGTAACGTCAATGATGCGCATTTT 1524

Qy 683 CTGAGACTAGCTGTGGAGTCCGAATCTGCTCCAGAGTAATCTGGTAACTA 742

Db 1523 TTGAAGACAGCTGTGGAGTCCAACTATGCTCTCCAGAGTATCTGTGTAATTA 1464

Qy 743 TATGCTGACCTGAGGTCGATGTATGAGTTGCGGCTGATCTTTATGCTCTTCTTGT 802

Db 1463 TATGCTGACCTGAGGTCGATGTATGAGTTGCGGCTGATGTATGCTCTTCTTGT 1404

Qy 803 GGAATCTTTCATTTGATGAGAAATATTCCTCAATCTGTTCAAAAAAATTAAAGGAGGT 862

Db 1403 GGTACTCTTTCATTTGATGAGAAATATTCCTCAATCTGTTCAAAAAAATTAAAGGAGGT 1344

Qy 863 ATCTACACTTCCAAAGTCAATTTGCTGCTTGGCCAGGATTTGATCCCAAGATGCTT 922

Db 1343 ATATATCTCTCCCAAGTCAATTTGCTGCTGCGCAGAGATTTGATCCCAAGATGCTT 1284

Qy 923 GTTGTGAGCTTATGAGAGAAATCAAAATTAGGAAATTGCGAGCATCAATGTTCCAG 982

Db 1283 GTTGTGATCCAAATGAGAGAAATCAAAATTGGAATTCGAGAGCATCAATGTTCCAG 1224

Qy 983 ATTGCGCTTCCACGTTACTTGGCAGTGCCTCCACAGATACGACACACAAGCCAAATG 1042

Db 1223 ATTGCGCTTCCGTTACTTAGCAGTGCCTCCACAGACACAGCACAAGCCAAATG 1164

Qy 1043 ATTGATGAGATACACTTCGAGATGTTGTTAATATGGATTTAACAAACCATGTGTGT 1102

Db 1163 ATTGATGAGATACCTCTCAAGATGTCGTTAACTTGGGTTATGAAAGAACCATGTGTGT 1104

Qy 1103 GAATCACTGTGACGACAGACTTCAAAATGAGGCAACTGTTGCATATTAATTAATTTGAC 1162

Db 1103 GAATCTCTGCGCAATGAGCTGAGAAATGAGCAACTGTTGCATATTAATTAATTTGAC 1044

Qy 1163 AATCGTTTAGAGCAACTAGTGGCTATCTTGGGCGAGATTATCAAGAAATCAATGACAGG 1222

Db 1043 AATCGATTCGAGCTACAGTGGCTATTTGGGAGCAGACTATCAAGAAATCTTTGAGAGG 984

Qy 1223 AATTTAAATCAGCTGGCGTCATCTGAATCTAGTTCTGTAGAGGAATTAATGTTCCA 1282

Db 983 AATTTAAATCAGCTTGTCTTCAATCAAGCAAGTCAATTAATCAAGCAATTAATCTTCCA 924

Qy 1283 GGAAGCAGTATCTCATAGCAGTGTGTTGGGCGCATATTAATCTGTTGAAAGAAATGG 1342

Db 923 GGAAGCAGTATCTCATAGCAGTGTGTTGGGCGCATATTAATCTGTTGAAAGAAATGG 864

Qy 1343 GCGCTTGAATCTCAGTCTGGGCGCCACCTCGTGAATTAATGTTGAGGTCTTAAAGCA 1402

Db 863 GCTCTTGAATCTCAGTCTGGGCGCCACCTCGGAGATTAATGAGGTCTTAAAGCA 804

Qy 1403 CTTCAAGATTAAGCGTCAGATGGAAGAAATGGGCACTACAACTGAATGCAAGATGG 1462

Db 803 CTTCAAGATTAATGTCTCTGGAAGAAATGAGCAGTACAACTGAATGCAAGATGG 744

Qy 1463 TGCCAGGCTTCTCGAAGTTAATGACACCTTAGATGCCAGCAACAGCTTCTTGCTGAC 1522

Db 743 AGCGTTGGG--ACTCAGGCCACTGATATGTTAGATGTTAAACAGCTTGTGATGAC 687

Qy 1523 TCTACCATCATGATTAATGATGATGCTAATGAGGCTTACTACTGTGATCAAGTTGAA 1582

Db 686 TCAATCAATATGATTAACGCTGATGTAATGAGGCTTACTGCTGATCAAGTTGAA 627

Qy 1583 TTCCAGCTTTACAAGACGAAAGACAGCAAGTACTCTTAGATATGACAGAGTTACTGGA 1642

Db 626 ATCCAGCTTTACAAGACGAAAGACAGCAAGTATCTGCTGATATGACAGAGTTACGGGG 567

Qy 1643 CCTCAGCTGCTCTTCTTGAATCTGTGCGGCTTCTTACCAAGCTTAGGTTCTATAG 1702

Db 566 CCTCAGCTGCTTCTTCTGACTTCTGTGCAAGTCTTACCAAGCTGAGGTTCTATAG 507

Qy 1703 TGGTCT 1708

Db 506 TACCCT 501

RESULT 7

US-10-437-963-49667

; Sequence 49667, Application US/10437963

; Publication No. US2004012343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 49667

; LENGTH: 2484

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_52229C.1

US-10-437-963-49667

Query Match 43.6%; Score 848.8; DB 17; Length 2484;

Best Local Similarity 70.5%; Pred. No. 5.9e-232;

Matches 1326; Conservative 0; Mismatches 217; Indels 337; Gaps 1;

Qy 161 GTAAGAGTGAATATGATGGAAGTAAAGGAGTGGCATTTGAGCATTTAAGAAC 220

Db 150 GTCACGTGAAAATGGAAGAAATGCTAGAGCGGTGGCATTTGAGGCACCTGAAGAAC 209

Qy 221 TACAACCTGGGAAGAACTTATGCTATCGGTACATTTGAAAAGTGAAGATTGACAGCAT 280

Db 210 TACAATCTAGGAAGAACTTATGCTATGCTTCAATTTGAAAAGTGAAGATTGACAGCAT 269

Qy 281 AAGCTTACTGACATAGAGGTTGCTATTAAGATCATCAACTGCCCAATGAGAAATATG 340

Db 270 AAGCTTACAGGCGACAGAGTTGCTATTAAGATCCTGAACGTCGCCAAATGAGAAATATG 329

Qy 341 GAAATGGAAGAGAAAGCAAGAGAAATTCAGATATTTGAAGTTGTTCAATCCACCCCAT 400

Db 330 GAAATGGAAGAGAAAGCAAGAGAAATTCAGATATTTGAAGTTGTTCAATCCACCCCAT 389

Qy 401 ATCATTCGGCTTATGAGGTATATACACACCTACAGATATATATGTTGTGATGGAATAT 460

Db 390 ATCATTCGGCTTATGAGGTATATACACCTCCTACGGAATATATATGTTGTGATGGAATAT 449


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Qy 461 TGTAGTATGCGAGTTATTGATTACATTGTTGAGAAAGGCAGATTACAGGAAGATGAA 520
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 450 TGCAAGTTTGAGAACTGTTGATTACATTGTGAGAAAGGCAGTTGACAGGAAGATGAG 509
Qy 521 GCTCGTGAATCTTCCAGCAGATCATATGCGCTCGAATACTGCGCAATAGAAACATGTT 580
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 510 GCTGCGGAATCTTCCAGCAGATTATATCTGGGGTTGAATACTGCCACAGAAACATGTTG 569
Qy 581 GTCCACCGTGACCTAAAGCCGGAACCTGTAATTGATTCAAAGTAAATGTAACACTT 640
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 570 GTTCATCGTGATCTGAAGCCAGAAAACCTGCTACTGATTCAAAGTAAACGTAAGCTT 629
Qy 641 GCGGATTTTGGTCTGAGCAATGTCATGATGAGCCCATTTTCTGAAGACTAGCTGTGG 700
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 630 GCTGACTTTGGTTTGAGTAATGTCATGCAATGAGCCCATTTTAAAGACAAGCTGCGGG 689
Qy 701 AGTCCGAATATGCTGCTCCAGAGGTAAATATCTGTTAACTATATGCTGGAACCTGAGTC 760
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 690 AGTCCGAATATGCTGCTCCAGAGGTAAATATATATATATGCTGGAACCCGAGGTT 749
Qy 761 GATGATGAGTGTGGGGTGAATCTTTATGCTCTTCTTGTGGAACCTTCCATTGAT 820
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 750 GATGATGAGCTGTGGAGTGATCTTATGCTCTCTTGTGTACTCTTCCATTGAT 809
Qy 821 GATGAGAATATCCCAATCTGTTCAAAAAAATTAAGGAGTATCTACACACTTCCAACT 880
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 810 GACGAGAATATCCCAACTATTTCAAAAAAGTAAAGGAGTATATATATCTCCCAAGT 869
Qy 881 CATTTGCTGCTTTGGCCAGGAGTTGATCCCAAGATGCTGTTGTGAGCCATGAG 940
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 870 CATTTATCTGCTCTGCGCAGGAGTTGATCCCAAGATGCTGTTGTGATCCCAATGAG 929
Qy 941 AGAATCACAATTAGGGAATTCGGGAGCATGATGTTCCAGATTGCGCTTCCACGTTAC 1000
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 930 AGAATCACAATTGCGTGAATTCGAGAGCATCAATGTTTCAGATTGCGCTTCCGTTAC 989
Qy 1001 TTGGCAGTGCCTCCACGATACGACACAAAGCCAAAT----- 1041
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 990 TTAGCAGTGCCTCCACGACACAGACAGACAGCAAGCCAAATGTAATTTGTGTCAATTTC 1049
Qy 1042 ----- 1041
Db 1050 TTAACGAGTTGTTCAATATGATCAAACTTATATATAATAATTTTCTTGAGATAT 1109
Qy 1042 ----- 1041
Db 1110 ACTTATAGATGATTAATAATGTTTGGCCAACATAAAACCGTATAAAGCAGTGTGAA 1169
Qy 1042 ----- 1041
Db 1170 AGGCATTTGAATAACATTTTATGATATGAGGCTGTGAGTATTTCTGCTAGTAGTA 1229
Qy 1042 ----- 1041
Db 1230 GTTATCTTAGCAAAATCCTTCATGAGATGTAAGAAAGACAGATAAGTTTCACTTGCA 1289
Qy 1042 ----- 1041
Db 1290 ATATCACTTATTAATGTTGATTTTATTAATATCTTGCCACTTTGCTAATATCTTGA 1349
Qy 1042 -----GATTGATGAAGATACCTTCGAGATGTTGTTAATATGGGATT 1083
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1350 TATATGACCTTCTTTGAAGATTGATGAAGATACCTTCAAGACGTTGTAACCTTGGGTTA 1409
Qy 1084 TAACAAGAACAATGTTGTTGATCACTGTGACAGACACTTCAAAATGAGGCAACTGTTGC 1143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1410 TGAAGAAGACCAATGTTGTGATCTCTGCGCAATAGACTGCAAAATGAGCAACTGTTGC 1469
Qy 1144 ATATTATTACTATTGGAACAATCGGTTTGAAGCAACTAGTGGCTATCTTGGGCGAGATTA 1203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1470 ATATTATTGTTGTTGGAACAATCGATTCCGAGCTAACAGTGGCTATCTGGGAGCAGACTA 1529
Qy 1204 TCAAGAATCAATGGAACGAATTTAAATCAGCTGGCGTCAATCTGAATCATCTAGTTCTGC 1263
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Db 1530 TCAAGATCATTTGAGAGGAATCTTAATCGCTTGTCTTCATCAGAAATCAGCAAGTCAAA 1589
Qy 1264 TACGAGAATTAATGTTCCAGGAAGCAGTATCCTCATAGCAGTGTGTTGGCGCATATTA 1323
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1590 TACAGGCATTAATCTCCAGGAAGCAGTATCCTCATGCGAGTGTGTTGGCGCCACATTA 1649
Qy 1324 TCCTGTTGAAAGAAATGGGCGCTTGGACTTCAGTCTCGGGCCCACTCGTGAATTAAT 1383
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1650 TCCTGTTGAAAGAAATGGGCGCTTGGACTTCAGTCTCGAGCTCAGCCTCGCGAGATTAAT 1709
Qy 1384 GGTGAGGCTTTAAAGCACTTCAAGATTAACCGTCAGATGGAAGAAATGGGCACTTA 1443
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1710 GATTGAGGCTTAAAGCACTTGAAGACTTAATATGCTGCTGGAAGAAATGAGACAGTA 1769
Qy 1444 CAACGTGAATGCAGATGTTGCCAGGGGTTTCTGAAAGTTAATGACACGTTAGATGCCAG 1503
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1770 CAACATGAAGTCAGATGAGCGTTGGGTATCCTCAGGCCAATGATATGTTAGATGTCAA 1829
Qy 1504 CAACAGCTTCTTGGTGAATCTACCATCATGATGAATGAATGCTAATGGAGGCTACC 1563
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1830 CCACAGCTTGTGTTGATGACTCAATTAATAGATAATGGCGAATGAACGGAGGTTACC 1889
Qy 1564 TACTGTGATCAAGTTTGAATTCAGCTTTACAAGACGAAGACGAACAAGTACTCTTAGA 1623
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1890 TGCTGTGATCAAGTTTGAATTCAGCTTTACAAGACGAAGACGAAGAAGTATCTGTGGA 1949
Qy 1624 TATGACAGAGTTACTGGAACCTCAGCTGCTCTTCTGACTTCTGTGCGGCTTCTTAC 1683
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1950 TATGACAGAGTTACGGGGCTCAGCTCTTCTTCTGACTTCTGTGACGCTTCTTAC 2009
Qy 1684 CAACGTTAGGTTCTATAGT 1703
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2010 CAACGTGAGGTTCTATAGT 2029
```

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RESULT 8
US-10-437-963-80980
; Sequence 80980, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 80980
; LENGTH: 2224
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MFT4530_80552C.1
US-10-437-963-80980
```

```
Query Match 42.0%; Score 817.4; DB 17; length 2224;
Best Local Similarity 72.4%; Pred. No. 5.6e-223;
Matches 1074; Conservative 0; Mismatches 406; Indels 3; Gaps 1;
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Qy 221 TACAACCTGGGAAGAACTTTAGGTATCGGTACATTTGGAAGAGTGAAGATTCAGAGCAT 280
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 238 TACCGGATTTGGCAAAACCTTAGGAGTTGGGTCAATTTGGCAAGTGAAGATCGCGAGCAT 297
Qy 281 AAGCTTACTGACATAGAGGTTGTATAAAGATCATCAACTGCCGCAATGAGAAATATAG 340
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 298 ATATTGACTGGTCACAAGGTGGCAATCAAGATCCTCAATCGCCGTAAGATCAAGACATG 357
QY 341 GAAATGGAAGAAAAGCAAGAGAGAAATTCAGATATTTGAAGTTGTTCAATTCACCCCAT 400
Db 358 GAGATGGAAGAGAAAGTTAAAGAGAAATCAAGATACTTAGATTATTATGCAACCCACAT 417
QY 401 ATCATTCGGCTTTAGAGTGCATATACACACCTACAGATATATATGTTGATGGAATAT 460
Db 418 ATCATTCGCCCTTATAGAGGTGATAGACACCCGAGCTGATATTATGTTGTTATGAGATAT 477
QY 461 TGTAGTATGGCGAGTTATTGATTACATGTTGAGAAAGGACAGATTACAGAGATGAA 520
Db 478 GTCAATCTGGAGAGTTGTTGATTACATCGTTGAGAAAGGAGAGACTGCAAGAGAGAA 537
QY 521 GCTCGTGAATCTTCCAGCAGATCATATCTGGCGTCGAATACTGCCATAGAAACATGCTT 580
Db 538 GCTCGACGCTTTTCCAGCAGATCATATCTGGTGTGAATATTGCCATAGAAACATGCTG 597
QY 581 GTCCACCGTGACCTTAAAGCCGGAAAACTTGTACTTGATTCAAAGTATAAATGTAACCTT 640
Db 598 GTTCATCGTGAATCTTAAAGCCAGAGAACCTTCTTTTGAAGCTCCAAATGCAATGTAAAGATT 657
QY 641 GCGATTTTGGTGTGAGCAATGTGCATGATGAGCCATTCTTCTGAAGACTAGCTGTGG 700
Db 658 GCAGACTTGGCTTGAGTAATGTTATGCGTGAAGTCACTTTCTGAAGACAAGTTGTGT 717
QY 701 AGTCCGAATATGCTGCTCCAGAGTAATATCTGTTAACTATATATGCTGAGCCTGAGGTC 760
Db 718 AGCCCAATATATGCAGACACCTGAGGTGATATCTGTTAACTATATGCTGAGCCTGAGGTT 777
QY 761 GATGATGAGATTGTGGGGTGATCTTTATGCTCTTCTTTGTGGAATCTTCCATTGAT 820
Db 778 GATGATGAGATTGTGGGGTGATCTTTATGCTCTTCTTTGTGGAATCTTCCATTGAT 837
QY 821 GATGAGAAATATCCCAATCTGTTCAAAAAAATTAAGGAGGTATCTACACACTTCCAAGT 880
Db 838 GACGAGAAATATCCCACTTTTAAAGAAATAAAGGGTGATATATATCCCTTCCAGT 897
QY 881 CATTGTCTGCTTTGGCCAGGAGATTGATCCCAAGATGCTTGTGTTGAGCCTTGAAG 940
Db 898 CATTGTCACTTTGGCAAGGAGATTGATCCAGAATGCTTGTGTTGATCCCATGAG 957
QY 941 AGAATCACAATTAGGAAATTCGGAGCATCAATGTTCCAGATTGCCCTCCACGTTAC 1000
Db 958 AGGATCACCATAGTGGAATCCGTGAACATCAGTGTTCACAGTTGTTCCGCGTTAT 1017
QY 1001 TTGGCAGTGCCTCCACAGATAGCACACACAAACCAAAATGATTGATGAAGATACACTT 1060
Db 1018 TTAGCTGTGCCACTCTCTGACACTGCACACAGGTTAAAAAGCTCGACGATGAAAACTCTG 1077
QY 1061 CGAGATGTTGTTAATATGGGATTTAACAAGAACCATGTGTGTAATCACTGTGCAGCAGA 1120
Db 1078 AATGATGTTATCAATATGGGGTTTGACAAGAAATCAGCTAATCGAATCACTTCAACAAGAGA 1137
QY 1121 CTTCAAAATGAGGCAACTGTGTCATATTATTACTATTGACAATCGTTTAGACAACCT 1180
Db 1138 CTGCAAAAAGGCGACAGATTGCTACTATTTACTATTGACAATAGGCTGCGACAAC 1197
QY 1181 AGTGCTATCTTGGGGCAGATTATCAAGAAATCAATGAGACAGAAATTTAATCAGCTGGCG 1240
Db 1198 AGTGCTACCTTGAGAGCTGAGTCCATGAATCTATGGAATCTTCTCGCTCAAGTACT 1257
QY 1241 TCATCTGAATCATCTAGTCTGTGTCGAGAGAAATATGTTCCAGAGACAGTGCATCTCAT 1300
Db 1258 CCAGCTGAGACACCAAACTCAGCCACTGATCATCGGACAGCATGGGCATATGGAATCTCCT 1317
QY 1301 AGCAGTGTGGCGCCCATATTATCTGTGTAAGAAATGGGCGCTTGGAATTCAGTCT 1360
Db 1318 GGGTTTGGCTTGAGGCATCATTTCCGACGCTGACAGAAATGGGCGCTTGCTTCAAGTCT 1377
QY 1361 CGGGCCCACTCTGTGAATAATGTTGAGGCTTTAAAGCACTTCAAGAAATTAACGTC 1420
Db 1378 CGAGCATATCAAGAGAAATATTAAGTTCTTAAAGCTCTGACAGAGCTAAATGTT 1437

QY 1421 AGATGGAAGAGAATGGGCACTACAACGTGAATGCAGATGTTGCCAGGGTTCTCGAA 1480
Db 1438 TGCTGGAAGAAGATTGGACATTTATTAATGAATGCAGATGGAGTCTTAGTTTCCAGT 1497
QY 1481 GTTAATGACACGTTAGATGCCAGCAACGCTTCTTGTTGACTCTAACATCATGATAT 1540
Db 1498 CATGAGAGTATGATGCATTAACAACCATGGCTTTGGTGCAGAATCTGCTAATTAAGAACT 1557
QY 1541 GATGATGCTAATGGAGGCTTACCTGATGATCAAGTTTGAATTCAGCTTTACAAGACG 1600
Db 1558 GATGACAGTGAAGAAATCAACCCACACTGTG--AAATTGAATTCAGCTTTACAAGAA 1614
QY 1601 AAGACGACAAGTACCTCTTAGATATGACAGAGATTACTGACCTGACCTGCTTCTT 1660
Db 1615 AGGATGAATAATACCTTCTTGACTTGCAAAAGGTCAGTGACCAAGCTTCTTCTG 1674
QY 1661 GACTTCTGTGGCCCTTCTTACCAAGCTTAGGTTCTATAGT 1703
Db 1675 GACCTGTGCTGTGCTTCTTCTAATCTGAGAGAGTCTTAAAT 1717

RESULT 9
US-10-425-114-35131
; Sequence 35131, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 35131
; LENGTH: 1991
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE089A07_FL1
US-10-425-114-35131

Query Match 41.8%; Score 814.6; DB 13; Length 1991;
Best Local Similarity 69.7%; Pred. No. 3.3e-222;
Matches 1150; Conservative 0; Mismatches 489; Indels 12; Gaps 3;
QY 53 CCCTCCGCCCGGCTCTCCCATCTAGGTGTTCTCCCGCTCCGCGCACTCGCTC 112
Db 9 CCTTCCCTCCCTGCGGGCTTCTCTCAAGACTCCCGGCTTCCGCGCGCCACC 68
QY 113 GTCCGCGGCAAGAGTTGACCTGTGAGGGCGCGGCAACCGGTAAGT--AAGAGTG 169
Db 69 GCCGCGCGCGCGGCTGTCCGCGGGCGGAGCCAGCTGCGAGCGTCTCCCTGCG 128
QY 170 AAAATGATGAAGTAGTAAGGAGAGTGGGCATTCTGAAGCATTTAAGAACTACAACCTG 229
Db 129 GCGAGGTACACGATGAGGAGCGGGAAGAGATGCCAACCTTTGAGCGGTTACAGAAAT 188
QY 230 GGAAGAACTTTAGTATCGGTACATTTGGAAGAGTGAAGATTGCAGACATAAGCTTACT 289
Db 189 GGCAAAACCTTGGGAATTTGGGTCTCGGTAAAGTGAAGATCGAAGACATATATGACT 248
QY 290 GGAATAGGCTTGTATTAAGATTCATCACTGCCGCAATGAGAAATATGAAGATGAA 349
Db 249 GGTATTAAGTGGCGATCAAGATTCATCAATCGAAGAGATCAGAAAGCATGATATGAG 308
QY 350 GAGAAAGCAAGAGAGATTCAAGATTTGAAGTTGTTCAATTCACCCCATATCATTCGG 409

Db 309 GAGAAAGTTAAGAGAAATCAAGATACTGAGATTATTATGCATCTCATATCATACCGC 368
Qy 410 CTTTATGAGGTGATATACACACCTACAGATATATATGTTGATGGAATATTGTAAGTAT 469
Db 369 CTTTATGAGGTGATAGATACACCTGCTGATATTATGTTGATGAGATGTTAAATCT 428
Qy 470 GCGAGTTATTGATTACATTGTTGAGAAAGCAGATTACAGAGAAATGAAGCTCGTGA 529
Db 429 GGAGAGTTGTTGATTACATCGTTGAGAAAGGAGCTACACGAAAGAGAAAGCCGCGCAC 488
Qy 530 ATCTTCAGCAGATCATATCTGCGCTGAGATACTGCCATAGAAACATGTTGTCCACCGT 589
Db 489 TTTTTCAGCAGATCATATCTGCGTGTGAATAATTGCCATAGGAACATGTTGCTCACCGT 548
Qy 590 GACCTTAAAGCCGGAATACTGTTACTTGAATTCAAAGTATATGTAATACTTGCGGATTTT 649
Db 549 GATTTAAAGCCAGAGAAATCTTCTTTTGGATTCAAAATACAAATATTAGATTGCCGATTTT 608
Qy 650 GGCTTGAGCAATGTCATGCATGATGGCCATTTTCTGAAGACTAGCTGTGGAGTCCGAAC 709
Db 609 GGCTTAAGTAATGTTATGCGTGATGGTCACTTCTTAAGACGAGTTGTGTAGCCCGAAT 668
Qy 710 TATGCTGCTCAGAGGTATATCTGTGTAATCTATATGCTGACCTGAGCTGATGTATGG 769
Db 669 TATGACAGCAGCTGAGGTATATCTGTGTAATCTATATGCTGCTGCTGAGATTGATGTCG 728
Qy 770 AGTTGGGGTGATCTTTATGCTCTTCTTGTGGAACCTTCCATTGATGATGAGAAT 829
Db 729 AGCTGTGAGTATCTTTACGCTCTTCTTGTGGCACTCTCCCAATTGATGATGAGAAT 788
Qy 830 ATTCCCAATCTGTCAAAAAAATTAAAGGAGTATCTACACACTTCCAGTCAATTGTTGCT 889
Db 789 ATTCCAACCTTTTCAAGAAATAAAGGAGTATATATACCCTTCTAGTCAATTGTTGCTCA 848
Qy 890 GCTTGGCCAGGATTTGATCCCAAGATGCTGTTGTTGAGCCCTATGAAGAGAAATCACA 949
Db 849 CTTTCAAGCGAGGACTTGATTTCCCAAGATGCTGTTGTTGATCCAAATGAAGAAAGATTACA 908
Qy 950 ATTAGGAAATTCGGGAGCATCAATGTTCCAGATTGCGCTTCCAGTTACTTGGCAGTGT 1009
Db 909 ATACGTGAATCCGTGAACATGTGTGTTCAAGATCCGACTTCCAGCTATTTGGCTGTG 968
Qy 1010 CCTCCACCAATACGACACACAAGCCAAATGATTGATGAAGATTAACCTTCGAGATGTT 1069
Db 969 CCGCTCCAGACACTGCTCAACAAGTTAAAGTGCAGAGAGAACTCTTAATGATGTT 1028
Qy 1070 GTTAATATGGATTTAACAAGAACCATGTGTGTAATCACTGTGACAGACACTTCAAAAT 1129
Db 1029 ATTAAGATGGTTTGAACAAGATCAAGCTAATGTAATCTCTGCAAAACAGATTGCAGAAT 1088
Qy 1130 GAGGCAACTGTTGCATATATTACTATTTGACAATCGGTTAGAGCACTAGTGCGTAT 1189
Db 1089 GAGGCAACAGTTGCTTATTTACTCTTTGACAATAGGCTTCGCAACAACAGTGTAT 1148
Qy 1190 CTTGGGCGAGATTATCAAGATCAATGACAGAGAAATTTAAATCAAGTGGCGTCACTGA 1249
Db 1149 CTTGGATCTGAGTTTCAAGAACTATGAGCTCATCTTTCTCTCA---AGTAATCGCTGAA 1205
Qy 1250 TCATCTAGTTCTGCTACGAGAAATTATGTTCCAGGAAGCAGTATCTCATAGCAGTGT 1309
Db 1206 ACACCAACTTCAGCAACTGAACTTCGTACAGATGGGTTTTCAGAAATCTCCGGGGTCTGGC 1265
Qy 1310 TTGCGGCATATATCTGTTGAAAAGAAAATGGGCGCTTGACCTGAGCTCTCGGGCCAC 1369
Db 1266 TTGAGGCGAGCTTTTGACGCTGAAAAGAAATGGGCCCTTGCTTCAGTCTCGAGCACAT 1325
Qy 1370 CCTCGTGAATAATGTTGAGGTCTTAAAGCACTTCAAGAATTAAACGTCAAGTGAAG 1429
Db 1326 CCACGAGAAATTAATAGTGAAGTGTCTTAAAGCTCTGCAAGAACTGAATGTTTACTGAAA 1385
Qy 1430 AAGAATGGGCACTACAACGTGAATGCAATGCTGCCAGGGTTTCTGAACTTAATGAC 1489
Db 1386 AAGATTGGGCACTACAACATGAATGCAATGAGTCCGTGGCTGCTTGAAGAGT----- 1439

Qy 1490 ACGTTAGATCCAGCAACAGCTTCTTGTGACTCTACCATCATGATATGATGCT 1549
Db 1440 ATGATGATTAACAGTATAGCTTCAAGTGGAGTCTGCTATAATTGAACATGATGTTTC 1499
Qy 1550 AATGGAGGCTACCTACTGTGATCAAGTTTGAATTCACGCTTTACAAGACGAAGACGAC 1609
Db 1500 ATGGAGAAATCAACCCCTACAGTGAAGTTTGAGATTCAAGCTTTACAAAACGAGGGATGAG 1559
Qy 1610 AAGTACCTTTAGATATGCAAGAGTTACTGACCTCAGCTGCTCTTCTTGACTTCTGT 1669
Db 1560 AAGTACCTTTGACCTGCAAGGGTCAAGTGAATCAGATCAGATCTTCTTCTTGACTTGTGT 1619
Qy 1670 GCGGCTTCTTACCAAGCTTAGGGTCTAT 1700
Db 1620 TCCGCTTCTTAACCTCAGCTGAGAGTCTTT 1650

RESULT 10
US-10-425-114-2148
; Sequence 2148, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2148
; LENGTH: 1778
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700204782_FLI
US-10-425-114-2148

Query Match 41.5%; Score 807.6; DB 13; Length 1778;
Best Local Similarity 72.1%; Pred. No. 3.1e-220;
Matches 1082; Conservative 0; Mismatches 409; Indels 9; Gaps 2;

Qy 201 ATTCTGAAGCATTAAGGAAGTCAACCTGGGAAGAACTTTAGGTATCGGTACATTTGAA 260
Db 147 ATGCCAACCTTTGGCGGTTACCGAATTTGGCAAAACCTTAGGAATTTGGTCTTGGTA 206
Qy 261 AAGTGAAGATTGCAGAGCATTAAGCTTACTGACATAGGGTTGCTATAAGATCATCAACT 320
Db 207 AAGTGAAGATCGCGAATCATTAATTGACTGGCCATTAAGGTGGCAATCAAGATCTCAATC 266
Qy 321 GCCGCAATGAGAAATATGAAATGGAAGAGAAAGCAAGAGAGAAATTCAGATATTGA 380
Db 267 GCCGTAAAGATCAGAAGCATGGAATGGAAGAGAAAGTGAAGAGAAATCAAGATACCTGA 326
Qy 381 AGTTGTCATTCACCCCATATCATTCGCTTTATGAGGTGATATACACACCTACAGATA 440
Db 327 GATTAATTATGATCTCTCATATCATACGCTTTATGAGGTGATAGATACACCTGCTGATA 386
Qy 441 TATATGTTGATGAGATATTGTAAGTATGCGAGTTATTGATTAATGATGTTGAGAAAG 500
Db 387 TTTATGTTGTTATGAGATGTTAAATCTGAGAGTGTGTTGATTAATGTTGAGAAAG 446
Qy 501 GCAGATTACAGGAAGATGAAGCTGCTGCAATCTTCCAGCAGATCATATCTGGCGTGAAT 560
Db 447 GAAGACTACATGAAGAGAAAGCCGGCGCTTTTTCAGCAGATCATATCTGGTGTGAAT 506
Qy 561 ACTGCCATAGAAACATGTTGTCCACCGTGAACCTTAAAGCCGAAAACTGTTACTTGATT 620

Db 507 ATTGCCATAGGAACATGGTGTGCTCACCGTGATTTAAAGCCAGAGAATCTTTTGATT 566

Qy 621 CAAGTATATATGTAACCTGCGGATTTGGTCTGAGCAATGTGATGATGGCCATT 680

Db 567 CGAANTGCAACATTAAGATTGCTGATTTGGCTTAAGTAATGTATGCTGATGGTCACT 626

Qy 681 TTCTGAAGACTAGCTGTGGAGTCCGAACATGCTGCTCCAGAGGTAATATCTGTAAAC 740

Db 627 TTCTTAAGACGAGTGTGGTAGCCCGAATTAAGACACCTGAGGTCAATCTGTAAAC 686

Qy 741 TATATGCTGACCTGAGCTGATGTATGAGTTGTGGGTGATTTATGCTCTTCTT 800

Db 687 TATATGCTGTCTGAAAGTTGATGTCTGAGCTGCGCGTATTTATGCTCTTCTT 746

Qy 801 GTGAACCTCTTCATTTGATGATGAGAATATCCCAATCTGTTCAAAAAATTAAAGGAG 860

Db 747 GTGGCACTCTTCATTTGACGATGAGAATATTTAAACCTTTTAAAGAAATAAAGGGTG 806

Qy 861 GTATCTACACACTTCCAAGTCAATTTGCTGCTTGGCCAGGATTTGATCCCAAGATGC 920

Db 807 GAATATATACCTTCTCCTAGTCAATTTGTCACTTACGAGGAGACTGATTCCTAGAATGC 866

Qy 921 TTGTTGTGAGCCTATGAAGAAATCAAAATTAGGAAATTCGGAGCATCATGTTCC 980

Db 867 TGGTGTGATCCGATGAAGAAAGATTACATACTGAATCCGTGAACATGTGTGTTCA 926

Qy 981 AGATTGCGCTTCCACGTACTTGGCAGTGCCTCCACCAGATACGACACAACAGCCAAA 1040

Db 927 AATTCACCTTCCGCGCTATTAGCTGTACCGCTCCGACACTGACACAACAGTTAAGA 986

Qy 1041 TGATTGATGAGATACACTTCGAGATGTTGTAATATGGGATTTAACAAGAACCATGTGT 1100

Db 987 AGCTGACGAGGAAACCTTAATGATGTTAATTAAGATGGGTTTGACAAGAAATCACTAA 1046

Qy 1101 GTGAATCACTGTGACGACGACTTCAAAATGAGGCAACTGTTGCATATTAATTAATTTG 1160

Db 1047 TTGAATCTCTGCACAACAGATTGCAAGATGAGCAACAGTTGCTATTAATTAATCTCAT 1106

Qy 1161 ACAATCGGTTAGACCAACTAGTGGCTATCTTGGGCGAGATTAATCAAGATCAATGACA 1220

Db 1107 ACAATAGGCTTCGTACAACCAAGTGTATCTTGATCTGAGTTTCAAGATCTATGACC 1166

Qy 1221 GGAATTAATCAGCTGGCGCTCATCTGAATCACTAGTTCTGTAGAGGAATTAATGTTT 1280

Db 1167 CATCTTCTCTCA--AGTACATGCTGAACAACCAACTTCAGCACTGAACATCGACAGC 1223

Qy 1281 CAGGAAGCAGTATCTCATAGCAGTGTGCGGCCATATTAATCTGTTGAAAAGAAAT 1340

Db 1224 ATGTGTTTACGAATCTCCGGGCTGTGTTGAGGCGAGCATTTTGCACTGAAAAGAAAT 1283

Qy 1341 GGGCGCTTGACTTCAGTCTGGGCCCACTCTGTGAATTAATGTTGAGGCTTTAAAG 1400

Db 1284 GGGCCCTGTGCTCAGTCTCGAGCACATCCACGAGAATTAATGAAGTCTTAAAG 1343

Qy 1401 CACTTCAAGATTAACGTCAGATGGAAGAAATGGGCACTACAACGTGAATGCAGAT 1460

Db 1344 CACTGCAAGAACTGAATGTTTACTGAAAAGATTTGACACTACACATGAATGCAGAT 1403

Qy 1461 GGTGCCCAAGGTTTCTGAAGTTAATGACGTTAGATGCCAGCAACGTTTCTGCTG 1520

Db 1404 GGAGTCCGTGCTGCTTGAAGT-----ATGATGCATACTGTGATGCTTTAGTGACG 1457

Qy 1521 ACTTACCATCATGATATGATGATGCTTAATGGGAGGCTACCTACTGTGATCAAGTTTG 1580

Db 1458 AGTCTGCTTAATTTGAAGACTGATGATCTCATAGCGAAATCAACCCGTATAGTGAAGTTTG 1517

Qy 1581 AATTCCAGCTTTTACAAGAGCAAGCAAGTAACCTCTTAGATATGAGAGAGAGTACTG 1640

Db 1518 AGATTCACTTTTACAAAACGAGGAGTGAAGTAACCTTCTTGACCTGCAAAAGGCTCAGTG 1577

Qy 1641 GACCTCAGCTGCTCTCTTCTGACTTCTGTGCGGCTTCTTACCAAGCTTAAGGTTCTAT 1700

Db 1578 GACCACAACCTCTTCTTCTGACTGTGTTCGCGCTTCTTAACGCAAGCTGAAGATTTCTT 1637

RESULT 11

US-10-183-687-237

; Sequence 237, Application US/10183687

; Publication No. US20030204870A1

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve

; APPLICANT: Allen, William B.

; APPLICANT: Cahoon, Rebecca

; APPLICANT: Epelbaum, Sabine

; APPLICANT: Famodu, Omolayo O.

; APPLICANT: Harvell, Leslie T.

; APPLICANT: Jones, Todd

; APPLICANT: Kinney, Tony

; APPLICANT: Klein, Ted

; APPLICANT: Li, Changjiang

; APPLICANT: Oliveira, Igor Cunha

; APPLICANT: Sakai, Hajime

; APPLICANT: Shen, Bo

; APPLICANT: Tarczyński, Mitchell C.

; TITLE OF INVENTION: Alteration Of Oil Traits In Plants

; FILE REFERENCE: B01458 US NA

; CURRENT APPLICATION NUMBER: US/10/183,687

; CURRENT FILING DATE: 2002-06-27

; PRIOR APPLICATION NUMBER: 60/301,913

; PRIOR FILING DATE: 2001-06-29

; NUMBER OF SEQ ID NOS: 532

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 237

; LENGTH: 2107

; TYPE: DNA

; ORGANISM: Zea mays

US-10-183-687-237

Query Match 41.3%; Score 804.2; DB 13; Length 2107;

Best Local Similarity 71.7%; Pred. No. 3.3e-219;

Matches 1084; Conservative 0; Mismatches 418; Indels 9; Gaps 2;

Qy 190 AGGAGTGGGCAATTTGAAAGCATTAAGGAATCAACCTGGGAAGAACTTTAGTATCG 249

Db 238 AGCGGAAGAGATGCCAACCTTTGACCGGTTACAGAATTTGGCAAAACCTGGGAATTGG 297

Qy 250 TACATTTGAAAAAGTGAAGATTGCAGACATAAGCTTACTGACATAGGGTGTCTATAAA 309

Db 298 GTGTTGCGTAAAGTGAAGATCGCGCAACATATATTGACTGTGCATAAAGTGGCATCAA 357

Qy 310 GATCATCAACTGCCGCCAAATGAGAAATATGGAATGGAAGAGAAACAAAGAGAGAAAT 369

Db 358 GATTCTCAATCGCAAGAGATCAGAAACATGATATGGAAGAGAAAGTTAAGAGAGAAAT 417

Qy 370 CAAGATATTGAAGTTGTTCAATTCACCCCCATATCATTCGGCTTTATGAGTCAATACAC 429

Db 418 CAAGATACGAGATTATTATGCACTCTCATATCATACGCGCTTTATGAGGTGATAGATAC 477

Qy 430 ACCTACAGATATATATGTTGTGATGGAATATTGTAAGTATGGGAGTTATTGATTACAT 489

Db 478 ACCTGCTGATATCTGTGTTGTTATGAGATGTTAAATCTGAGAGTGTGTTGATTACAT 537

Qy 490 TGTGAGAAAGCAGATTACAGAGAGATGAAGCTGCTGCAATCTCCAGCAGATCATATC 549

Db 538 CGTTGAGAAAGGAGGCTACACGAGAGAGAAAGCCGACACTTTTTCAGCAGATCATATC 597

Qy 550 TGGCGTGAATACTGCCATAGAAACATGTTGTCCACCGTGAACCTTAAAGCCGAAAACTT 609

Db 598 TGGTGTGAATATTGCCATAGAACATGTTGCTCACCGTATTTAAAGCCAGAGAAATCT 657

Qy 610 GTTACTTGATTTCAAGTATATTAATAAATCTGCGGATTTTGGTCTGAGCAATGTATGCA 669

Db 658 TCTTTTGATTTCAAAATGCAATGTTAAAGATTGCCGATTTTGGCTTAAAGTATATATGCG 717

Qy 670 TGATGGCAATTTTCTGAAGACTAGCTGTGGAGTCCGAACATATGCTGCTCCAGAGGTAAT 729

Db 718 TGATGTCACCTTCTTAAGACGAGTTGTGTAGCCCGAATTATGACGACACCTGAGTTCAT 777
QY 730 ATCTGTAACTATATGCTGACCTGAGTGCATGTATGAGTTGGGGTGAATCTTTA 789
Db 778 ATCTGTAACTATATGCTGTGCTGAGTTGACGCTGAGCTGTGAGTTATCTTTA 837
QY 790 TGCTCTTCTTGTGGAACCTCTCCATTGTATGATGAGATATTTCCAACTCTGTTCAAAA 849
Db 838 TGCTCTTCTTGTGCACTCTCCATTGTACGATGAGATATTTCCAACTTTCAAGAA 897
QY 850 AATTAGGAGGTATCTACACACTTCCAGTCAATTTGTCTGTGCTTGGCCAGGATTGTAT 909
Db 898 AATAAAGGGTGAATATATACCCTTCTAGTCATTTGTACACCTTCAGCGAGGACTTGAT 957
QY 910 CCCACGAATGCTTGTGTGAGCCCTATGAAGAATCACAATTAGGAAATTCGGAGCA 969
Db 958 TCCCAGAAATGCTGTTGTGTGATCCAAATGAAGATTACAAATACGTGAATCCGTGAACA 1017
QY 970 TCAATGGTTCAGATTGCGCCTTCCAGTTACTTGGCAGTGCCTCCACGATACGACACA 1029
Db 1018 TGTGTGTTCAAGATCCGACTTCCGCTAATTTGGCTGTGCGCCTCCAGACACTGCTCA 1077
QY 1030 ACAAGCCAAATGATTGATGAAGATACACTCGAGATGTTGTTAATATGGATTAAACA 1089
Db 1078 ACAAGTTAAAGGTGACGACGAGAACTCTTAATGATGTTATTAAGATGGGTTTGACAA 1137
QY 1090 GAACCATGTGTGATCACTGTGACGACACTTCAAAATGAGGCACTGTTCATATTA 1149
Db 1138 GAATCAGCTAATTGAATCTCTGCAAAACAGATTGCAAGATGAGGCAACAGTTGCCATTA 1197
QY 1150 TTACTATATGACAAATCCGTTTATGAGCACTAGTGGCTATCTTGGGCGAGATTATCAGA 1209
Db 1198 TTACTCTTGGACAATAGGCTTCTGACCAACAGTGGTTATCTTGATCTGAGTTCAAGA 1257
QY 1210 ATCAATGACAGGAATTTAAATCAGCTGGGCTCATCTGAATCATCTAGTTCTGTACGAG 1269
Db 1258 ATCTATGACTCATCTTGTCTCA--AGTAAATCGCTGAAACACCACTTCAGCAACTGA 1314
QY 1270 GAATTATGTTCCAGAAAGCAGTATCTCATAGCAGTGGTTTGGGCCATATTATCTGT 1329
Db 1315 ACTTCGTACGATGGGTTTTCAGAACTCCAGGTTCTGGCTTGAAGCAGCATTTTGACGC 1374
QY 1330 TGAAGAAAAATGGGCGCTTGAAGTTCAAGTCTGGGCCACCCCTGTGAATAATGTTGA 1389
Db 1375 TGAAGGAATGGGCCCTTGTGCTTCAAGTCTCGAGCACATCCAGAGAAATAATAAGTGA 1434
QY 1390 GGCTTAAAGCACTTCAAGATTAAAGTCAAGTGAAGAAGAAATGGGCACTACAACGT 1449
Db 1435 AGTCTTAAAGCTCTGCAAGAACTGAATGTTTACTGAAAAAGATTGCACTACAACAT 1494
QY 1450 GAAATGCAGATGCTGCCCAAGGTTCCCTGAAGTTAATGACACGTTAGATGCCAGCAACAG 1509
Db 1495 GAAATGCAGATGAGTCTGCTGCTGCTGAGAGT-----ATGATGATTAACAGTGATAG 1548
QY 1510 CTTTCTTGTGACTCTACCATCATGATGAATAATGATGCTTAATGGGAGGCTACCTACTGT 1569
Db 1549 CTTTCAAGTGGAGTCTGCTATTAATGAATGATGTTTTCATGAGAAATCAACCCCGAC 1608
QY 1570 GATCAAGTTTGAATTCAGCTTTTACAAGACGAGAGACGACAAGTACTCTTAGATATGCA 1629
Db 1609 AGTGAAGTTTGAATTCAGCTTTACAAGAGAGGAGATGAGAACTACTCTTGACCTGCA 1668
QY 1630 GAGAGTTACTGACCTCAGCTGCTTCTTGAATCTGTGCGGCTTCTTACCAAGCT 1689
Db 1669 AAGGCTCAGTGATCACATCTTCTTCTGAGCTTGTGTCCGCTTCTAATCACTCAGCT 1728
QY 1690 TAGGTTCTAT 1700
Db 1729 GAGAGTTCTTT 1739

RESULT 12
US-10-183-687-239

; Sequence 239, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B1458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 239
; LENGTH: 2052
; TYPE: DNA
; ORGANISM: Zea mays
; US-10-183-687-239

Query Match 40.7%; Score 793.4; DB 13; Length 2052;
Best Local Similarity 72.4%; Pred. No. 4e-216;
Matches 1079; Conservative 0; Mismatches 391; Indels 21; Gaps 3;

QY 210 CATTAGGAACCTACCACTGGAGAACTTTAGTATCGGTACATTGGAAAAGTGAGA 269
Db 244 CGTTGAGAAATTATCGAATTGGCAAGACTCTCGAATTGGCTCATTCGGAAGTGAAA 303
QY 270 TTGACAGCATTAAGCTTACTGACATAGGTTGCTATTAAGATCATCAACTGCCCAAA 329
Db 304 TTGCGAGCATATCAGACTGACACACAAGGTGCAATCAAGATCTCAACCGCGTAAA 363
QY 330 TGAGAAATATGGAATGGAAGAGAAAGCAAGAGAGAAATTCAGATATTGAAGTTGTTCA 389
Db 364 TCAGAGGATGAGATGGAAGAGAAAGTTAAAGAGAGATTAAAGATATTGAGGTTATTTA 423
QY 390 TTCACCCCATATCATTTCCGCTTTATGAGTCAATATACACCTACAGATATATGTTG 449
Db 424 TGCATCCATATTATCCGCTTATGAGGTTATAGACACACCGGCTGATATTATGTTG 483
QY 450 TGATGAATATTGTAAGTATGGGAGTTATTGATTACATGTTGAGAAAAGGAGATTAC 509
Db 484 TTATGAGTATGTTAAGTGTGGGAATTATTGATTACATGTTGAGAAAAGTAGGCTGC 543
QY 510 AGGAGATGAAGCTCGTGAATCTTCCAGACAGATCATATCGCGTGAATACTGCCATA 569
Db 544 AAGGAGAGAAGCTCGCCGTTCTTCCACAGATTATATCCGCTGTAATATGCCATA 603
QY 570 GAAACATGTTGTCCACCGTGACCTTAAAGCCGAAAAGCTTTACTTGATTCAAAGTATA 629
Db 604 GAAACATGTTGTGTCCATCGTGAATCTTAAAGCCAGAAAAGCTTCTTATGATTCAAAATGCA 663
QY 630 ATGTAAACTTGGCGAATTTGGTCTGAGCAATGTCATGATGAGCCATTTCTGAAGA 689
Db 664 ATGTAAAGTTGACAGATTTGGCTTAAAGTATGTTAAGCGGATGCTCATTTCTGAAGA 723
QY 690 CTAGCTGGAGTCCGAATATGCTGCTCCAGAGGTAAATATCTGTAACCTATATGCTG 749
Db 724 CAAGTTGTGTAGCCCAATATGCTGCTCCAGGTGATATCTGTAACCTATATGCTG 783
QY 750 GACCTGAGGTGATGATGAGTTGTGGGTGATTTCTTAAGTCTTCTTGTGGAAGTCTC 809

Db 784 GACCTGAAGTTGATGTGAGCTGTGGGTTATTCTTATGCTCTTTATGTGACTC 843
 Qy 810 TTCCATTGATGATGAGATATCCCAATCTGTTCAAAAAAATTAAGGAGTATCTACA 869
 Db 844 TGCCATTGATGACGAGACATACCAAACTTTTAAAGAAATAAAGGTGAATATATA 903
 Qy 870 CACTTCCAGTCAATTTGCTGCTTTGGCCAGGATTTGATCCCAAGATGCTTGTGTTG 929
 Db 904 CCTTCCAGCCATTGTTGCTGTGAGCAAGGGAATTTGATTCCAAAGATGCTAGTTGTCG 963
 Qy 930 AGCCTATGAAGAGATCACAATTAGGAAATTCGGAGCATCAATGGTTCAGATTGCGC 989
 Db 964 ATCTATGAAGCGGATCACCATTGCTGAATTCGCGAACATGATTGTTCAAAATTCCTTC 1023
 Qy 990 TTCCAGTTACTTGGCAGTGCCTCCACGATACGACACAACAAGCCAAATGATTGATG 1049
 Db 1024 TCCCGCGCTATTGACTGTGCTCCTCCAGATAGTGCAGCAAGTCAAAAAGTTGATG 1083
 Qy 1050 AAGATACACTTGAAGATGTTGTTAATAGGATTTTAAACAAGAACCATGTGTGATCAC 1109
 Db 1084 AGGAACCTCTCCGTGAGGTTTAAAGTATGATGACAGAACCCTGTGTGATGATCAA 1143
 Qy 1110 TGTGACAGCACTTCAAAATGAGGCACTGTTCATATTTATTTACTATTGGAATCGGT 1169
 Db 1144 TCCAAAAAAGGCTGCAAAATGAGGCACTGTTCATATTTACTTCTTGGACAATAGGC 1203
 Qy 1170 TTAGAGCACTAGTGGCTATCTTGGGGCAGATTATCAAGAATCAATGGAACAGAAATTAA 1229
 Db 1204 TCCGTACACACAGTGGCTATCTTGAAGTGAATGTCAAGAAAGCTATGCACTCCTCATTC 1263
 Qy 1230 ATCAGCTGGCTCATCTGAATCATCTAGTTCTGTGACGAGAAATTAATGTTCCAGAAACA 1289
 Db 1264 CAAACATCGCATCATATGAAACACCAAGTTCACACGCTGGAATGACACAAATATTTA 1323
 Qy 1290 GTGATCCTCATAGCAGTGTGCGGCCAATATATCTGTTGAAGAAATGGCGCTTG 1349
 Db 1324 TGGAGTCTC---CAGTTGGCTTGAGACCATCTTCCAGCTGAGAGAAATGGGCTCTTG 1380
 Qy 1350 GACTTCACTCTCGGGCCCAACCCTCGTGAATTAATGTTGAGGTCTTAAAGCACTTCAAG 1409
 Db 1381 GTCTTCACTCTCGAGCACATCCAAAAGAAATTAATGTCTGAAGTCTGAAAGCTCTGCAAG 1440
 Qy 1410 AATTAAAGTCAATGATGGAAGAAATGGGCACTACAAAGTGAATGAGATGTCGCCAG 1469
 Db 1441 AATTAAATGTTTAACTGAAAAAGATAGTCACTAATACATGAAGTGAATGAGTCTCTG 1500
 Qy 1470 GGTTCCTGAAGTTAATGACACGTTAGATGCCAGCAACAGCTTCTTGTGACTCTACCA 1529
 Db 1501 GCTTCTCTCTCAAAATTCATTAACAATCACTTCA-----GTGCAAGGT 1545
 Qy 1530 TCATGATTAATGATGATGCTAATGGAGGCTACTGATGATCAAGTTGAATTCAGC 1589
 Db 1546 CCATGAACTGATAGCCTGAGTGAAGGTTA--AGTTAATTAAGTTGAATTCAGC 1602
 Qy 1590 TTTACAAGCAAGAGACGACAGTAACCTTTAGATATGACAGAGTTACTGACCTCAGC 1649
 Db 1603 TGTACAAAACAAGAGACGAGAAATACCTCTCGATTGCAAAAGTCAAGTGGGCCACAGC 1662
 Qy 1650 TGCTCTTCTTGACTTCTGTGCGGCTTCTTAACCAAGCTTGAAGTTCTAT 1700
 Db 1663 TCCTCTTCTTGAAGTGTGCGGCTTCTTAACCACTGAGAGTTCTTT 1713

RESULT 13
 US-10-425-114-4365
 ; Sequence 4365, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jindong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(5313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 4365
 ; LENGTH: 1742
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700355426_FLI
 US-10-425-114-4365

Query Match 40.7%; Score 793.2; DB 13; Length 1742;
 Best Local Similarity 72.9%; Pred. No. 4.1e-216;
 Matches 1071; Conservative 0; Mismatches 378; Indels 21; Gaps 3;

Qy 231 GAAGACTTTAGGTATCGGTACATTTGGAAGAAAGTGAAGATTGCGAGCATTAAGCTTACTG 290
 Db 1 GCAAGACTCTCGGAATTTGCTCATTCGGAAGGTGAAGAAATTCGGAAGCATATCAGCACTG 60
 Qy 291 GACATGAGGTGCTATTAAGATCATCACTGCCGCCAAATGAGAAATATGAAATGAAAG 350
 Db 61 GACACAAGGTGGCAATCAAGATCTCAACCGCGTAAAAATCAGAGGCATGAGATGAAAG 120
 Qy 351 AGAAGCAAGAGAGAAATTCAGATTTGAAGTTGTTCAATTCACCCCATATCATTCGGC 410
 Db 121 AGAAGTTAAAGAGAGATTAAGATATTGAGGTTATTATGATCCACATATTATCCGCC 180
 Qy 411 TTTATGAGTATATACACACCTACAGATATATATGTTGTGATGAATATTTGAATGATG 470
 Db 181 TCTATGAGTTATAGACACACCGCGTGAATTTATGTTGTTATGAGATGATGTTAAGTGTG 240
 Qy 471 GCGAGTTATTTGATTACATTTGTTGAGAAAGGCGAGATTACAGAAAGTGAAGCTGTCGAA 530
 Db 241 GGAATTAATTTGATTACATTTGTTGAGAAAGGTAGGCTGCAAGAGAAAGGCTGCGCTT 300
 Qy 531 TCTTCAGCAGATCATATCTGCGGTGGAATACTGCCATAGAAACATGTTGCCACCGTG 590
 Db 301 TCTTCCACAGATTATATCCGGTGTGAATATTGCCATAGAAACATGTTGTCATCGTG 360
 Qy 591 ACCTAAGCCGGAACCTGTTACTGATTCAAGATTAATGTAACCTTGCGGATTTTG 650
 Db 361 ATCTAAGCCAGAAACCTCTTAATGATTCAAAATGCAATGTTAAGATTGACATTTTG 420
 Qy 651 GTCGACCAATGTCATGATGAGCCATTTTCTGTAAGACTGCTGGAGTCCGAAT 710
 Db 421 GCTTAAGTAAATGTTATGCGGGATGTCATTTTCTGAAGCAAGTGTGTAAGCCCAATT 480
 Qy 711 ATGCTGCTCCAGAGGTAATATCTGTTAACTATATGCTGACCTGAGTGCATGTATGA 770
 Db 481 ATGCTGCTCCAGAGGTAATATCTGTTAACTATATGCTGACCTGAAAGTTGATGTGGA 540
 Qy 771 GTTGGGGGTGATCTTTATGCTCTCTTGTGGAACCTTTCATTTGATGATGAGAAATA 830
 Db 541 GCTGCGGGTTATTCTTATGCTCTTTATGTGTTACTGCTGCAATTTGATGACGAGAAACA 600
 Qy 831 TTCCCAATCTGTTCAAAAAAATTAAGGAGGATCTACACACTTCCAAGTCATTTGCTG 890
 Db 601 TACCAACCTTTTAAAGAAATTAAGGATGAATATATACCTTCCAGCCATTTGTCG 660
 Qy 891 CTTGGCCAGGATTTGATCCACGATGCTTGTGTTGAGCCTATGAAGAAATCAGAA 950
 Db 661 GTGCAAGCAAGGATTTGATCCAGAATGCTAGTTGTGATCTATGAAGCGGATCACCA 720
 Qy 951 TTAGGAAATTCGGAGCATCAATGTTCCAGATTGCGCTTCCACGTTACTTGGCAGTGC 1010
 Db 721 TTGCGAAATTCGGAACATGATGTTCAAAATTTCTTCTCCCGGCTATTTGACTGTGC 780
 Qy 1011 CTCACCAAGATACGACACAACAGCCAAATGATTGATGAAGATACACTTCGAGATGTTG 1070

Db 781 CTCCTCCAGATAGTGCAGCAACAGTCAAAAAAGGTTGATGAGAACTCTCCGTAGGTTT 840
Qy 1071 TTAATATGGGATTTAACAAGAACCATGCTGTGATCACTGTGACAGACCTTCAAAATG 1130
Db 841 TAGGTATGGGATATGACAAGAACCTGTGTGGAATCAATCCAAAAAAGGCTGCAAAATG 900
Qy 1131 AGGCACTGTTCATATATTATTATTAATGACAATCGTTAGACAATAGTGTATC 1190
Db 901 AGGCACTGTTCATATATTATTATTAATGACAATAGGCTCCGTACAACCAAGTGTATC 960
Qy 1191 TTGGGGCAGATTATCAAGAATCAATGACAGAAATTTAATCAGCTGGGCTCATCTGAAT 1250
Db 961 TTGGAGCTGAATGTCAAGAAAGCTATGACTCTCATTTCTCAACATCGCATATATGAAA 1020
Qy 1251 CATCTAGTTCTGTGACGAGGAATTAATGTTCCAGGAAGCAGTGATCTCATAGCAGTGT 1310
Db 1021 CACCAAGTTCAGCAGTGGGAATAGACAGCAAAATTTATGAGTCTC--CAGTTGGCT 1077
Qy 1311 TGCGGCCATATTATCTGTGAAAGAAAATGGGCGCTTGACTTCAGTCTCGGCCACAC 1370
Db 1078 TGAGACCAATCTTCACAGCTGAGAGAAATGGGCTCTGTCTTCAGTCTCGAGCACATC 1137
Qy 1371 CTGTGAATTAATGTTGAGGTCTTAAAGCACTTCAAGAATTAAAGTCAGATGAAGA 1430
Db 1138 CAAAAGAAATAATGTCTGAAGTCTGAAGCTCTGCAAGAATTAAATGTTACTGAAAA 1197
Qy 1431 AGAATGGGCACTACAAGCTGAATGCAGATGGTGGCCAGGTTTCTGAAGTTAATGACA 1490
Db 1198 AGATAGGTCACTAATAATGAATGAGTGCAGATGAGTCTGCTTCTGCTCAATTCATA 1257
Qy 1491 CGTTAGATGCCAGCAACAGCTTCTTGGTGACTCTACCATCATGATGAATGATGATCTA 1550
Db 1258 ACAATCATTAATCTCA-----GTGCAGGGTCCATTGAATGATAGCCTGA 1302
Qy 1551 ATGGAGGCTAAGCTAAGTGTGATCAAGTTGAATTCAGCTTTACAGAAGAGAGAGACA 1610
Db 1303 GTGAGAGGTTA--AGTTAATTAAAGTTGAATTCAGCTGTACAAAACAAGAGAGAGACA 1359
Qy 1611 AGTACCTCTTGAATATGACAGAGTTTACAGCTCAGCTGCTCTTCTTGAATCTGTG 1670
Db 1360 AATACCTCTTGAATTTGCAAAAGAGTCAAGTGGGACACAGCTCTCTTCTGGAATGTGCG 1419
Qy 1671 CGGCTTCTTACCAAGCTTAGGGTTCTAT 1700
Db 1420 CGGCTTCTTCACTCAACTGAGAGTTCTTT 1449

RESULT 14
US-10-183-687-247
; Sequence 247, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B1458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532

; SOFTWARE: Microsoft Office 97
; SEQ ID NO 247
; LENGTH: 2123
; TYPE: DNA
; ORGANISM: Glycine max
US-10-183-687-247

Query Match 40.2%; Score 782.6; DB 13; length 2123;
Best Local Similarity 71.1%; Pred. No. 5.2e-213;
Matches 1072; Conservative 0; Mismatches 414; Indels 21; Gaps 2;

Qy 213 TAAGGAATCAACCTGGGAAGACTTTAGGTATCGGTACATTTGAAAAAGTGAAGATTG 272
Db 169 TACCAATTATTAATTGGAAAAACACTCGGATTGGATCTTTGGCAAGGTGAAAATTG 228
Qy 273 CAGAGCATTAAGCTTACTGACATAGGTTGCTATTAAGATCATCACTGCCGCAAAATGA 332
Db 229 CAGAACATGTGTGACTGGCCATAAGTTGCGATCAAGATCTTAAACGACGAAGATTA 288
Qy 333 GAAATATGAATGAAGAGAAAGCAAGAGAGAAATTCAGATATTTGAAGTTGTTCAATC 392
Db 289 AGAACATGAATGAAGAAAAAGTGAAGAGAAATCAAAATTTAAGATTGTTCATGC 348
Qy 393 ACCCCCATATCATTCGGCTTATGACGTCAATATACACACCTACAGATATATATGTGTGA 452
Db 349 ATCTCATATTAATTCGACTTTATGAAATCATAGAAACTCCAACTGACATATATGTGTCA 408
Qy 453 TGAATATTTGTAAGTATGGCGAGTTATTTGATTACATTTGTGAGAAAAAGCAGATTACAG 512
Db 409 TGGAGTATGTGAAGTCTGAGAGCTTTTGCATTACATAGTAGAGAAAGGTAGTTGCAGG 468
Qy 513 AAGATGAAGCTCGTCAATCTTCAGCAGATCATATCTGCGTGAATACTGCCATAGAA 572
Db 469 AAGATGAAGCTCGTAATTTTTCAGCAGATTAATCTGCGGTGAAGTACTGTACAGGA 528
Qy 573 ACATGTTGTCCACCGTGACCTAAAGCCGAAAACTTGTACTGATTCAAGATTAATAG 632
Db 529 ATATGTTGTTATAGATTTGAAGCTGAGAAATTTACTTTTGAATCCAAATGTAATG 588
Qy 633 TAAACTTGGGATTTTGTGTGAGCAATGTCATGATGATGCCATTTTCTGAAGACTA 692
Db 589 TCAAGATTGCTGATTTTGGCTTGAGCAACATCATGCGTGAATGCTTTCTTAAAAACAA 648
Qy 693 GCTGTGGAGTCCGAATATGCTGCTCCAGAGGTAATATCTGTAAACTATATGCTGAG 752
Db 649 GTTGTGAAGCCCTAATGACATGACGCTCTGAGGTTATCTGTGGAAATGTATGCTGAG 708
Qy 753 CTGAGTGTGATGATGAGTGTGGGCTGATTTCTTATGCTCTTTGTGGAATCTTTC 812
Db 709 CTGAATGAGATGCTGAGAGCTGTGGTGAATTTTATATGCCCCCTTTTGTGTGACACCCCTTC 768
Qy 813 CATTTGATGATGAGAAATATCCCAATCTGTTCAAAAAAATTAAGGAGTATCTACACAC 872
Db 769 CTTTGTGATGAATAATATTCAAATCTCTTCAAGAAAAATAAGGTGGATTATACACTC 828
Qy 873 TTCCAAGTCAATTTGTCTGCTTTGGCCAGGAGTTTGAATCCCAAGATGCTTGTGTGAGC 932
Db 829 TTCCCAATCATCTATCACCCGGTCTAGAGATTGATACCAAGGATGCTTGTGTGAGC 888
Qy 933 CTATGAAGAGAAATCAATTAAGGAAATTCGGAGCATCAATGTTCCAGATTGCGCTTC 992
Db 889 CTATGAGAGAAATGACCATACCTGAGATCCGTCAACACCCGATGTTCCAGCTGACCTTC 948
Qy 993 CACGTACTTGGCAGTGCCTCCACAGATACGACACCAACCAAGCCAAATGATGTGAGAG 1052
Db 949 CACGTATTTAGCTGTGACACCAAGATTAATGCAACAGGCCAAAAAGATTGATGAGG 1008
Qy 1053 ATACACTTGAAGATGTTGTTAATATGGAATTTAACAAGAACATGTGTGAATCACTGT 1112
Db 1009 AGATCTTCAAGAAAGTGTGAATAAGGAAATTTGACAGGAATCAATGTTGAATCTCTTG 1068
Qy 1113 GCAGAGACTTCAAAATGAGCAACTGTGTCATATTTACTATTGAGCAATCGGTTTA 1172

Db 1069 GGAACAGGATACAAAATGAGGGTACTGTGGCACTAATTGTTATTGGACACCGATTTC 1128
QY 1173 GAGCAACTAGTGGCTATCTTGGGCGAGATTATCAAGAATCATGACAGAAATTAAATC 1232
Db 1129 GTGTTCCAGTGGCTATCTTGGAGCTGAGTTTCAAGAACCATGATCCGGTTTAAATC 1188
QY 1233 AGCTGGCGTCATCTGAATCATCTAGTCTGGTACGAGGAATTATGTTCCAGGAAGCACTG 1292
Db 1189 AATGCATCTCAGTGAACCTGCTTCTTCAGTGTGGAAACCGCTTTCAGGCTACATGG 1248
QY 1293 ATCCTCATAGCAGTGGTTTGGCGCCATATTATCTGTGAAGAAATGGGCGCTTGAC 1352
Db 1249 AATATCCAGAGATGAGATCGAGGCAACAGTTCCTGTGTGAAGGAATGGGCGCTTGAGC 1308
QY 1353 TTCAGTCTCGGGCCCACTCTGTAATAATGTTGAGGCTTTAAAGCACTTCAAGAA 1412
Db 1309 TTCACTTCGAGCCCATCTCTGTAATAATGACTGAGGTTCTTAAAGCTTTGCAAGAA 1368
QY 1413 TAAACGTGAGTGAAGAAGATGGGCACTACACGTGAATGCAGATGGTCCAGGGT 1472
Db 1369 TAAATGTTGTTGGAAGAAGATTGTCACCTACACATGAAGTGTAGTGGTGTGCGCA 1428
QY 1473 TTCTGTG-----AAGTTAATGACAGTTAGATGCCAGCAACGCTTCTTG 1517
Db 1429 TTCTGTGTACCAACGAGGAAGATGTTAACAAATATGTGCATAGTAAATCATTACTTTGAG 1488
QY 1518 GTGACTCTACCATCATGATGATGATGCTTAATGGGAGGCTACCTACTGTGATCAAGT 1577
Db 1489 ATGATTCCAACATTAATGGAATGATGCTGTCTT-----ACTTCAATGTGTCAAGT 1542
QY 1578 TTGAATTCAGCTTTTACAAGACGAAGGACGACAGTAACCTTAGATATGACAGAGTTA 1637
Db 1543 TTGAAGTGACGCTTTTCAAAAACCGGGAAGAAAGTATCTGCTTGAATCTTCAAAAGGTC 1602
QY 1638 CTGACCTCAGCTGCTCTTCTGACTTCTGTGGGCGCTTCTTACCAAGCTTAGGGTTC 1697
Db 1603 AGGTCACAGTTTCTTCTTGGATCTATGCTGCTTCTTGACACAGCTTCGTGTCC 1662
QY 1698 TATAGTG 1704
Db 1663 TCTAGAG 1669

RESULT 15
US-09-938-842A-162
; Sequence 162, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jelf
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 162
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-162

Query Match 40.1%; Score 780.2; DB 9; Length 1539;
Best Local Similarity 70.2%; Pred. No. 2e-212;
Matches 1046; Conservative 0; Mismatches 443; Indels 0; Gaps 0;

QY 212 TTAAGGAACCTACACCTGGAGAACTTTAGGTATCGGTACATTTGGAAAAGTGAAGATT 271
Db 49 TTACCGAATTACAAGCTTGGTAAACTCTTTGGAATTTGGGCTTTTGGGAAAGTGAAATA 108
QY 272 GCAGAGCATTAAGCTTACTGGACATAGGGTTGCTATAAAGATCATCACTGCCCAATG 331
Db 109 GCAGAGCATGTTGTCAAGGCGCATTAAGGTTGCTATCAAAATCCTTAATCGTCTGAAGATC 168
QY 332 AGAATATGGAATGGAAGAAAGCAAGAGAAATTCAGATATGAAGTTGTTCAAT 391
Db 169 AAGAACATGAGATGGAAGAAAGTGAAGAGGAGATTAAAGATTACGGTTGTTATG 228
QY 392 CACCCCATATCATTCGGCTTTATGAGGTCATATACACACCTACAGATATATATGTTGTG 451
Db 229 CATCCTCATATTATTCGGCAGTATGAGTTAATAGACACAGATGACATTTATGTTGTG 288
QY 452 ATGAATATGTAAGTATGCGGAGTTATTGATTTACATTTGTGAAAGCGAGATTACAG 511
Db 289 ATGAGATATGTAAGTCTGGAGAGCTCTTTGATTTATTTGTGAAAGCGAGATTACAA 348
QY 512 GAAGATGAAGCTCGTGAATCTTCCAGAGATCATATCTGGCGTCAATCTGCCATAGA 571
Db 349 GAAGATGAGGCTCGTAACCTTTTCCAGAGATAATATCTGGTGAAGTACTGCCATCGT 408
QY 572 AACATGTTGTCCACCGTGACCTAAAGCCGAAACCTGTTACTGTAATCAAGTATAAT 631
Db 409 AATATGTTGTCCATAGAGACCTGAAGCTGAAGATTACTATTTGATTCGAGTGTAAAT 468
QY 632 GTAAACCTTGGGATTTTGTCTGAGCAATGTCATGATGAGGCCATTTTCTGAAGACT 691
Db 469 ATTAAGATGACACTTTGGGTGAGTAATGTTATGCGGAGTGTCAATTTCTAAAGACG 528
QY 692 AGCTGGGAGTCCGAATATGCTGCTCCAGAGTAATATCTGTTAACTATATGCTGGA 751
Db 529 AGTTGTGAAGCCCCAAGTACGCTGCTCCGAGGTTATATCAGGTAATATATGCTGGA 588
QY 752 CCTGAGGTCATGATGAGAGTGTGGGGTGAATCTTTATGCTCTTCTTGTGGAATCTT 811
Db 589 CTTGAAGTATGATGAGAGTTGCGGAGTTATTTATGACGCTCTAATATGCGGTACTCTT 648
QY 812 CCATTGATGATGAGATATTTCCCAATCTGTCAAAAAAATTAAGGAGGATCTACACA 871
Db 649 CTTTGTATGATGAAAAACATTTCCCACTTTTCAAGAAAAATTAAGGTGGGATTTACACT 708
QY 872 CTTCCAAGTCAATTTGCTGCTTGGCGAGGATTTGATCCACGAATGCTTGTGTGAG 931
Db 709 CTTCCAAGTCAATTTATCATCTGAGGCTAGAGACCTGATCCCAAGATGCTTATAGTTGAC 768
QY 932 CCTATGAAGAGATCAACATTTAGGAAATTCGGGAGCATCAATGTTCCAGATTGCGCTT 991
Db 769 CCGGTGAACGAATCAACATTTCTGAGATCCGTCAACACCGTTGGTTCCAGACTCATCTC 828
QY 992 CCACGTTACTTGGCAGTGCCTCCACAGATACGACACACAACCAAGCCAAATGATGAA 1051
Db 829 CTTGTTATCTTGTGCTGCTCTCCACCGGATACAGTAGAGCAGGCTTAAAAAGATCAATGAG 888
QY 1052 GATACACTTGAAGATGTTGTTAATATGGAATTTAAACAAGAACCAATGTGTGATCACTG 1111
Db 889 GAGATAGTTCAAGAAGTGTGAACATGGGATTTGATAGAACCAGGTTTGAATCTCTA 948
QY 1112 TGCAGCAGCTTCAAAATGAGGCACTGTGCATATTATTATTACTATTGGAACAATCGTTT 1171
Db 949 CGCAACAGAACACAAAAGATGCTACTGTTACATACTACCTGTTATTGGATTAACCGGTT 1008
QY 1172 AGAGCAACTAGTGGCTATCTTGGGCGAGATTATCAAGAAATCAATGACAGAAATTTAAAT 1231
Db 1009 CGTGTTCGAAGTGGCTATCTAGAAATCCGAGTTTCAGAGAGACAACAGAGTGTTCAT 1068
QY 1232 CAGCTGGCGTCATCTGAATCATCTAGTTCTGTTAGCAGGAATTAATGTTCCAGGAAGCAGT 1291
Db 1069 CCTATGCGCACACCTGAAGCGGGCGCTTCACTGTAGGCCACTGGAATTCCTGCACATGTG 1128

| | | | | |
|----|--|------|--|------|
| OY | | 1292 | GATCCTCATAGCAGTGGTTTGCCGCCATATTATCTGTGGAAGAAAATGGCGCCTTGGAA | 1351 |
| Db | | 1129 | GATCACTACGGGTTGGGAGCAAGATCACAAAGTCCTGTGATCGAAAATGGGCTCTTGGAA | 1188 |
| OY | | 1352 | CTTCAGTCTCGGGCCCCACCCTCGTGAATAATGTTGAGGCTTTAAAGCACTTCAAGAA | 1411 |
| Db | | 1189 | CTTCAGTCTCATGCGCATCTCTCGTAATCATGAATGAAGTTTGAAGCTCTTCAAGAA | 1248 |
| OY | | 1412 | TTPAACGTCAGATGGAAGAAGATGGGCACCTACAACGTGAATGCAGATGTCGCCAGGG | 1471 |
| Db | | 1249 | CTCAATGTGTGTGGAAGAAGATTGGTCACACTACAACATGAATGTCGATGGGTTCTGGT | 1308 |
| OY | | 1472 | TTTCCTGAAGTTAATGACACGTTAGATGCCAGCAAAGCTTCTTGATCACTTCAACATC | 1531 |
| Db | | 1309 | TTAGCTGATGTCAGAAATCACTATGTCACAACATCAGCTGCACCTTCAGAGATGAATCCAGC | 1368 |
| OY | | 1532 | ATGATATATGATGATGCTAATGGAGGCTACCTACTGTGATCAAGTTTGAATTCAGCTT | 1591 |
| Db | | 1369 | ATCATTGAGGATGACTGTGCCATGACTTCACCCACTGTCAATCAATTTGAAC TTCAGCTA | 1428 |
| OY | | 1592 | TACAAGACGAAGGACGACAACTACTTAGATATGCAGAGATTACTGCACTCAGCTG | 1651 |
| Db | | 1429 | TACAAGACCCGGGAAGAGAACTACTTGCTGGATATACAGAGATTAAACGGTCCGCACTT | 1488 |
| OY | | 1652 | CTCTTCCTGACTTCTGTGCGGCTTCCCTTACCAAGCTTAAGGCTTAT | 1700 |
| Db | | 1489 | CTCTTCCTTGATCTATGCGCGCTTCTTACAGAGCTTCGTGTGATCT | 1537 |

Search completed: July 9, 2004, 15:28:10
Job time : 926 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:50:54 ; Search time 59 Seconds
(without alignments)
2437.571 Million cell updates/sec

Title: US-09-857-522B-4
Perfect score: 2693
Sequence: 1 MDGSSKSGSHSEALRNYNLG.....GPQLLFUDFCAFLTKRLV 509

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|----------|---------------------|
| 1 | 2693 | 100.0 | 509 | 3 | AAB03416 | Aab03416 Corn puta |
| 2 | 2693 | 100.0 | 509 | 6 | ABR40708 | Abrr40708 Zea mays |
| 3 | 2422 | 89.9 | 509 | 6 | ABR40809 | Abrr40809 Oryza sat |
| 4 | 2378 | 88.3 | 531 | 6 | ABR40718 | Abrr40718 Triticum |
| 5 | 1977 | 73.4 | 505 | 6 | ABR40810 | Abrr40810 Oryza sat |
| 6 | 1974.5 | 73.3 | 514 | 3 | AAB03420 | Aab03420 Soybean p |
| 7 | 1974.5 | 73.3 | 514 | 6 | ABR40714 | Abrr40714 Glycine m |
| 8 | 1969.5 | 73.1 | 512 | 6 | ABR44015 | Abrr44015 Human SNF |
| 9 | 1963 | 72.9 | 504 | 6 | ABR40815 | Abrr40815 Cucumis s |
| 10 | 1958 | 72.7 | 570 | 6 | ABR40710 | Abrr40710 Zea mays |
| 11 | 1939 | 72.0 | 515 | 3 | AAB03422 | Aab03422 Soybean p |
| 12 | 1939 | 72.0 | 515 | 6 | ABR40716 | Abrr40716 Glycine m |
| 13 | 1931 | 71.7 | 579 | 3 | AAB03417 | Aab03417 Corn puta |
| 14 | 1931 | 71.7 | 579 | 6 | ABR40709 | Abrr40709 Zea mays |
| 15 | 1923 | 71.4 | 511 | 2 | AAR40842 | Aarr40842 SHPP. 8/2 |
| 16 | 1903.5 | 70.7 | 512 | 3 | AAG36157 | Aag36157 Arabidops |
| 17 | 1899.5 | 70.5 | 512 | 5 | AAO17663 | Aao17663 A thalian |
| 18 | 1891.5 | 70.2 | 512 | 5 | AAO17664 | Aao17664 A thalian |
| 19 | 1890.5 | 70.2 | 523 | 3 | AAB03425 | Aab03425 Wheat put |
| 20 | 1890.5 | 70.2 | 523 | 6 | ABR40719 | Abrr40719 Triticum |
| 21 | 1881.5 | 69.9 | 514 | 6 | ABR40816 | Abrr40816 Glycine m |
| 22 | 1809.5 | 67.2 | 512 | 5 | AAM50578 | Aam50578 Arabidops |
| 23 | 1734 | 64.4 | 454 | 3 | AAG36158 | Aag36158 Arabidops |
| 24 | 1724 | 64.0 | 452 | 3 | AAG36159 | Aag36159 Arabidops |
| 25 | 1545.5 | 57.4 | 494 | 3 | AAG39432 | Aag39432 Arabidops |

| | | | | | | |
|----|--------|------|-----|---|----------|---------------------|
| 26 | 1405.5 | 52.2 | 437 | 3 | AAG39433 | Aag39433 Arabidops |
| 27 | 1368.5 | 50.8 | 420 | 3 | AAG39434 | Aag39434 Arabidops |
| 28 | 1184 | 44.0 | 244 | 3 | AAB03424 | Aab03424 Wheat put |
| 29 | 1144 | 42.5 | 552 | 2 | AAR64312 | Aarr64312 Rat liver |
| 30 | 1119 | 41.6 | 548 | 7 | ADD48046 | Add48046 Rat Prote |
| 31 | 1115 | 41.4 | 550 | 7 | ADD48048 | Add48048 Human Pro |
| 32 | 1109 | 41.2 | 582 | 4 | ABB59603 | Abbs59603 Drosophil |
| 33 | 1101.5 | 40.9 | 565 | 7 | ADB61363 | Adb61363 Protein o |
| 34 | 1015.5 | 37.7 | 345 | 2 | AAW29894 | Aaw29894 Mammalian |
| 35 | 1013.5 | 37.6 | 633 | 6 | ABR52941 | Abrr52941 Protein s |
| 36 | 971 | 36.1 | 304 | 7 | ADC07762 | Adc07762 Rice prot |
| 37 | 940 | 34.9 | 257 | 2 | AAW29899 | Aaw29899 Mammalian |
| 38 | 861.5 | 32.0 | 257 | 2 | AAW43926 | Aay43926 Yeast pro |
| 39 | 749 | 27.8 | 783 | 4 | AAG65764 | Aag65764 Human pro |
| 40 | 749 | 27.8 | 783 | 4 | AAB85786 | Aab85786 Human kin |
| 41 | 746 | 27.7 | 744 | 5 | AAE19049 | Aae19049 Human PAR |
| 42 | 746 | 27.7 | 823 | 3 | AAW90879 | Aaw90879 Human ker |
| 43 | 745 | 27.7 | 729 | 2 | AAW37158 | Aaw37158 Human Twe |
| 44 | 745 | 27.7 | 729 | 4 | AAB65628 | Aab65628 Novel pro |
| 45 | 745 | 27.7 | 729 | 6 | AAE33552 | Aae33552 Human mic |

ALIGNMENTS

RESULT 1
AAB03416
ID AAB03416 standard; protein; 509 AA.
XX
AC AAB03416;
XX
DT 03-JAN-2001 (first entry)
XX
DE Corn putative carbon catabolite repression protein SNF1 #2.
XX
KW Corn; carbon catabolite repression; sucrose non-fermenting protein 1;
KW SNF1; plant growth.
XX
OS Zea mays.
XX
PN WO200036115-A2.
XX
PD 22-JUN-2000.
XX
PF 15-DEC-1999; 99WO-US029824.
XX
PR 16-DEC-1998; 98US-0112563P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ;
PI Miao G;
XX
DR WPI; 2000-431593/37.
DR N-PSDB; AAA52768.
XX
PT New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
PT involved in carbon catabolite repression in plants and seeds, useful for
PT controlling carbon and nitrogen partitioning pathways during plant growth
PT and development.
XX
PS Claim 10; Page 35-36; 59pp; English.
XX
CC The present sequence is a putative sucrose non-fermenting protein SNF1
CC protein sequence from corn. Its coding sequence was isolated by searching
CC a corn tassell shoot cDNA library for sequences similar to those encoding
CC SNF1 in Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza
CC sativa. The protein is involved in carbon catabolite repression, and so
CC the gene and protein can be used in plants to control the nitrogen and
CC carbon partitioning pathways during plant growth and development. They
CC can also be used to alter the accumulation of carbohydrates, lipids and
CC proteins during plant growth
XX

Sequence 509 AA;

Query Match 100.0%; Score 2693; DB 3; Length 509;
Best Local Similarity 100.0%; Pred. No. 1e-246;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSSKSGSHSEALRNYNLGRITLGITFGKVKIAEHKLTGHRVAIKIINCRQRMNMEME 60
DB 1 MDGSSKSGSHSEALRNYNLGRITLGITFGKVKIAEHKLTGHRVAIKIINCRQRMNMEME 60
QY 61 KAKREFKILKFIHPHIIIRLYEVIYPTDIYVVMYCKYGELFDYIVEKGRLOEDEARRI 120
DB 61 KAKREFKILKFIHPHIIIRLYEVIYPTDIYVVMYCKYGELFDYIVEKGRLOEDEARRI 120
QY 121 FQOIIISGVEYCHRNWVHRDLKPENLLDSKYNVKLADFGLSNVMHDGHLKTS CGSPNY 180
DB 121 FQOIIISGVEYCHRNWVHRDLKPENLLDSKYNVKLADFGLSNVMHDGHLKTS CGSPNY 180
QY 181 AAPEVISGKLYAGPEVDVWSCGVILYALCGTLPDDENIPNLFKKIKGIIYTLPSHLSA 240
DB 181 AAPEVISGKLYAGPEVDVWSCGVILYALCGTLPDDENIPNLFKKIKGIIYTLPSHLSA 240
QY 241 LARDLIPRMLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQOAKMIDEDTLRDVV 300
DB 241 LARDLIPRMLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQOAKMIDEDTLRDVV 300
QY 301 NMGFNKNHVCESLCSRLQNEATVAYLLDNFRATSGYL GADYQESMDRNLNQLASSES 360
DB 301 NMGFNKNHVCESLCSRLQNEATVAYLLDNFRATSGYL GADYQESMDRNLNQLASSES 360
QY 361 SSSGTRNYPGSSDPHSSGLRPIYPVERKWA LGQSRAPREIMVEVLKALQELNVRWK 420
DB 361 SSSGTRNYPGSSDPHSSGLRPIYPVERKWA LGQSRAPREIMVEVLKALQELNVRWK 420
QY 421 NGHYNVCKRWCPGFPEVNDTLDASNSFLGDSITMDNDANGRLPTVIKFEFQLYKTKDDK 480
DB 421 NGHYNVCKRWCPGFPEVNDTLDASNSFLGDSITMDNDANGRLPTVIKFEFQLYKTKDDK 480
QY 481 YLLDMQRTGPQLFLDFCAAFITKLRVL 509
DB 481 YLLDMQRTGPQLFLDFCAAFITKLRVL 509

RESULT 2

ABR40708 standard; protein, 509 AA.

AC ABR40708;
XX
DT 16-MAY-2003 (first entry)
XX
DE Zea mays oil trait related protein sequence SEQ ID NO:236.
XX
KW Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CKC-like transcription factor; antisense inhibition; co-suppression;
KW transgenic plant.
XX
OS Zea mays.
XX
PN WO2003002751-A2.
XX
PD 09-JAN-2003.
XX
PF 27-JUN-2002; 2002WO-US020152.
XX
PR 29-JUN-2001; 2001US-0301913P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;

PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczynski MC;
XX
DR WPI; 2003-201509/19.
DR N-PSDB; ACC00743.
XX
PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
PS Claim 12; Page 273-274; 542pp; English.

CC The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
XX

Sequence 509 AA;

Query Match 100.0%; Score 2693; DB 6; Length 509;
Best Local Similarity 100.0%; Pred. No. 1e-246;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDGSSKSGSHSEALRNYNLGRITLGITFGKVKIAEHKLTGHRVAIKIINCRQRMNMEME 60
DB 1 MDGSSKSGSHSEALRNYNLGRITLGITFGKVKIAEHKLTGHRVAIKIINCRQRMNMEME 60
QY 61 KAKREFKILKFIHPHIIIRLYEVIYPTDIYVVMYCKYGELFDYIVEKGRLOEDEARRI 120
DB 61 KAKREFKILKFIHPHIIIRLYEVIYPTDIYVVMYCKYGELFDYIVEKGRLOEDEARRI 120
QY 121 FQOIIISGVEYCHRNWVHRDLKPENLLDSKYNVKLADFGLSNVMHDGHLKTS CGSPNY 180
DB 121 FQOIIISGVEYCHRNWVHRDLKPENLLDSKYNVKLADFGLSNVMHDGHLKTS CGSPNY 180
QY 181 AAPEVISGKLYAGPEVDVWSCGVILYALCGTLPDDENIPNLFKKIKGIIYTLPSHLSA 240
DB 181 AAPEVISGKLYAGPEVDVWSCGVILYALCGTLPDDENIPNLFKKIKGIIYTLPSHLSA 240
QY 241 LARDLIPRMLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQOAKMIDEDTLRDVV 300
DB 241 LARDLIPRMLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQOAKMIDEDTLRDVV 300
QY 301 NMGFNKNHVCESLCSRLQNEATVAYLLDNFRATSGYL GADYQESMDRNLNQLASSES 360
DB 301 NMGFNKNHVCESLCSRLQNEATVAYLLDNFRATSGYL GADYQESMDRNLNQLASSES 360
QY 361 SSSGTRNYPGSSDPHSSGLRPIYPVERKWA LGQSRAPREIMVEVLKALQELNVRWK 420
DB 361 SSSGTRNYPGSSDPHSSGLRPIYPVERKWA LGQSRAPREIMVEVLKALQELNVRWK 420
QY 421 NGHYNVCKRWCPGFPEVNDTLDASNSFLGDSITMDNDANGRLPTVIKFEFQLYKTKDDK 480
DB 421 NGHYNVCKRWCPGFPEVNDTLDASNSFLGDSITMDNDANGRLPTVIKFEFQLYKTKDDK 480
QY 481 YLLDMQRTGPQLFLDFCAAFITKLRVL 509
DB 481 YLLDMQRTGPQLFLDFCAAFITKLRVL 509

RESULT 3
ABR40809
ID ABR40809 standard; protein; 509 AA.
XX
AC ABR40809;
XX
DT 16-MAY-2003 (first entry)
XX
DE Oryza sativa oil trait related protein sequence SEQ ID NO:401.
XX
KW Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CKC-like transcription factor; antisense inhibition; co-suppression;
KW transgenic plant.
XX
OS Oryza sativa.
XX
PN WO2003002751-A2.
XX
PD 09-JAN-2003.
XX
PF 27-JUN-2002; 2002WO-US020152.
XX
PR 29-JUN-2001; 2001US-0301913P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczyński MC;
XX
DR WPI; 2003-201509/19.
XX
PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
PS Claim 12; Page 433-434; 542pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV) or
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 509 AA;
Query Match 89.9%; Score 2422; DB 6; Length 509;
Best Local Similarity 88.6%; Pred. No. 6.1e-221;
Matches 451; Conservative 35; Mismatches 23; Indels 0; Gaps 0;

QY 121 FQOIIISGVEYCHRNWVVRDLKPENTLLDSKYNVLADEGLSNVMDHGHFLKTS CGSPNY 180
D 121 FQOIIISGVEYCHRNWVVRDLKPENTLLDSKYNVLADEGLSNVMDHGHFLKTS CGSPNY 180
QY 181 AAPEVISGKLYAGPEVDVWSCGVIYLLALCGTLPPDENIPNLFKKIKGCIYTLPSHLSA 240
D 181 AAPEVISGKLYAGPEVDVWSCGVIYLLALCGTLPPDENIPNLFKKIKGCIYTLPSHLSA 240
QY 241 LARDLIPRMLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQQA KIDEDTLRDV 300
D 241 LARDLIPRMLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQQA KIDEDTLRDV 300
QY 301 NMGFNKNHVCESLCSRLQNEATVAYLLDNRPRATSGYL GADYQESMDRNLNQLASSES 360
D 301 NLGYEKDHVCESLRNLQNEATVAYLLDNRPRATSGYL GADYQESLRNLNRPASSES 360
QY 361 SSSGTRNYPGSSDPHSSGLRPYPYVERKWKALGLQSRAPREIMWEVLKALQELNVRWK 420
D 361 ASSNTRHYLLPGSSDPHSSGLRPHYPVERKWKALGLQSRAPREIMIEVLKALQELNVRWK 420
QY 421 NGHYNVCKRCWCPGFPEVNDTLDA NSFLGDSITMDNDANGRLPTVIKFEFQLYKTKDK 480
D 421 NGQYNMCKRWSVGYPQATDMLDVNHSFVDDSLTMDNGDVNGRLPAVIKFEIQLYKSRDEK 480
QY 481 YLLDMQRTGPPQLFLDFCAAFLTCLRVL 509
D 481 YLLDMQRTGPPQLFLDFCAAFLTCLRVL 509

RESULT 4
ABR40718
ID ABR40718 standard; protein; 531 AA.
XX
AC ABR40718;
XX
DT 16-MAY-2003 (first entry)
XX
DE Triticum aestivum oil trait related protein sequence SEQ ID NO:256.
XX
KW Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CKC-like transcription factor; antisense inhibition; co-suppression;
KW transgenic plant.
XX
OS Triticum aestivum.
XX
PN WO2003002751-A2.
XX
PD 09-JAN-2003.
XX
PF 27-JUN-2002; 2002WO-US020152.
XX
PR 29-JUN-2001; 2001US-0301913P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczyński MC;
XX
DR WPI; 2003-201509/19.
DR N-PSDB; ACC00753.
XX
PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
PS Claim 12; Page 296-298; 542pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a

CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 531 AA;

| | | | | |
|-----------------------|------------------|---------------------|-----------|-------------|
| Query Match | 88.3% | Score 2378; | DB 6; | Length 531; |
| Best Local Similarity | 86.8%; | Pred. No. 9.9e-217; | | |
| Matches 442; | Conservative 34; | Mismatches 33; | Indels 0; | Gaps 0; |

| | | | |
|----|-----|---|-----|
| QY | 1 | MDGSSKSGSHSEALRNYNLGRTLGIGTEGKVYKIAEHKLTHGRVAIKI INCRQMRNMEMEE | 60 |
| Db | 23 | MEGNTRGGSHDALKNYNVGRTLGIGTEGKVR IAEHKHTGHKVAIKILNBRQMRTEMEE | 82 |
| QY | 61 | KAKREFKILKLFIIHPHIIRLYEVIYTPDIYVMEYCKYGELEFDYIVEKGRLOEDEARRI | 120 |
| Db | 83 | KAKREIKILRLFIHPHIIRLYEVIYTPDIFVMEYCKYGELEFDICIVEKGRLOEDEARRI | 142 |
| QY | 121 | FOQIISGEVEYCHRNMVVHRDLKPENLILDSKYNVKLADFGLSNVMDHGHFLKTS CGSPNY | 180 |
| Db | 143 | FOQIISGEVEYCHRNMVVAHRDLKPENLILDSKYNVKLADFGLSNVMDHGHFLKTS CGSPNY | 202 |
| QY | 181 | AAPEVISGKLYAGPEVDVWSCGVLVALLCGTLPFDDENIPNLFKKIKG3IYTLPSHLSA | 240 |
| Db | 203 | AAPEVISGKLYAGPEVDVWSCGVLVALLCGTLPFDDDNIPKLFKKIKG3IYTLPSHLSA | 262 |
| QY | 241 | LARDLIPRLVVEPMKRITIREIREHQWFQIRLPRYLAVPPPTDQQAKMIDEDTLRDVY | 300 |
| Db | 263 | LARDLIPRLVVDPMKRITIREIREHPWFQIRLPRYLAVPPPTDQAQAKMIDEDTLKEIV | 322 |
| QY | 301 | NMGFNKNHVCESLCSRLQNEATVAYLLLDNRFRAATSGYLGADYQESMDRNINQLASSES | 360 |
| Db | 323 | NLGIDKDHVCESLCSRLQNEATVAYLLLDNRFRAATSGYLGADYLOSMGRSTNOFTSLES | 382 |
| QY | 361 | SSSGTRNVVPGSSDPHSSGLRPYPVERKMAJGLOSRAPREIMVEVLKALQELNVRWKK | 420 |
| Db | 383 | ASPESTRQYLLPASNDSQSGSLRPYPVERKMAJGLOSRAPREIMIEVLKALQELNVCWKK | 442 |
| QY | 421 | NGHYNVKCRWCPGFPPEVNDTLDASNSFLGDSTIMDNDANGRLPTVIKPEFQLYTKDDK | 480 |
| Db | 443 | NGHYNMKCRWCPGFPQVSMDLDANHSFVDDSTIMDNGDANGRLPAVIKPEIQLYTKYDDK | 502 |
| QY | 481 | YLLDMQRTGPQLLFLDFCAAFITKLRLV | 509 |
| Db | 503 | YLLDMQRTGPQLLFLDFCAAFITNLRLV | 531 |

| RESULT 5 | |
|----------|---|
| ABR40810 | |
| ID | ABR40810 standard; protein; 505 AA. |
| XX | |
| AC | ABR40810; |
| XX | |
| DT | 16-MAY-2003 (first entry) |
| XX | |
| DE | Oryza sativa oil trait related protein sequence SEQ ID NO:402. |
| XX | |
| KW | Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; receptor-like protein kinase; mitogen activated protein kinase; oil; LIP5-like transcription factor caleosin; ATP citrate lyase; SNF1; CKC-like transcription factor; antisense inhibition; co-suppression; |
| KW | |

| | |
|----|---|
| KW | transgenic plant. |
| XX | |
| OS | Oryza sativa. |
| XX | |
| PN | WO2003002751-A2. |
| XX | |
| PD | 09-JAN-2003. |
| XX | |
| PF | 27-JUN-2002; 2002WO-US020152. |
| XX | |
| PR | 29-JUN-2001; 2001US-0301913P. |
| XX | |
| PA | (DUPO) DU PONT DE NEMOURS & CO E I. |
| PA | (PION-) PIONEER HI-BRED INT INC. |
| XX | |
| PI | Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT; |
| PI | Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B; |
| PI | Tarczynski MC; |
| XX | |
| DR | WPI; 2003-201509/19. |
| XX | |
| PT | Novel nucleotide fragment encoding polypeptides having receptor-like |
| PT | protein kinase activity, caleosin-like activity, useful for altering oil |
| PT | phenotypes in plants such as sunflower, coconut, soybean, wheat and rice. |
| XX | |
| PS | Claim 12; Page 434-436; 542pp; English. |

The present invention describes an isolated nucleotide fragment (I) comprising a nucleic acid sequence (NS) chosen from a NS encoding a polypeptide (PP) having receptor-like protein kinase activity, mitogen activated protein (MAP)-kinase activity, LIP15-like transcription factor activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like activity and CKC-like transcription factor activity. Also described: (1) complement (II) of (I); (2) a chimeric construct (III) comprising (I) or (II), operably linked to a regulatory sequence; (3) a plant (IV) comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5) oil obtained from (V). (I) or its part can be used in antisense inhibition or co-suppression in a transformed plant. (III) is useful for altering the oil phenotype in a plant such as corn, soybean, wheat, rice, canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for creating transgenic plants having altered lipid profiles. (I) can also be used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to ABR40879 represent sequences used in the exemplification of the present invention

| | | | | |
|-----------------------|------------------|---------------------|-----------|-------------|
| Query Match | 73.4%; | Score 1977; | DB 6; | Length 505; |
| Best Local Similarity | 74.1%; | Pred. No. 1.2e-178; | | |
| Matches 377; | Conservative 52; | Mismatches 76; | Indels 4; | Gaps 2; |

| | | | |
|----|-----|--|-----|
| Qy | 1 | MDGSSKSGHSEALRNYNLGRITLGIGTEGVKIAEHKLTGHRVAIKIINCRÖMNNMEMEE | 60 |
| Db | 1 | MEGAGR---DGNPLGGYRIKTLGIGSFVKIAEHLTGHKVAIKILNRKIKSMEEMEE | 57 |
| Qy | 61 | KAKREKILKLFIHPHIIRLYEVIYTPUDIYVMEYCKYGELFDYIVEKGRLOEDEARRI | 120 |
| Db | 58 | KYKREIKILRLFMHPHIIRLYEVIDTPADIYVMEYKSGELFDYIVEKGRLOEEARRF | 117 |
| Qy | 121 | FQOIISGVEYCHRNMVVHRDLKPENLILDSKNVKLADFGLSNVMDGHFLKTSOSSPNY | 180 |
| Db | 118 | FQOIISGVEYCHRNMVVHRDLKPENLILDSKCNVKIADFGLSNVMRDGHFLKTSOSSPNY | 177 |
| Qy | 181 | AAPEVISGKLYAGPEVDWMSGVILYALLCGTLPEDDENIPNLFKKIKGIIYTLPSHLSA | 240 |
| Db | 178 | AAPEVISGKLYAGPEVDWMSGVILYALLCGTLPEDDENIPNLFKKIKGIIYTLPSHLSA | 237 |
| Qy | 241 | LARDLIPRLVVEBPMKRITIREIREHÖWFQIRLPXYLAVPPPDPTQÖAKMIDEDTLRDVY | 300 |
| Db | 238 | LARDLIPRLVVDPMKRITIREIREHÖWFTVGLPRYLAVPPPDPTAQÖVKKLDEDETLDVY | 297 |
| Qy | 301 | NMGFNKGVHVCESLCSRLÖNEATVAYVYLLDNFRFRATSGYLGADYÖESMDRNINÖLASSES | 360 |

DB 298 NMGFDKNQLIESLHKRLQNEATVAYYLLLDNRRLRTSGYLGAEFHESMESSLAQVTPAET 357
QY 361 SSSGTRNYVPGSSDPHSSGLRPYPYVERKWAALGQSRAPREIMVEVLKALQELNVRWK 420
DB 358 PMSATDHRQGHMESPGFGLRHFAADRKWALGQSRAPREIITEVLKALQELNVCWK 417
QY 421 NGHYNVKCRWCPGFPREVNDTLDA NSFLGDSSTIMDNDANGRLPTVIKFEFQLYKTKDK 480
DB 418 IGHYNMKCRWSPSPFSGHSMHNNHGFGEASAIETDDSEKSTHTV-KFEIQLYKTRDEK 476
QY 481 YLLDMQRTVGPQLFLDFCAAFITKLRVL 509
DB 477 YLLDLQRVSGPQLFLDLCSAFLTLQRLV 505

RESULT 6

AAB03420
ID AAB03420 standard; protein; 514 AA.

AC AAB03420;

DT 03-JAN-2001 (first entry)

DE Soybean putative carbon catabolite repression protein SNF1 #2.

XX KM Soybean; carbon catabolite repression; sucrose non-fermenting protein 1;
XX SNF1; plant growth.

OS Glycine max.

PN WO200036115-A2.

PD 22-JUN-2000.

PF 15-DEC-1999; 99WO-US029824.

PR 16-DEC-1998; 98US-0112563P.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

PI Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ;
PI Miao G;

DR WPI; 2000-431593/37.

DR N-PSDB; AAA52772.

PT New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
PT involved in carbon catabolite repression in plants and seeds, useful for
PT controlling carbon and nitrogen partitioning pathways during plant growth
PT and development.

PS Claim 10; Page 43-45; 59pp; English.

CC The present sequence is a putative sucrose non-fermenting protein SNF1
CC protein sequence from the soybean. Its coding sequence was isolated by
CC searching a pod cDNA library for sequences similar to those known to
CC encode SNF1 in Arabidopsis thaliana, Cucumis sativus, Glycine max and
CC Oryza sativa. The protein is involved in carbon catabolite repression,
CC and so the gene and protein can be used in plants to control the nitrogen
CC and carbon partitioning pathways during plant growth and development.
CC They can also be used to alter the accumulation of carbohydrates, lipids
CC and proteins during plant growth

XX SQ Sequence 514 AA;

Query Match 73.3%; Score 1974.5; DB 3; Length 514;
Best Local Similarity 74.0%; Pred. No. 2.2e-178;
Matches 382; Conservative 49; Mismatches 76; Indels 9; Gaps 3;

QY 1 MDGSS--KSGSHSEALRNYNLGRTLGITGFGKYVIAEHKLTGHRVAIKIINROMRNMEM 58
DB 1 MDGPARGGAGLDMFLPNYKLGKTIGISFGKYVIAEHVLTGHKVAIKILNRKIKNMEM 60

QY 59 EEKAKREFKILKFIHPHIIRLYEVIYPTDIYVMMEYCKYGEFLDYIVEKRLQDEAR 118
DB 61 EEKVRREIKILRFMHPIIRLYEVIETPTDIYVMMEYKSGELFDYIVEKRLQDEAR 120
QY 119 RIFQOIIISGVEXCHRNMVVRDLKPENLILDSKNVKAADFGLSNVMDGHFLKTS CGSP 178
DB 121 NFOQOIIISGVEXCHRNMVVRDLKPENLILDSKNVKAADFGLSNVMDGHFLKTS CGSP 180
QY 179 NYAAPEVISGKLYAGPEVDVWSCGVLLVALLCGTLFPDDENIPNLFKIKGIIYTLPSHL 238
DB 181 NYAAPEVISGKLYAGPEVDVWSCGVLLVALLCGTLFPDDENIPNLFKIKGIIYTLPSHL 240
QY 239 SALARDLIPRMIVPEPMKRITIREIREHQWFQIRLPYLA VPPPDITQOAKMIDEDTLRD 298
DB 241 SPGARDLIPGMLVVDPMRMTIPEIRQHPWFQARLPYLA VPPPDITQOAKKIDEIILQE 300
QY 299 VNMGFNKNHVCESLCSRLQNEATVAYYLLLDNFRATSGYLGA DYQESMDRNLNQLASS 358
DB 301 VVKMGFDRNQLVESLGNRIQNEGTVAAYYLLLDNFRVSSGYLGA EFQETWDSGFNQMHSS 360
QY 359 ESSSGTRNYVPGSSDPHSSGLRPYPYVERKWAALGQSRAPREIMVEVLKALQELNVRW 418
DB 361 ELASSVGNRFPGYMEYPGVSGRQGFVERKWAALGQSRAPREIMVEVLKALQELNVCW 420
QY 419 KNGHYNVKCRWCPGFP-----EVDNTLDASNSFLGDSSTIMDNDANGRLPTVIKFEFQ 473
DB 421 KKI GHYNMKCRWVAGIPGHHEGMVNNVNSHNYFGDDSNIIENDAVS--TSNVVKFEVQL 478
QY 474 YKTKDDKYLDMQRTVGPQLFLDFCAAFITKLRVL 509
DB 479 YKTRREKYLDLQRVGPGQLFLDLCSAFLTLQRLV 514

RESULT 7

ABR40714
ID ABR40714 standard; protein; 514 AA.

AC ABR40714;

DT 16-MAY-2003 (first entry)

DE Glycine max oil trait related protein sequence SEQ ID NO:248.

XX KM Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
XX receptor-like protein kinase; mitogen activated protein kinase; oil;
XX LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
XX CKC-like transcription factor; antisense inhibition; co-suppression;
XX transgenic plant.

OS Glycine max.

PN WO2003002751-A2.

PD 09-JAN-2003.

PF 27-JUN-2002; 2002WO-US020152.

PR 29-JUN-2001; 2001US-0301913P.

PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.

PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;

PI Tarczyński MC;

DR WPI; 2003-201509/19.

DR N-PSDB; ACC00749.

PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.

Qy 472 QLYKTKDDKYLDMQRTVGPQLFLDFCAFLTKLRVL 509
| | | | : | | | | : | | | | : | | | | : | | | |
Db 475 QLYKTRDDKYLDDLQRVGPOFLFLDLCAAFLAQLRVL 512
| | | | : | | | | : | | | | : | | | | : | | | |
RESULT 9
ABR40815
ID ABR40815 standard; protein; 504 AA.
XX
AC ABR40815;
XX
DT 16-MAY-2003 (first entry)
XX
DE Cucumis sativus oil trait related protein sequence SEQ ID NO:407.
XX
KW Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CKC-like transcription factor; antisense inhibition; co-suppression;
KW transgenic plant.
XX
OS Cucumis sativus.
XX
PN WO2003002751-A2.
XX
PD 09-JAN-2003.
XX
PF 27-JUN-2002; 2002WO-US020152.
XX
PR 29-JUN-2001; 2001US-0301913P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczynski MC;
XX
DR WPI; 2003-201509/19.
XX
PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
PS Claim 12; Page 442-444; 542pp; English.
XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 504 AA;
Query Match 72.9%; Score 1963; DB 6; Length 504;
Best Local Similarity 74.8%; Pred. No. 2,6e-177;
Matches 374; Conservative 53; Mismatches 65; Indels 8; Gaps 4;
Qy 16 NYNLGRTLGIGTGGKVKIAEHKLGTGRVAIKINCRQMRNMEMEKEAKBEFKILKFTIHP 75
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Db 7 NYKLGKTLGIGSGFKVIAEHALTGHKVAIKILNRKIKNLDMEKXVRRIRKILRLFMHP 66
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |

Qy 76 HIIRLYEVITYPTDIYVMEYCKYGELEFDYIVEKGRLOEDEARRIFQOIIISGEYCHRM 135
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Db 67 HIIRLYEVIETPSDIYVMEYKSGLEFDYIVEKGRLOEDEARNFFQOIIISGEYCHRM 126
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Qy 136 VVHRDLKPENLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNYAADEVISGLYAGPE 195
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Db 127 VVHRDLKPENLLDSKCNVKIADFGLSNMRDGHFLKTS CGSPNYAADEVISGLYAGPE 186
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Qy 196 VDVWSCGVIYALLCGTLPFDDENIPNLFKKIKGIYTLPSHLSALARDLIPRMLVVEPM 255
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Db 187 VDVWSCGVIYALLCGTLPFDDENIPNLFKKIKGIYTLPSHLSGARELIPSMLVVDPM 246
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Qy 256 KRITIREIREHOWFOIRLPXYLAVPPEDTTOQAKMIDEDTLRDVYVMGFNKNHVCESLCS 315
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Db 247 KRITIREIRQHPWFQAHLPXYLAVPPEDTMOQAKKIDEDILQEVYVMGFDRNQLVESLRN 306
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Qy 316 RLQNEATVAYILLIDNRFRTATSGYLGADYQESMDRNLNQLASSSESSSGTRNYVPGSSDP 375
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Db 307 RIQNEATVAYILLIDNRFRTATSGYLGADYQESMDRNLNQLASSSESSSGTRNYVPGSSDP 366
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Qy 376 HSSGLRPYPYVERKWAALGLQSRAPREITVEVLKALQELNVRWKKNGHYNVKCRWCPCGFP 435
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Db 367 QGMGLRAQFVVERKWAALGLQSRAPREITVEVLKALRELNVAMWKIGHYNMKCRWLPGIP 426
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Qy 436 -----EVNDTLDASNSFLGD-STIMDNDANGRLPTVIKFEFQLYKTKDKYLLDMQRTV 489
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Db 427 GHHEGMINNPVH-SNHYFGDKSTIENDGV-VKSPNVIKFEVQLYKTREEKYLLDLQRTV 484
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Qy 490 GPQLFLDFCAFLTKLRVL 509
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |
Db 485 GPQLFLDLCAFLAQLRVL 504
| | | | : | | | | : | | | | : | | | | : | | | | : | | | |

RESULT 10
ABR40710
ID ABR40710 standard; protein; 570 AA.
XX
AC ABR40710;
XX
DT 16-MAY-2003 (first entry)
XX
DE Zea mays oil trait related protein sequence SEQ ID NO:240.
XX
KW Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CKC-like transcription factor; antisense inhibition; co-suppression;
KW transgenic plant.
XX
OS Zea mays.
XX
PN WO2003002751-A2.
XX
PD 09-JAN-2003.
XX
PF 27-JUN-2002; 2002WO-US020152.
XX
PR 29-JUN-2001; 2001US-0301913P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczynski MC;
XX
DR WPI; 2003-201509/19.
DR N-PSDB; ACC00745.
XX
PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.


```

QY      361 SSSGTRNYVFGSSDPHSSGLRPYYPVERKKAIGLQSRAPREIMVEVLKALQELNVWKK 420
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      433 PTSATELRQHGFESESPGSGLRQHPAAERKWAIGLQSRAPREIISEVLKALQELNVWKK 492

QY      421 NGHYNVKCRWCPGFPPEVNDTLDASNSFLGDSTIMDNDANGRLPTVIKPEFQLYKTKDDK 480
      ||| : ||| ||| : ||| : | : : | : : : | : : ||| : ||| : : |
Db      493 IGHYNNKCRWSPGCLL--SMHMNSDSFSAESIETDVFMEEKSTPYVKFEIQLYKTRDEK 550

QY      481 YLDMQRVTGPQLLFLDFCAAFITKLRVL 509
      ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db      551 YLIDLQRVSGSHLLFLDLCSAFLTQLRVL 579

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| | | |
|----|---|----------------------------|
| XX | RESULT 15 | |
| XX | AAAR40842 | |
| ID | AAAR40842 | standard; protein; 511 AA. |
| XX | | |
| AC | AAAR40842; | |
| XX | | |
| DT | 27-AUG-2003 | (revised) |
| DT | 02-MAR-1994 | (first entry) |
| XX | | |
| DE | SHP. | |
| XX | | |
| KM | Yeast; SNF1; homologous protein; SHPP; Nicotinia tabacum; invertase. | |
| XX | | |
| OS | Saccharomyces cerevisiae. | |
| PN | JP05199884-A. | |
| XX | | |
| PD | 10-AUG-1993. | |
| XX | | |
| PF | 13-DEC-1991; 91JP-00330417. | |
| XX | | |
| PR | 13-DEC-1991; 91JP-00330417. | |
| XX | | |
| PA | (SUMO) SUMITOMO CHEM CO LTD. | |
| XX | | |
| DR | WPI; 1993-284682/36. | |
| DR | P-PSDB; AAAR40842. | |
| XX | | |
| PT | Yeast SNF1 homologous protein phosphorylase gene of SOLANACEAE plants - | |
| PT | useful for controlling expression of invertase for the increase of crop | |
| PT | yield. | |
| XX | | |
| PS | Claim 1; Page 6; 7pp; Japanese. | |
| XX | | |
| CC | This sequence is encoded by the yeast SNF1 homologous protein gene | |
| CC | (SHP). The yeast SHPP gene may be obtained from Nicotinia tabacum and | |
| CC | may be used to control expression of invertase for the increase of crop | |
| CC | yield. (Updated on 27-AUG-2003 to correct OS field.) | |
| XX | | |
| SQ | Sequence 511 AA; | |

```

Query Match          71.4%; Score 1923; DB 2; Length 511;
Best Local Similarity 72.1%; Pred. No. 1.7e-173;
Matches 372; Conservative 60; Mismatches 72; Indels 12; Gaps 7;

Qy      1 MDGSS--KSGSHSEALRNYNLGRTLGIGTFGKVKIAEHKLTHGRAVAIKIINCRÖRMNEM 58
        |||||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      1 MDGSTVQGSSSVESFLRNKYLGKTGLIGSFGVKVIAEHTLTGHKAVAKITLRNKIKNMEM 60

Qy      59 BEKAKREFKILKLFIFPHIIRLYEVITYPTDIYVMVEYCKYGELFDYIVEKGRLQEDEAR 118
        |||||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      61 EEKVRREIKILRLFMMPHIIRLYEVETPSDIYVMVEYKSGELFDYIVEKGRLQEDEAR 120

Qy      119 RIFOQIIISGV EYCHRRNMVVHRDLKPENLLDSKYNVKLTADFGLSNMVHIDGHLKTS CGSP 178
        :|||||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db      121 KFFQQIIISGV EYCHRRNMVVHRDLKPENLLDSKMNVKIADFGLSNIMRDGHFLKTS CGSP 180

Qy      179 NYAAPEVISGKLYAGPEVDVWSCVILYALLCGTLPFDDDENIPNLFKIKGGIYTLP SHL 238
        |||||:|||||:::|||||:::|||||:::|||||:::|||||:::|||||

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Db      181 NYAAPEVISGKLYAGPEVDVWSCGVLLYALLCGTLPEDDENIPNLFKKIKGMISSPSHL 240

QY      239 SALARDLIPRLVVEPMKRITIREIREHWFQIRLPRYLAVPPPDITTOAKMIDEDTLRD 298
        || ||||| : : : : || || || || || || || || || || || || || || || : :
Db      241 SAGARDLIPRLIVDPMKRMTIPEIRMHMPWFQAHLPRLAVPPPDITMOQAKKIDEDILQE 300

QY      299 VVNGFENKNHVCESLCSRLONEATVAYLLLDNRFRATSGYLGADYQESMDRNLNQJLASS 358
        || || : : : : || : : : : || || || || || || || || || || || || ||
Db      301 VYKRGFDRNSLVASLCNRVONEGIVAYLLLENQFRASSGYMGALEFQETMEYGYHQINSS 360

QY      359 ESSSSGTRNYPGSSDPHSSGLRPYYEVERKWAJGLOSRAHPREIMVEVLKALQELNVRW 418
        || || : : || || || || || || || || || || || || || || || || || || ||
Db      361 EVLLP-CWQHLPGIMDFQOVGAR-QPEVERKWAJGLOSRAHPREIMTEVLKALQGINVRW 418

QY      419 KKNQHNVVKCRWCPCGPFPEVNDTLBASNS----FLG-DSTIMDNDDANGRLPTVIKEEFQJL 473
        || || : : : : || || || || || || || || || || || || || || || || || ||
Db      419 KKIGBYNMKCQWPGVPGHHEGM-SNNSIHIOFFGDDSTVIENGVT--IPNAVKEFVQL 475

QY      474 YKTKDDKYLLDMQRTVGPQLFLDFCAAFITKLRLV 509
        || || : : || || || || || || || || || || || || || || || || || || ||
Db      476 YKTBEEKYLLDLQRVQGPQFLFLDLCAAFIAQLRLV 511

```

Search completed: July 7, 2004, 17:55:08
Job time : 61 secs

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This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 7, 2004, 17:52:24 ; Search time 45 Seconds
(without alignment)
3568.861 Million cell updates/sec

Title: US-09-857-522B-4

Perfect score: 2693

Sequence: 1 MDGSSKSGHSEALRNYNLG.....GPQLFLDFCAFLTKRLVL 509

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|------------|---------------------|
| 1 | 2422 | 89.9 | 509 | 10 Q9ZRUJ3 | O9ZRUJ3 oryza sativ |
| 2 | 2422 | 89.9 | 509 | 10 Q852Q1 | O852Q1 oryza sativ |
| 3 | 2411.5 | 89.5 | 508 | 10 Q9ZNT4 | O9ZNT4 oryza sativ |
| 4 | 2411.5 | 89.5 | 508 | 10 Q852Q0 | O852Q0 oryza sativ |
| 5 | 2356.5 | 87.5 | 510 | 10 Q40740 | O40740 oryza sativ |
| 6 | 2100 | 78.0 | 513 | 10 Q81992 | O81992 oryza sativ |
| 7 | 2080 | 77.2 | 513 | 10 Q40029 | O40029 hordeum vul |
| 8 | 2072 | 76.9 | 513 | 10 Q40030 | O40030 hordeum vul |
| 9 | 1977 | 73.4 | 505 | 10 Q9ZRUJ1 | O9ZRUJ1 oryza sativ |
| 10 | 1977 | 73.4 | 505 | 10 Q852Q2 | O852Q2 oryza sativ |
| 11 | 1969.5 | 73.1 | 535 | 10 Q8RWD2 | O8RWD2 arabidopsis |
| 12 | 1963 | 72.9 | 504 | 10 P93113 | P93113 cucumis sat |
| 13 | 1960.5 | 72.8 | 514 | 10 Q9M726 | Q9M726 lycopersico |
| 14 | 1945 | 72.2 | 484 | 10 Q43475 | Q43475 hordeum vul |
| 15 | 1923 | 71.4 | 511 | 10 Q40544 | Q40544 nicotiana t |
| 16 | 1909 | 70.9 | 503 | 10 Q9ZTF6 | Q9ZTF6 oryza sativ |

| | | | | | |
|----|--------|------|-----|------------|---------------------|
| 17 | 1903.5 | 70.7 | 512 | 10 P92958 | P92958 arabidopsis |
| 18 | 1903.5 | 70.7 | 514 | 10 O04122 | O04122 solanum tub |
| 19 | 1899.5 | 70.5 | 512 | 10 P92968 | P92968 arabidopsis |
| 20 | 1881.5 | 69.9 | 514 | 10 Q9XF25 | Q9XF25 glycine max |
| 21 | 1727 | 64.1 | 504 | 10 Q41485 | Q41485 solanum tub |
| 22 | 1545.5 | 57.4 | 494 | 10 Q9FL23 | Q9FL23 arabidopsis |
| 23 | 1195.5 | 44.4 | 258 | 10 Q9ZRUJ2 | Q9ZRUJ2 oryza sativ |
| 24 | 1146 | 42.6 | 552 | 6 Q7YRX9 | Q7YRX9 sus scrofa |
| 25 | 1137 | 42.2 | 472 | 8 Q98RL9 | Q98RL9 guillardia |
| 26 | 1117.5 | 41.5 | 560 | 13 Q8UW8 | Q8UW8 xenopus lae |
| 27 | 1116.5 | 41.5 | 291 | 10 Q9ZRA0 | Q9ZRA0 arabidopsis |
| 28 | 1109 | 41.2 | 582 | 5 O18645 | O18645 drosophila |
| 29 | 1106.5 | 41.1 | 530 | 11 Q8BRK8 | Q8BRK8 mus musculu |
| 30 | 1101.5 | 40.9 | 574 | 4 Q86V51 | Q86V51 homo sapien |
| 31 | 1096 | 40.7 | 348 | 10 Q41491 | Q41491 solanum tub |
| 32 | 1087 | 40.4 | 626 | 5 Q95ZQ4 | Q95ZQ4 caenorhabdi |
| 33 | 1080 | 40.1 | 562 | 5 Q86FL6 | Q86FL6 caenorhabdi |
| 34 | 1080 | 40.1 | 624 | 5 Q22068 | Q22068 caenorhabdi |
| 35 | 1048 | 38.9 | 718 | 5 Q9XYP6 | Q9XYP6 dictyosteli |
| 36 | 992 | 36.8 | 602 | 3 P87209 | P87209 kluyveromyc |
| 37 | 979 | 36.4 | 777 | 3 Q872H0 | Q872H0 neurospora |
| 38 | 940.5 | 34.9 | 880 | 3 Q9Y880 | Q9Y880 cochlodolu |
| 39 | 932 | 34.6 | 765 | 3 Q9Y7V4 | Q9Y7V4 sclerotinia |
| 40 | 927 | 34.4 | 671 | 3 Q96W17 | Q96W17 trichoderma |
| 41 | 899.5 | 33.4 | 706 | 3 Q8J2N0 | Q8J2N0 fusarium ox |
| 42 | 828 | 30.7 | 175 | 10 Q8S9G0 | Q8S9G0 triticum ae |
| 43 | 768.5 | 28.5 | 833 | 5 Q8S5X5 | Q8S5X5 dictyosteli |
| 44 | 749 | 27.8 | 783 | 4 Q86YJ2 | Q86YJ2 homo sapien |
| 45 | 738 | 27.4 | 725 | 13 Q804T2 | Q804T2 xenopus lae |

ALIGNMENTS

RESULT 1
ID Q9ZRUJ3 PRELIMINARY; PRT; 509 AA.
AC Q9ZRUJ3;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE OSK4.
GN OSK4.
OS Oryza sativa (Rice).
OC Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99086251; PubMed=9870704;
RA Takano M., Kaiya-Kanegae H., Funatsuki H., Kikuchi S.;
RT "Rice has two distinct classes of protein kinase genes related to SNF1
RT of Saccharomyces cerevisiae, which are differently regulated in early
RT seed development.";
RL Mol. Gen. Genet. 260:388-394(1998)
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D82035; BAA36299.1; -
DR HSSP; Q63450; 1A06.
DR Gramene; Q9ZRUJ3; -
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase Cterm.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; pkinase; 1.

GN OSK3 OR OSK5.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OK NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99086251; PubMed=9870704;
RA Takano M., Kajiya-Kanegae H., Funatsuki H., Kikuchi S.;
RT "Rice has two distinct classes of protein kinase genes related to SNF1
RT of Saccharomyces cerevisiae, which are differently regulated in early
RT seed development.";
RL Mol. Gen. Genet. 260:388-394(1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D82038; BAA36297.1; -.
DR EMBL; D82036; BAA36295.1; -.
DR HSSP; Q63450; 1A06.
DR Gramene; Q9ZNT4; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 508 AA; 58250 MW; E935262080B39A59 CRC64;

Query Match 89.5%; Score 2411.5; DB 10; Length 508;
Best Local Similarity 89.0%; Pred. No. 7.4e-198;
Matches 453; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

QY 1 MDGSSKSGHSEALRNYNLGRTLGIGTFGKVKIAEHKLTGHRVAIKINCROMNMEME 60
Db 1 MDGNAKGSGHSEALKYNLGRTLGIGSGFKVKIAEHKLTGHRVAIKILNRQRMNMEME 60

QY 61 KAKREFKILKLFIPHIIRLYEVIYTPTDIYVMEYCKYGGELFDYIVEKRLQEDEARRI 120
Db 61 KAKREIKILRLFIPHIIRLYEVIYTPTDIYVMEYCKFGELFDYIVEKRLQEDEARRI 120

QY 121 FQOIISGVEYCHRNMVVHRDLKPENLLDSKYNVKLADFGLSNVMHDGHLKTSGSPNY 180
Db 121 FQOIISGVEYCHRNMVVHRDLKPENLLDSKYNVKLADFGLSNVMHDGHLKTSGSPNY 180

QY 181 AAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPDDENIPNLFKKIKGGIYTLPSHLSA 240
Db 181 AAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPDDENIPNLFKKIKGGIYTLPSHLSA 240

QY 241 LARDLIPRMLVVEPMKRTIREIREHOWFOIRLPYLAVPPDDTQQAAMIDEDTLRDVY 300
Db 241 LARDLIPRMLVVDPMKRTIREIREHOWFOIRLPYLAVPPDDTQQAAMIDEDTLQDVY 300

QY 301 NMGFNMKNHVCESLCSRLONEATVAYYLLLDNRFRTSGYLGADYQESMDRNLQLASSES 360
Db 301 NLGYGKDHVCESLRNRLONEATVAYYLLLDNRFRTSGYLGADYQESLERNFRFASSES 360

QY 361 SSSGTRNYVPGSSDPHSSGLRPYPYVERKWA LGLSRAHPREIMVEVLKALQELNVRWK 420
Db 361 SSSGTRNYVPGSSDPHSSGLRPYPYVERKWA LGLSRAHPREIMVEVLKALQELNVRWK 420

Db 361 ASSNTRHYTLPGSSDPHASGLRPHYVERKWA LGLSRAQPREIMIEVLKALQDLNWSWK 420

QY 421 NGHYNVKCRWCPGPEVNDTLDASNSFLGSDTIMDNDANGRLPTVTKREFOLYTKDK 480
Db 421 NGQYNMKCRWSVG-TQATDMLDVNNSFVDSIIMDNGDVNGRLPAVIKEIQLYKTRDEX 479

QY 481 YLLDMQRYTGPQLLFLDFCAFLTKLRVL 509
Db 480 YLLDMQRYTGPQLLFLDFCADFLTKLRVL 508

RESULT 4
Q852Q0
ID Q852Q0 PRELIMINARY; PRT; 508 AA.
AC Q852Q0;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, last annotation update)
DE SnRK1b protein kinase.
GN OSK35.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OK NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Norin 8;
RA Kanegae H., Takano M.;
RT "Rice SnRK1s.";
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB101657; BAC56590.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW Kinase.
SQ SEQUENCE 508 AA; 58250 MW; E935262080B39A59 CRC64;

Query Match 89.5%; Score 2411.5; DB 10; Length 508;
Best Local Similarity 89.0%; Pred. No. 7.4e-198;
Matches 453; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

QY 1 MDGSSKSGHSEALRNYNLGRTLGIGTFGKVKIAEHKLTGHRVAIKINCROMNMEME 60
Db 1 MDGNAKGSGHSEALKYNLGRTLGIGSGFKVKIAEHKLTGHRVAIKILNRQRMNMEME 60

QY 61 KAKREFKILKLFIPHIIRLYEVIYTPTDIYVMEYCKYGGELFDYIVEKRLQEDEARRI 120
Db 61 KAKREIKILRLFIPHIIRLYEVIYTPTDIYVMEYCKFGELFDYIVEKRLQEDEARRI 120

QY 121 FQOIISGVEYCHRNMVVHRDLKPENLLDSKYNVKLADFGLSNVMHDGHLKTSGSPNY 180
Db 121 FQOIISGVEYCHRNMVVHRDLKPENLLDSKYNVKLADFGLSNVMHDGHLKTSGSPNY 180

QY 181 AAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPDDENIPNLFKKIKGGIYTLPSHLSA 240
Db 181 AAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPDDENIPNLFKKIKGGIYTLPSHLSA 240

Db 181 AAPEVISGKLYAGPEVDWVSCGVIYLLALCGTLPFDDENIPLNFKKIKGIIYTLPSHLSA 240
QY 241 LARDLIPRLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQQAAMIDEDTLRDV 300
Db 241 LARDLIPRLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQQAAMIDEDTLQDV 300
QY 301 NMGFNKNHVCESLCSRLQNEATVAYLLLDNFRATSGYLQADYQESMDRNLNQLASSES 360
Db 301 NLGYGDHVCESLRNRLQNEATVAYLLLDNFRATSGYLQADYQESLRNFRFASSES 360
QY 361 SSSGTRNYVPGSSDPHSSGLRPYPYVERKMWALGLQSRAPREIMVEVLKALQELNVRWK 420
Db 361 ASSNTRHYLPGSSDPHASGLRPHYVERKMWALGLQSRAPREIMIEVLKALQDLNVSWK 420
QY 421 NGHYNVKRCWCPGPEVNDTLDASNSFLGDSITMDNDANGRLPTVIKEEFQLYKTKDDK 480
Db 421 NGQYNMKCRWSVG-TQATDMLDVNNSFVDDSIIMDNGDVNGRLPAVIKEIQLYKTRDEK 479
QY 481 YLLDMQRTVGPQLLFLDFCAFLTKRLV 509
Db 480 YLLDMQRTVGPQLLFLDFCADFLTKRLV 508

RESULT 5
Q40740 PRELIMINARY; PRT; 510 AA.
ID Q40740
AC Q40740;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SNF1-related protein kinase.
GN RSK1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Erihartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=tn5-8; TISSUE=Endosperm;
RA Tsai T.-H., Le H.-T.;
RT "SNF1-related protein kinase of rice."
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U55768; AAB05457.1; -.
DR PIR; T04145; T04145.
DR HSSP; Q63450; 1A06.
DR Gramene; Q40740; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR01772; Kinase Cterm.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; kinase; 1.
DR Pfam; PF00627; UBA; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 510 AA; 58258 MW; 51048A9C0D0CF2CB CRC64;

Query Match 87.5%; Score 2356.5; DB 10; Length 510;
Best Local Similarity 87.1%; Pred. No. 3.9e-193;
Matches 444; Conservative 32; Mismatches 33; Indels 1; Gaps 1;

QY 1 MDSSKSGSHSEALRNYNLGRITLIGTEGKVKIAEHKLTGHRVAIKINCRQRMNEMEE 60
Db 1 MDGNKGGSHSEALKNNYLGRTLGSGFGKVKIAEHKLTGHRVAIKILNRQRMNEMEE 60
QY 61 KAKREFKLKLFHPHITRLYEVTYPTDIYVMEYCKGELFDYIVEKRLQEDE-ARR 119
Db 61 KAKREIKILRLFIHPHITRLYEVTYPTDIYVMEYCKGELFDYIVEKRLQEDRVALLR 120
QY 120 IFQOISGVEYCHRMNVHRDLKENLLDSKYNVKLADFGISNVMDGHFLKTS CGSPN 179
Db 121 IFSQIISAVEYCHRMNVAHRDLKENLLDSKYNVKLADFGISNVMDGHFLKTS CGSPN 180
QY 180 YAAPEVISGKLYAGPEVDWVSCGVIYLLALCGTLPFDDENIPLNFKKIKGIIYTLPSHLS 239
Db 181 YAAPEVISGKLYAGPEVDWVSCGVIYLLALCGTLPFDDENIPLNFKKIKGIIYTLPSHLS 240
QY 240 ALARDLIPRLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQQAAMIDEDTLRDV 299
Db 241 ALARDLIPRLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQQAAMIDEDTLQDV 300
QY 300 VNMGFNKNHVCESLCSRLQNEATVAYLLLDNFRATSGYLQADYQESMDRNLNQLASSE 359
Db 301 VNLGYGDHVCESLRNRPQNEATVAYLLLDNFRATSGYLQADYQESLRNFRFASSE 360
QY 360 SSSGTRNYVPGSSDPHSSGLRPYPYVERKMWALGLQSRAPREIMVEVLKALQELNVRWK 419
Db 361 SASNTRHYLPGSSDPHASGLRPHYVERKMWALGLQSRAPREIMIEVLKALQDLNVSWK 420
QY 420 KNGHYNVKRCWCPGPEVNDTLDASNSFLGDSITMDNDANGRLPTVIKEEFQLYKTKDD 479
Db 421 KNGQYNMKCRWSVGYPQATDILDVNSFVDDSIIMDNGDVNGRLPAVIKEIQLYKSRDE 480
QY 480 KYLLDMQRTVGPQLLFLDFCAFLTKRLV 509
Db 481 KYLLDMQRTVGPQLLFLDFCAFLTKRLV 510

RESULT 6
O81992 PRELIMINARY; PRT; 513 AA.
ID O81992
AC O81992;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SNR1-type protein kinase (Fragment).
GN KIN12A.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Sundance; TISSUE=Seed minus seed coat;
RA Slocumbe S.P., Bertini L., Beaudoin F., Dickinson J.R., Halford N.G.;
RT "Molecular cloning of Bsn1p, a novel putative SNF4-related protein
RT identified in a two-hybrid screen with barley seed snr1 protein
RT kinase."
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ007990; CAA07813.1; -.
DR HSSP; P00518; 1PHK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR01772; Kinase Cterm.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_kinase.

DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW NON_TER
SQ SEQUENCE 513 AA; 58801 MW; 37DEFEDBAB6295AD CRC64;

Query Match 78.0%; Score 2100; DB 10; Length 513;
Best Local Similarity 75.8%; Pred. No. 3.7e-171;
Matches 389; Conservative 61; Mismatches 59; Indels 4; Gaps 2;

QY 1 MDGSSKSGHSEALRNVLGRTLGITFGKVKIAEHKLTGHRVAIKIINCROMRMEMEE 60
DB 1 MDGNNRGCGHSEVLKNYNLKTGLTGFQDVKAHEKLTGORVAIKILNRRKMETMEMEE 60
QY 61 KAKREFKILK--FIHPHIIIRLYEVITYPTDIYVMEYCKYGELEFDYIVEKGRLOEDEA 117
DB 61 KANREIKIMRLFIDFIHPHIIIRLYEVITYPTDIYVMEYCKYGELEFDYIVEKGRLOEDEA 120
QY 118 RRIFOQIISGVEYCHRMNVVHRDLKPENLLDISKYNVKLADFGLSNVMDGHFLKTS CGS 177
DB 121 RRIFOQIISGVEYCHRMNVVHRDLKPENLLDISKYNVKLADFGLSNVMDGHFLKTS CGS 180
QY 178 PNYAAPEVISGKLYAGPEVDVWSCGVLVYALLCGTLPFDENIPNLFKKIKGITYLPSH 237
DB 181 LNYAAPEIISSKLYAGPEVDVWSCGVLVYALLCGSVPFDDNIPSLFRKIKGITYLPSY 240
QY 238 LSALARDLIPRLVVEPMKRITIREIREHQMFOIRLPRYLAVPPDPTQOAKMIDEDTLR 297
DB 241 LSDSARDLIPKLNIDPMKRITIREIRVHPFKNHLPCYLAVPPPYKEQOAKMIDEDILR 300
QY 298 DVVNMGFNKNHVCESLCSRLQNEATVAYLLLDNFRATSGYLQADYQESMDRLNQLAS 357
DB 301 EVVNLGYDKDHVCESLNMRLQNEETVAYLLLDNFRSTSGYLGADHQLMDRSFNEFTL 360
QY 358 SSSSSGTRNYPGSSDPHSSGLRPYPYVERKWAIGLOSRAHPREIMVEVLKALQELNVR 417
DB 361 SESASPSTRNYLPGINDSGGGLRPYPYVQRKWAIGLOSRAHPRDIMIEVLKALKEINVC 420
QY 418 WKNNGHYNVKCRWCPGFPEVND-TLDASNSFLGDSITMDNDANGRLPTVIKFEFQLYKT 476
DB 421 WKNGLYNMKCRWCPGFPOVSMDLLDSNHNFDVDSITMDNGNADGRLPAVVKFEIQLYKT 480
QY 477 KDDKYLLDMQRTVGPQLLFLDFCAFLTKLRVL 509
DB 481 KDNKYLLDIOGRTVGPQLLFLDFCAFLTKLRVL 513

RESULT 7

Q40029 PRELIMINARY; PRT; 513 AA.
AC Q40029;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Protein kinase.
GN BKIN12.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Sunbar;

RX MEDLINE=93258420; PubMed=1302632;
RA Halford N.G., Vicente-Carbajosa J., Sabelli P.A., Shewry P.R.,
RA Hannappel U., Kreis M.,
RT "Molecular analyses of a barley multigene family homologous to the
RT yeast protein kinase gene SNF1."
RL Plant J. 2:791-797(1992).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; X65606; CAA46556.1; -.
DR PIR; S60303; S60303.
DR HSSP; P00518; IPHK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 513 AA; 58715 MW; 3DF7820303365630 CRC64;

Query Match 77.2%; Score 2080; DB 10; Length 513;
Best Local Similarity 75.0%; Pred. No. 1.9e-169;
Matches 385; Conservative 62; Mismatches 62; Indels 4; Gaps 2;

QY 1 MDGSSKSGHSEALRNVLGRTLGITFGKVKIAEHKLTGHRVAIKIINCROMRMEMEE 60
DB 1 MDGNNRGCGHSEVLKNYNLKTGLTGFQDVKAHEKLTGORVAIKILNRRKMETMEMEE 60
QY 61 KAKREFKILK--FIHPHIIIRLYEVITYPTDIYVMEYCKYGELEFDYIVEKGRLOEDEA 117
DB 61 KANREIKIMRLFIDFIHPHIIIRLYEVITYPTDIYVMEYCKYGELEFDYIVEKGRLOEDEA 120
QY 118 RRIFOQIISGVEYCHRMNVVHRDLKPENLLDISKYNVKLADFGLSNVMDGHFLKTS CGS 177
DB 121 RRIFOQIISGVEYCHRMNVVHRDLKPENLLDISKYNVKLADFGLSNVMDGHFLKTS CGS 180
QY 178 PNYAAPEVISGKLYAGPEVDVWSCGVLVYALLCGTLPFDENIPNLFKKIKGITYLPSH 237
DB 181 LNYAAPEIISSKLYAGPEVDVWSCGVLVYALLCGSVPFDDNIPSLFRKIKGITYLPSY 240
QY 238 LSALARDLIPRLVVEPMKRITIREIREHQMFOIRLPRYLAVPPDPTQOAKMIDEDTLR 297
DB 241 LSDSARDLIPKLNIDPMKRITIREIRVHPFKNHLPCYLAVPPPYKAPRAKMIDEDILR 300
QY 298 DVVNMGFNKNHVCESLCSRLQNEATVAYLLLDNFRATSGYLQADYQESMDRLNQLAS 357
DB 301 DVVNLGYDKDHVCESLNMRLQNEETVAYLLLDNFRSTSGYLGADHQLMDRSFNEFTL 360
QY 358 SSSSSGTRNYPGSSDPHSSGLRPYPYVERKWAIGLOSRAHPREIMVEVLKALQELNVR 417
DB 361 SESASPSTRNYLPGINDSGGGLRPYPYVQRKWAIGLOSRAHPRDIMIEVLKALKEINVC 420
QY 418 WKNNGHYNVKCRWCPGFPEVND-TLDASNSFLGDSITMDNDANGRLPTVIKFEFQLYKT 476
DB 421 WKNGLYNMKCRWCPGFPOVSAMLLDSNHNFDVDSITMDNGNADGRLPAVVKFEIQLYKT 480
QY 477 KDDKYLLDMQRTVGPQLLFLDFCAFLTKLRVL 509
DB 481 KDNKYLLDIOGRTVGPQLLFLDFCAFLTKLRVL 513

RESULT 8

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Q40030 PRELIMINARY; PRT; 513 AA.
ID Q40030
AC Q40030;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Protein kinase (Fragment).
GN BKIN12.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Hordeum.
OC Triticaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Sundance;
RX MEDLINE=93258420; PubMed=1302632;
RA Halford N.G., Vicente-Carabajosa J., Sabelli P.A., Shewry P.R.,
RA Hannappel U., Kreis M.;
RT "Molecular analyses of a barley multigene family homologous to the
RT yeast protein kinase gene SNF1.";
RL Plant J. 2:791-797(1992).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; X65604; CAA46554.1; -.
DR PIR; S60304; S60304.
DR HSSP; P00518; 1PHK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; kinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON TER 513
SQ SEQUENCE 513 AA; 58855 MW; BDE5AB9DDC50984 CRC64;
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Query Match 76.9%; Score 2072; DB 10; Length 513;
Best Local Similarity 74.7%; Pred. No. 9.3e-169;
Matches 383; Conservative 64; Mismatches 62; Indels 4; Gaps 2;
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QY 1 MDGSSKSGHSEALRNVLGRTLGIGTGKVKIAEHKLTGHRVAIKINCROMMEME 60
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 1 MDGNRRGGHSEVLKNVNLGTLGLTGFQDVKAERNVTGQRAIKILNRRKQETMEME 60
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
QY 61 KAKREFKIKL--FIHPHILRLYEVIYPTDIYVMEYCKYGLFDYIVKGRLODEA 117
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 61 KANREIKIMRLFDIFHPIHILRYVEVIETPKDIFVMEYCNNGELLDYITENGRLQDEA 120
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
QY 118 RRIFOOISGVEYCHRNWVVRDLKPENLILDSKVNVLADFGLSNVMDGHLKTS 177
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 121 RRIFOOILAGVEYCHRMVVRDLKPENLILDSRVNVLADFGLSNVMDGHLKTS 180
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
QY 178 PNYAAPEVISGKLYAGPEVDVWSCGVLILYALLCGTLPPDENIPNLFKKIKGTY 237
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 181 LNYAAPEIISSKLYAGPEVDVWSCGVLILYALLCGSLVPFDDNIPSLFRKIKGTY 240
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
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QY 238 LSALARDLIPRLVVEPMKRITIREIREHWFQIRLPRYLAVPBDTTOQAKMIDEDT 297
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 241 LSDSARDLIPKLLINIDPMKRITFHEIRVHPWPKNHLPCYLAVPBPYKEQAKMIDED 300
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
QY 298 DVVNMGNKRVNVCESLCSRLQNEATVAYVLLLDNFRATSGYLQADYQESMDRLNQLAS 357
    :|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 301 EVVNLGYDHDVCESLMNLQNEATVAYVLLLDNFRSTSGYLQADHQLMDRSFNEFTL 360
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
QY 358 SESSSGSTRNVYPGSSDPHSSGLRPYVVERKWAIGLOSRAHREIWEVLKALQELNVR 417
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 361 SESASPTSNVLPFINDSGGGLRPYVQKKWAIGLOSRAHPRDIMIEVLKALKEINVC 420
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
QY 418 WKNGHYNVKRCWCPGPEVND-TLDASNSFLGDSTIMDNDANGRLPTVIKPEFQLYKT 476
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 421 WKNGLYNMKRCWCPGFPQVSDMLDSNHFVDSTIMDNGNADGRLPAVVKFEIQLYKT 480
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
QY 477 KDDKYLDMQRYVTGPQLFLDFCAFLTKLRLV 509
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
Db 481 KDNKYLDDIQRYVTGPQLFLDFCAFLTKLRLV 513
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::
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RESULT 9

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Q9ZRJ1 PRELIMINARY; PRT; 505 AA.
ID Q9ZRJ1
AC Q9ZRJ1;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE OSKI.
GN OSKI.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99086251; PubMed=9870704;
RA Takano M., Kajiya-Kanegae H., Funatsu H., Kikuchi S.;
RT "Rice has two distinct classes of protein kinase genes related to SNF1
RT of Saccharomyces cerevisiae, which are differently regulated in early
RT seed development.";
RL Mol. Gen. Genet. 260:388-394(1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D82039; BAA36298.1; -.
DR HSSP; Q63450; 1A06.
DR Gramene; Q9ZRJ1; -.
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DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; kinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 505 AA; 57614 MW; 5631D07F591FD951 CRC64;
```


RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shin P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.,
CC Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AY093170; AAM13169.1; -.
DR HSSP; P24941; IBUH.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR01772; Kinase Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAl; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 535 AA; 61181 MW; FFFC383223FD8317 CRC64;

Query Match 73.1%; Score 1969.5; DB 10; Length 535;
Best Local Similarity 72.8%; Pred. No. 6e-160;
Matches 377; Conservative 52; Mismatches 74; Indels 15; Gaps 4;

QY 1 MDGSSKG--SGHSEALRNVNLGRTLGIGTFGKVIAEHKL TGHRAVAIKI INCRQMRNMEM 58
DB 24 MDGSGTGRSGVESILPNYKLGRTLGIGSFGRVKAIEHALTGHKVAIKI INRRKIKNMEM 83
QY 59 EEKAKREFKILKLFTHPHIIRLYEVITYPTDIYVMEYCKYGELEFDYIVKGRLOEDEAR 118
DB 84 EEKVRREIKILRLFMHPHIIIRLYEVIETPTDIYVMEYVNSGELFDYIVKGRLOEDEAR 143
QY 119 RIFQOIIISGVEYCHRNWVVRDLKPENL LLSKYNVKLADFGLSNVMDGHFLKTS CGSP 178
DB 144 NFFQOIIISGVEYCHRNWVVRDLKPENL LLSKCNVKIADFGLSNIMRDGHFLKTS CGSP 203
QY 179 NYAAPEVISGKLYAGPEVDVWSCGVL YALLCGTLPFDDENIPNLFKKIKGIYTLPSHL 238
DB 204 NYAAPEVISGKLYAGPEVDVWSCGVL YALLCGTLPFDDENIPNLFKKIKGIYTLPSHL 263
QY 239 SALARDLIPRMLVVEPMKRITIREIREHOWFOIRLPRYLAVPPDPTTQOAKMIDEDTLRD 298
DB 264 SPGARDLIPRMLVVDPMKAVTIPEIRQHPWFQAHLPYLA VPPDPTVQOAKKIDEEILQE 323
QY 299 VVNMGFNKNHVCESLCSRLQNEATVAYYLLDNFRATSGYL GADYQESMDRNLNQ LASS 358
DB 324 VINMGFDRNHLIESLNFNTQNDGTVTYYLLIDNFRASSGYL GAEFQETME-CTPRMHPA 382
QY 359 ESSSSGTRNYPGSSSDPHSSGLRPYPYVERKWKALGQSRAHPREIMVEYLKALQELNVRW 418
DB 383 ESVASPVSHRLPGIMEYQGVLRQYPERKWKALGQSRAHPREIMTEVLKALQDINVCW 442
QY 419 KKNGHYNVKCRWCPGFPVNDTLDA-----SNSFLGSDSTIMDNDANGRLPTVIKFEF 471
DB 443 KKIGHYNMKCRWVP-----NSSADGMLSNMSHDNNYFGDESSIIENEA AVKSPNVVKFEI 497
QY 472 QLYTKDDKYLLDMQRYTGPOLLFLDFCAAFITKLRVL 509
DB 498 QLYKTRDDKYLLDLQRVGPGQFLFLDLCAAFITKLRVL 535

RESULT 12
P93113
ID P93113 PRELIMINARY; PRT; 504 AA.
AC P93113;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SNF1-related protein kinase.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosids I; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxID=3659;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cotyledon;
RA Gumpel N.J.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; Y10036; CAA71142.1; -.
DR PIR; T10449; T10449.
DR HSSP; Q63450; 1A06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAl; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 504 AA; 57839 MW; 4CB485ACCD59C384 CRC64;

Query Match 72.9%; Score 1963; DB 10; Length 504;
Best Local Similarity 74.8%; Pred. No. 2e-159;
Matches 374; Conservative 53; Mismatches 65; Indels 8; Gaps 4;

QY 16 NYNLGRTLGIGTFGKVIAEHKL TGHRAVAIKI INCRQMRNMEERAKREFKILKLFTHP 75
DB 7 NYKLGKTLGIGSFQKVIAEHALTGHKVAIKI INRRKIKNLDMEKVRREIKILRLFMHP 66
QY 76 HIIRLYEVITYPTDIYVMEYCKYGELEFDYIVKGRLOEDEAR RIFQOIIISGVEYCHRNW 135
DB 67 HIIRLYEVIETPSDIYVMEYKSGELFDYIVKGRLOEDEARNFFQOIIISGVEYCHRNW 126
QY 136 VVHRDLKPENL LLSKYNVKLADFGLSNVMDGHFLKTS CGSPNYAAPEVISGKLYAGPE 195
DB 127 VVHRDLKPENL LLSKCNVKIADFGLSNIMRDGHFLKTS CGSPNYAAPEVISGKLYAGPE 186
QY 196 VDVWSCGVL YALLCGTLPFDDENIPNLFKKIKGIYTLPSHL SALARDLIPRMLVVEPM 255
DB 187 VDVWSCGVL YALLCGTLPFDDENIPNLFKKIKGIYTLPSHL SGAARELIPSM LVVDPM 246
QY 256 KRITIREIREHOWFOIRLPRYLAVPPDPTTQOAKMIDEDTLRDV VVNMGFNKNHVCESLCS 315
DB 247 KRITIREIRQHPWFQAHLPYLA VPPDPTVQOAKKIDEDITLQEVVYMGFDRNQLVESLRN 306
QY 316 RLQNEATVAYYLLDNFRATSGYL GADYQESMDRNLNQ LASSSSSSGTRNYPGSSDP 375

Db 307 RIQNEATVAYYLLDNRFRVSSGYLGAEFQETMETGFNRMHPSDPTNPAGVHLLPGYMDY 366
QY 376 HSSGLRPYPVERKVALGLQSRAPREIMVEVLKALQELNVRWKNNGHYNAKRCWCPGFP 435
Db 367 QGMGLRAQFVERKVALGLQSRAPREIMTEVLKALRELNVAMKIGHYNAKRCWLPGIP 426
QY 436 -----EVNDTLDAASNFLGD-STIMDNDANGRLPTVIKFEFQLYKTKDDKXLLDMQRYT 489
Db 427 GHHEGMINNPVH-SNHYFGDKSTIENDGV-VKSPNVIKEFVQLYKTREEKYLLDLQRYQ 484
QY 490 GPQLLFLDFCAAFLTCLRVL 509
Db 485 GPQFLFLDLCAAFLAQLRVL 504
RESULT 13
Q9M726
ID Q9M726 .PRELIMINARY; PRT; 514 AA.
AC Q9M726;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SNF1.
GN SNF1.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamids; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RA Bradford K.J., Dahal P., Downie B., Nonogaki H., Alvarado V.;
RT "Yeast SNF1 kinase homolog from tomato."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AF143743; AAF66639.1; -.
DR HSSP; Q63450; 1A06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 514 AA; 58825 MW; 587765211B17FCAC CRC64;
Query Match 72.8%; Score 1960.5; DB 10; Length 514;
Best Local Similarity 72.9%; Pred. No. 3.3e-159;
Matches 376; Conservative 63; Mismatches 68; Indels 9; Gaps 6;
QY 1 MDGSS-KSGSHSEA-LRNVNLGRTLIGTFGKVAIEHKLTGHRVAIKINCQRMNMEM 58
Db 1 MDGTAVQGTSSVDSFLRNVKLGKTLGIGSFQKVAIEHTLTGKVAVKILNRKRIRNMDM 60
QY 59 EEKAKREFKILKPLFHPHIIIRLYEVITYPTDIYVVMKYCYGELFDYIVEKGRLOEDEAR 118

Db 61 EEKVRREIKILRFMHPIIRLYEVIETPSDIYVVMKYKSGELFDYIVEKGRLOEDEAR 120
QY 119 RIFQOIIISGEYCHRNMVVHRDLKPENLILDSKYNVGLADFGLSNVWHDGHLKTS CGSP 178
Db 121 NFFQOIIISGEYCHRNMVVHRDLKPENLILDSKYNVGLADFGLSNMRDGHFLKTS CGSP 180
QY 179 NYAAPEVISGKLYAGPEVDVWSCGVLVALLCGTLPFDDENIPNLFKKIKGIIYTLPSHL 238
Db 181 NYAAPEVISGKLYAGPEVDVWSCGVLVALLCGTLPFDDENIPNLFKKIKGIIYTLPSHL 240
QY 239 SALARDLIPRLVVEPMKRITIREIREHQMFOIRLPYLAAPPDPTQQAAMIDEDTLRD 298
Db 241 SAGARDLIPRLIVDPMKRMTIPEIRLHPWFQAHLPYLAAPPDPTQQAAMIDEDTLRD 300
QY 299 VVMGFNKNHVCESLCSRLQNEATVAYYLLDNRFRATSGYLGADYQESMDRNLNQLASS 358
Db 301 VVKMGFDRNNLTESLRNRVQNEGTVAYYLLDNRHRVSTGYLGAEFQESMEYGYNRINSN 360
QY 359 ESSSSGTRNNYVPGSSDPHSSGLRPYPYVERKVALGLQSRAPREIMVEVLKALQELNVRW 418
Db 361 ETAASPVGQRFPGIMDYQQAAGAR-QFPIERKVALGLQSRAPREIMTEVLKALQELNVCW 419
QY 419 KKNGHYNAKRCWCPGFPEVNDTLDA-----NSFLG-DSTIMDNDANGRLPTVIKFEFQL 473
Db 420 KKIQGYNAKRCRWVPSLPGHHEGMGVNSMGHGFQFGDDSSIENDGAT-KLTNVKFEVQL 478
QY 474 YKTKDDKXLLDMQRYTGPQLLFLDFCAAFLTCLRVL 509
Db 479 YKTREEKYLLDLQRLQGPQFLFLDLCAAFLAQLRVL 514
RESULT 14
Q43475
ID Q43475 .PRELIMINARY; PRT; 484 AA.
AC Q43475;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SNF1-related protein kinase (Fragment).
GN BKIN2.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triciceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Sundance; TISSUE=Endosperm;
RX MEDLINE=95284374; PubMed=7766906;
RA Hannappel U., Vicente-Carabajosa J., Barker J.H., Shewry P.R.,
RA Halford N.G.;
RT "Differential expression of two barley SNF1-related protein kinase
genes";
RL Plant Mol. Biol. 27:1235-1240(1995).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; X82548; CAA57898.1; -.
DR PIR; S59941; S59941.
DR HSSP; Q63450; 1A06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.

| DR | ProDom; PD000001; Prot_kinase; 1. |
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| DR | SMART; SM00220; S_TKC; 1. |
| DR | SMART; SM00165; UBA; 1. |
| DR | PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. |
| DR | PROSITE; PS50011; PROTEIN_KINASE_DOM; 1. |
| DR | PROSITE; PS00108; PROTEIN_KINASE_ST; 1. |
| DR | PROSITE; PS50030; UBA; 1. |
| KW | ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase. |
| FT | NON_TER 1 1 |
| FT | NON_TER 484 484 |
| SO | SEQUENCE 484 AA; 55322 MW; E83748B410C2EC53 CRC64; |

| | | | | |
|-----------------------|------------------|---------------------|------------|-------------|
| Query Match | 72.2%; | Score 1945; | DB 10; | Length 484; |
| Best Local Similarity | 76.0%; | Pred. No. 6.5e-158; | | |
| Matches 374; | Conservative 47; | Mismatches 61; | Indels 10; | Gaps 4; |

| | | | |
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| QY | 20 | GRTLGIGTFGKVXIAEHKLTGHRVAIKINCROMNMEMEEKAKREFKILKLFIPHIIIR | 79 |
| Db | 1 | GKTLGIGSGFKVXIAEHIITGHKVAIKILNRKKIKSMEMEEKVREIKILRFLMHPIIIR | 60 |
| QY | 80 | LYEVIYTPTDIYVVMKEYCKYGELEFDYIYVEKGRLOEDEARRIFQOIIISGVYCHRMVVR | 139 |
| Db | 61 | LYEVIDTPADIYVMEYVKSSELFDYIYVEKGRLOEBEARRFQOIIISGVYCHRMVVR | 120 |
| QY | 140 | DLKENLLDSSKYNVKLADFGLSNVMDGHFLKTS CGSPNYAAPEVISGKIYAGPEVDW | 199 |
| Db | 121 | DLKENLLDSSKCNVKIADFGLSNVMDGHFLKTS CGRPNYAAPEVISGKIYAGPEVDW | 180 |
| QY | 200 | SCGVIIYALLCGTLPFDDENIPNLFKIKGGIYTLPSHLSALARDLIPMLVVEPMKRIT | 259 |
| Db | 181 | SCGVIIYALLCGTLPFDDENIPNLFKIKGGIYTLPSHLSPLARDLIPMLVVDPMKRIT | 240 |
| QY | 260 | IREIREHQMFOIRLPRYLAVPPDPTTQOAXMIDEDTLRDVNMGFNKNHVESLCSRLQN | 319 |
| Db | 241 | IREIREHSMFKARLPRYLAVPPDPTAQYVKLDDDELNDVIMKGFCKNQLTESLQKRLQN | 300 |
| QY | 320 | EATVAYYLLLDNRFRATSGYLGADYQESMDRNLNQLA-SSESSSSGSTRNY-VPGSSDPHS | 377 |
| Db | 301 | EATVAYYLLLDNKLRTTSGYLGAEYQESMDSFSQISPETPSSASEARQYCSFG----- | 354 |
| QY | 378 | SGLRPYYPVERKMWALGLQSRAPREIMEVYLKALQELNVRWKKNGHYVVKRCMCPGFPEV | 437 |
| Db | 355 | FGLRQHFPAERKMWALGLQSRAPREITEVYLKALQELNVCKWKIGHYVVKCRMSPGFFE- | 413 |
| QY | 438 | NDTLDA SNSFLGDSTIMDND DANGRLPYIYKFEFQLYKTKDKYLLDMQRYTGPQLLFLD | 497 |
| Db | 414 | -NMHNNGFGVESAIIEADGLGDKSTHIVKFEIQLYKTRGDKYLLDLQRYVSGPQLLFLD | 472 |
| QY | 498 | FCAPFLTKLRVL 509 | |
| Db | 473 | LCSAFLTQLRVL 484 | |

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RESULT 15
Q40544
ID Q40544 PRELIMINARY; PRT; 511 AA.
AC Q40544;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)
DE Protein kinase.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA Machida Y.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94217693; PubMed=8164654;

```

RA Muranaka T., Banno H., Machida Y.;
RT "Characterization of tobacco protein kinase NPK5, a homolog of
RT Saccharomyces cerevisiae SNF1 that constitutively activates expression
RT of the glucose-repressible SUC2 gene for a secreted invertase of S.
RT cerevisiae.";
RL Mol. Cell. Biol. 14:2958-2965(1994).
CC -! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D26602; BAA05649.1; -.
DR PIR; A56009; A56009.
DR HSSP; Q63450; 1A06.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001772; Kinase Cterm.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_kinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAI; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 511 AA; 58339 MW; 1263939CDD753519 CRC64;

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|-----------------------|------------------|---------------------|------------|-------------|
| Query Match | 71.4%; | Score 1923; | DB 10; | Length 511; |
| Best Local Similarity | 72.1%; | Pred. No. 5.4e-156; | | |
| Matches 372; | Conservative 60; | Mismatches 72; | Indels 12; | Gaps 7; |

[illegible]

Search completed: July 7, 2004, 17:56:36
Job time : 47 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:52:54 ; Search time 20 Seconds
(without alignments)
2448.074 Million cell updates/sec

Title: US-09-857-522B-4

Perfect score: 2693

Sequence: 1 MDGSSKSGHSEALRNYNLG.....GPQLLFDFCAFLTKLRVL 509

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|--------|-------------|--------|----|--------|---------------------|
| 1 | 2356.5 | 87.5 | 510 | 2 | T04145 | serine/threonine p |
| 2 | 2080 | 77.2 | 513 | 1 | S60303 | serine/threonine-s |
| 3 | 2068 | 76.8 | 513 | 1 | S60304 | serine/threonine-s |
| 4 | 2062.5 | 76.6 | 502 | 1 | A41361 | serine/threonine-s |
| 5 | 1969.5 | 73.1 | 512 | 1 | JC1446 | serine/threonine-s |
| 6 | 1963 | 72.9 | 504 | 2 | T10449 | probable serine/th |
| 7 | 1923 | 71.4 | 511 | 1 | A56009 | serine/threonine-s |
| 8 | 1903.5 | 70.7 | 512 | 2 | T52633 | serine/threonine-s |
| 9 | 1900 | 70.6 | 473 | 1 | S59941 | serine/threonine-s |
| 10 | 1853.5 | 68.8 | 512 | 2 | T07788 | probable serine/th |
| 11 | 1727 | 64.1 | 504 | 2 | T07415 | probable serine/th |
| 12 | 1148 | 42.6 | 552 | 1 | S51025 | [hydroxymethyl]glut |
| 13 | 1144 | 42.5 | 552 | 1 | A53621 | [hydroxymethyl]glut |
| 14 | 1137 | 42.2 | 472 | 2 | B90100 | SNF-related kinase |
| 15 | 1096 | 40.7 | 348 | 2 | T07660 | probable serine/th |
| 16 | 1080 | 40.1 | 562 | 2 | T29858 | hypothetical prote |
| 17 | 1013.5 | 37.6 | 633 | 1 | A26030 | serine/threonine-s |
| 18 | 992 | 36.8 | 602 | 2 | S72513 | FOG2 protein - yea |
| 19 | 981.5 | 36.4 | 576 | 2 | T41587 | probable carbon ca |
| 20 | 894.5 | 33.2 | 622 | 1 | S44859 | serine/threonine-s |
| 21 | 730.5 | 27.1 | 798 | 2 | UC7500 | gik protein - chic |
| 22 | 725.5 | 26.9 | 713 | 2 | S27966 | probable serine/th |
| 23 | 724 | 26.9 | 887 | 2 | T20941 | hypothetical prote |
| 24 | 718 | 26.7 | 1192 | 2 | T18611 | probable serine/th |
| 25 | 718 | 26.7 | 1246 | 2 | G89287 | protein H39B23.1 l |
| 26 | 717.5 | 26.6 | 745 | 2 | G01025 | serine/threonine p |
| 27 | 710.5 | 26.4 | 481 | 2 | T49072 | protein kinase - m |
| 28 | 709.5 | 26.3 | 1398 | 2 | T13741 | hypothetical prote |
| 29 | 701.5 | 26.0 | 440 | 2 | T14736 | probable serine/th |

| | | | | | | |
|----|-------|------|------|---|--------|--------------------|
| 30 | 700 | 26.0 | 440 | 2 | T14735 | probable serine/th |
| 31 | 696.5 | 25.9 | 774 | 2 | I48609 | probable serine/th |
| 32 | 692.5 | 25.7 | 445 | 2 | T09903 | serine/threonine-s |
| 33 | 691.5 | 25.7 | 441 | 2 | C84667 | probable protein k |
| 34 | 682.5 | 25.3 | 480 | 2 | A86427 | probable serine/th |
| 35 | 676.5 | 25.1 | 915 | 2 | S74283 | probable protein k |
| 36 | 675.5 | 25.1 | 532 | 2 | T38326 | serine threonine p |
| 37 | 667.5 | 24.8 | 453 | 2 | G86141 | protein T25K16.13 |
| 38 | 667 | 24.8 | 651 | 2 | S52244 | p69Eg3 protein - A |
| 39 | 664 | 24.7 | 174 | 2 | G01743 | AMP-activated prot |
| 40 | 659.5 | 24.5 | 1142 | 2 | S59359 | GIN4 protein - yea |
| 41 | 644.5 | 23.9 | 1518 | 2 | S37928 | probable purine nu |
| 42 | 644 | 23.9 | 445 | 2 | T50802 | serine/threonine p |
| 43 | 627 | 23.3 | 401 | 2 | B90120 | SNF1-related prote |
| 44 | 626 | 23.2 | 1147 | 2 | S64930 | serine/threonine-s |
| 45 | 618.5 | 23.0 | 421 | 2 | E96522 | hypothetical prote |

ALIGNMENTS

| | | | | | | |
|--|-----|--|-----|--|--|--|
| RESULT 1 | | | | | | |
| T04145 | | | | | | |
| serine/threonine protein kinase homolog - rice | | | | | | |
| C/Species: Oryza sativa (rice) | | | | | | |
| C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000 | | | | | | |
| C/Accession: T04145 | | | | | | |
| R/Tsal, T.H.; Le, H.T. | | | | | | |
| submitted to the EMBL Data Library, April 1996 | | | | | | |
| A/Description: SNF1-related protein kinase of rice. | | | | | | |
| A/Reference number: Z15239 | | | | | | |
| A/Accession: T04145 | | | | | | |
| A/Status: preliminary; translated from GB/EMBL/DBJ | | | | | | |
| A/Molecule type: mRNA | | | | | | |
| A/Residues: 1-510 <TSA> | | | | | | |
| A/Cross-references: EMBL:U55768; NID:G1477683; PIDN:AAB05457.1; PID:G1477684 | | | | | | |
| A/Experimental source: strain tns-8, endospore | | | | | | |
| C/Genetics: | | | | | | |
| A/Gene: RSK1 | | | | | | |
| C/Superfamily: AMP-activated protein kinase; protein kinase homology | | | | | | |
| F;15-270/Domain: protein kinase homology <KIN> | | | | | | |
| Query Match | | | | | | |
| Best Local Similarity 87.5%; Score 2356.5; DB 2; Length 510; | | | | | | |
| Matches 444; Conservative 32; Mismatches 33; Indels 1; Gaps 1; | | | | | | |
| QY | 1 | MDGSSKSGHSEALRNYNLGRTLGITGFKVYIAEHKLTGHRVAIKIINCROMMEME | 60 | | | |
| Db | 1 | MDGNAGGGHSEALRNYNLGRTLGISGFKVYIAEHKLTGHRVAIKILNRQRMME | 60 | | | |
| QY | 61 | KAKREFKILKFIHPHIIRLYEVIYTPDIYVMEYCKYGEIYVEKRLQEDE-ARR | 119 | | | |
| Db | 61 | KAKREIKILRLFIHPHIIRLYEVIYTPDIYVMEYCKYGEIYVEKRLQEDRVALLR | 120 | | | |
| QY | 120 | IFQIIISGVYCHRNMVHRDLKPENLDDSKYNVKLADFGLSNVMDGHFLKTS | 179 | | | |
| Db | 121 | IFSQIISAVEYCHRNMVHRDLKPENLDDSKYNVKLADFGLSNVMDGHFLKTS | 180 | | | |
| QY | 180 | YAAPEVISGKLYAGPEVDVWSCGVIYALLCGTLPFDDENIPNLFKKIKGIGITLPS | 239 | | | |
| Db | 181 | YAAPEVISGKLYAGPEVDVWSCGVIYALLCGTLPFDDENIPNLFKKIKGIGITLPS | 240 | | | |
| QY | 240 | ALARDLIPRMVVEPMKRITIREIREHQFQIRLPYLAAPPPTTQOAKMIDEDTL | 299 | | | |
| Db | 241 | ALARDLIPRMVVEPMKRITIREIREHQFQIRLPYLAAPPPTTQOAKMIDEDTL | 300 | | | |
| QY | 300 | VNMGFNKNHVCESLCSRLONEATVAYLLLDNRPATSGYLGADYQESMDRLNQL | 359 | | | |
| Db | 301 | VNLGYGKHVCESLCSRLONEATVAYLLLDNRPATSGYLGADYQESMDRLNQL | 360 | | | |
| QY | 360 | SSSSGTRNYPGSSDPHSSGLRPYPYVERKVALGLQSRAPHPREINVEVLKALQ | 419 | | | |
| Db | 361 | SASSNTRHYLPGSSDPHSSGLRPYPYVERKVALGLQSRAPHPREINVEVLKALQ | 420 | | | |

Db 481 KDNKYLDDIQRVGTGPQLLFLEFCGAFLTNLRVL 513

RESULT 4

A41361
serine/threonine-specific protein kinase (EC 2.7.1.-) RKINI - rye
C;Species: Secale cereale (rye)
C;Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 11-Jun-1999
C;Accession: A41361
R;Alderson, A.; Sabelli, P.A.; Dickinson, J.R.; Cole, D.; Richardson, M.; Kreis, M.; She
Proc. Natl. Acad. Sci. U.S.A. 88, 8602-8605, 1991
A;Title: Complementation of snf1, a mutation affecting global regulation of carbon metab
A;Reference number: A41361; MUID:92020901; PMID:1924320
A;Accession: A41361
A;Molecule type: mRNA
A;Residues: 1-502 <ALD>
A;Cross-references: GB:M74113; NID:g169835; PIDN:AAA33921.1; PID:g169836
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; autophosphorylation; magnesium; phosphoprotein; phosphotransferase; ser
F;12-269/Domain: protein kinase homology <KIN>
F;20-28/Region: protein kinase ATP-binding motif
F;43,62,140,142/Active site: Lys, Glu, Asp, Lys #status predicted
F;145,149/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 76.6%; Score 2062.5; DB 1; Length 502;
Best Local Similarity 77.9%; Pred. No. 4.5e-81;
Matches 401; Conservative 37; Mismatches 58; Indels 19; Gaps 6;

QY 1 MDGSSKSGHSEALRNYNLGRTLGITGFGVKIAEHKLTGHRVAIKINCROMNMEME 60
1 MDG---GGEHSEALKNYYLGKILGVGTFAKVIIEAHKTRHKVAIKVLRNRRAPEMEE 57
QY 61 KAKREFKILKF---IHPIIRLYEVITYPTDIYVVMYCKYGGELFDYIVEKRLQDEA 117
58 KAKREIKIRLFIDLIHPHIIIRYEVIVTPKDIYVMEYCQNGDLIDYIEKRRLQDEA 117
QY 118 RRIFOIISGVEYCHRMNVVHRDLKPENLILDSKYNVKIADFGLSNVMDHGHFLKTS 177
118 RRTFOIISAVEYCHRNKVVHRDLKPENLILDSKYNVKIADFGLSNVMDHGHFLKTS 177
QY 178 PNYAPEVISGKLYAGPEVDVWSCGVIILYALLCGTLPFDDENIPNLFKKIKGIYTLPSH 237
178 LNYAPEVISGKLYAGPEIDVWSCGVIILYALLCGAVPFDDDNIPNLFKKIKGTYILPIY 237
QY 238 LSALARDLIPRMVLVVEPMKRITIREIREHWFQIRLPYLAVPDPDTQQAAMIDEDTLR 297
238 LSDLVRLISRMLIVDPMKRITIGEIRKHSWFQNRPLRYLAVPPDMQQAAMIDEDTLR 297
QY 298 DVVNMGFNKNHVCSLCSRLQNEATVAYYLLDNRFRATSGYLGAHYQEQPM----- 348
298 DVVKLGDKDVHVESLCSNRLQNEETVAYYLLDNRFRATSGYLGAHYQEQPM----- 348
QY 358 SESSSSGTRNYPGSSDPHSSGLRPYPYVERKVALGL-QSRAHPREIMVEVLKALQELNV 416
349 -ESASPSTRSYLPGSNDSSGSLRPYRVERKVALGLQSSRAPPRAIMIEVLKALKELNV 407
QY 417 RWKNGH-YNVCKRCWCPGPEVND-TLDASNSFLGSDTIMDNDANGRLPTVIKEFQLY 474
408 CWKNGDCYNMKCRWCPGFPVRVSDMLLDANHSFVDDCAIKDNGDANSRLPAVIKEIQLY 467
QY 475 KTKDDKYLDDMQRVGTGPQLLFLEFCGAFLTNLRVL 509
468 KTKDDKYLDDMQRVGTGPQLLFLEFCGAFLTNLRVL 502

RESULT 5
JC1446
serine/threonine-specific protein kinase (EC 2.7.1.-) AK21 - Arabidopsis thaliana
N;Alternate names: protein kinase SNF1 homolog
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 11-Jun-1999
C;Accession: JC1446; S58266; S66334
R;LeGuen, L.; Thomas, M.; Bianchi, M.; Halford, N.G.; Kreis, M.
Gene 120, 249-254, 1992

A;Title: Structure and expression of a gene from Arabidopsis thaliana encoding a protein
A;Reference number: JC1446; MUID:93013041; PMID:1339373
A;Accession: JC1446
A;Molecule type: DNA
A;Residues: 1-512 <LEB>
A;Cross-references: GB:M93023; NID:g166599; PIDN:AAA32736.1; PID:g166600
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
submitted to the EMBL Data Library, May 1995
A;Description: Differential accumulation of the transcripts of 22 novel protein kinase ge
A;Reference number: S58256
A;Accession: S58266
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 144-198 <THU>
A;Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
R;Thuemmler, F.; Kirchner, M.; Teuber, R.; Ditttrich, P.
Plant Mol. Biol. 29, 551-565, 1995
A;Title: Differential accumulation of the transcripts of 22 novel protein kinase genes in
A;Reference number: S66314; MUID:96123233; PMID:8534852
A;Accession: S66334
A;Molecule type: DNA
A;Residues: 144-198 <TH2>
A;Cross-references: EMBL:X86966; NID:g928909; PIDN:CAA60529.1; PID:g928910
C;Comment: This enzyme plays an important role in a signal transduction cascade regulatin
C;Genetics:
A;Gene: AKn10; AK21
A;Introns: 64/1; 125/3; 186/3; 230/3; 292/3; 322/3; 350/3; 396/3; 475/3

A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase ATP-binding motif
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 73.1%; Score 1969.5; DB 1; Length 512;
Best Local Similarity 72.8%; Pred. No. 4e-77;
Matches 377; Conservative 52; Mismatches 74; Indels 15; Gaps 4;

QY 1 MDGSSKG--SGHSEALRNYNLGRTLGITGFGVKIAEHKLTGHRVAIKINCROMNMEM 58
1 MDGSGTGRSGVESILPNYKLGRTLGISGFRVKIAEHALTGHRVAIKILNRKIKNMEM 60
QY 59 EEKAKREFKILKFIHPHIIIRLYEVITYPTDIYVVMYCKYGGELFDYIVEKRLQDEAR 118
61 EEKVRREIKIRLFEMPHIIRLYEVITYPTDIYVMEYVNSGELFDYIVEKRLQDEAR 120
QY 119 RIFQOIIISGVEYCHRMNVVHRDLKPENLILDSKYNVKIADFGLSNVMDHGHFLKTS 178
121 NFFQOIIISGVEYCHRMNVVHRDLKPENLILDSKYNVKIADFGLSNVMDHGHFLKTS 180
QY 179 NYAAPEVISGKLYAGPEVDVWSCGVIILYALLCGTLPFDDENIPNLFKKIKGIYTLPSHL 238
181 NYAAPEVISGKLYAGPEVDVWSCGVIILYALLCGTLPFDDENIPNLFKKIKGIYTLPSHL 240
QY 239 SALARDLIPRMVLVVEPMKRITIREIREHWFQIRLPYLAVPDPDTQQAAMIDEDTLRD 298
241 SPGARDLIPRMVLVVDPMKRVITPEIRQHPWFQAHLPYLAVPDPDTVQQAKKIDEIILQE 300
QY 299 VVNMGFNKNHVCSLCSRLQNEATVAYYLLDNRFRATSGYLGAHYQESMDRNLNLQASS 358
301 VINMGFDRNHILIESLRNRTQNDGTIVTYLLDNRFRASSGYLGAHFQETME-GTPRMHPA 359
QY 359 ESSSSGTRNYPGSSDPHSSGLRPYPYVERKVALGL-QSRAHPREIMVEVLKALQELNVRW 418
360 ESVASPVSHRLPGLMEYQGVGLRSQYVERKVALGLQSRAPPREIMTEVLKALQDLNVCW 419
QY 419 KNGHYNVCKRCWCPGPEVNDTLDA-----SNSFLGSDTIMDNDANGRLPTVIKEFE 471


```
Db      420 KKI GHY NMKCRWVP-----NSSADGMLSNSMHDNNNYFGDESSIIENEA VKSPNVKEFI   474
```

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Qy      472 QLYKTKDDKYLLDMQRVTGPQLLF LDFCAAFILTKLRVL    509
```

```
Dd      475 QLYKTRDCKYLIDLQRVQGPFLLFLDLCAAFILAQLRVL    512
```

RESULT 6

probable serine/threonine-specific protein kinase (EC 2.7.1.-) - cucumber
N/Alternate names: SNF1-related protein kinase
C/Species: Cucumis sativus (cucumber)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000
C/Accession: T10449
R/Gumpel, N.J.
submitted to the EMBL Data Library, December 1996
A/Reference number: Z17020
A/Accession: T10449
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-504 <GUM>
A/Cross-references: EMBL:Y10036
A/Experimental source: cv. Masterpiece; cotyledon
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C/Superfamily: AMP-activated protein kinase; protein kinase homology
C/Keywords: ATP, phosphotransferase; serine/threonine-specific protein kinase
F/6-260/Domain: protein kinase homology <KIN>

| | | | | |
|-----------------------|------------------|--------------------|-----------|-------------|
| Query Match | 72.9%; | Score 1963; | DB 2; | Length 504; |
| Best Local Similarity | 74.8%; | Pred. No. 7.5e-77; | | |
| Matches 374; | Conservative 53; | Mismatches 65; | Indels 8; | Gaps 4; |

[illegible]

serine/threonine-specific protein kinase (EC 2.7.1.-) NPK5 - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 16-Jun-2000
C;Accession: A56009
R;Murataka, T.; Banno, H.; Machida, Y.
Mol. Cell. Biol. 14, 2958-2965, 1994
A;Title: Characterization of tobacco protein kinase NPK5, a homolog of Saccharomyces cerevisiae.
A;Reference number: A56009; MUID:94217693; PMID:8164654
A;Accession: A56009
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-511 <MUR>
A;Cross-references: GB:D26602; NID:g496384; PIDN:BAA05649.1; PID:g496385
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>
F;25-33/Region: protein kinase ATP-binding motif
F;48,67,142,144/Active site: Lys, Glu, Asp, Lys #status predicted
F;147,151/Binding site: magnesium (Asn, Asp) #status predicted

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 71.4% | Score 1923; | DB 1; | Length 511; |
| Best Local Similarity | 72.1% | Pred. No. 3.8e-75; | | |
| Matches 372; | Conservative 60; | Mismatches 72; | Indels 12; | Gaps 7; |

| | | | |
|----|-----|--|-----|
| Qy | 1 | MDGSS--KSGSHSEALRNNYLGRTLGIGTFGKVKIAEHKLTGHRVAIKIINCRÖRMNEM | 58 |
| Db | 1 | MDGSTVÖGSSSVESFLRNYKLGKTLGIGSFGKVKIAEHTLTGHKVAVKILNRKIKNMEM | 60 |
| Qy | 59 | BEKAKREFKILKLFHPIHILRYEVIYTPTDIYVWMEYCKYGEFDYIVEKGRLOEDEAR | 118 |
| Db | 61 | BEKVRREIKILRLFMHPHILRLYEVEVETPSDIYVWMEYKSGELFDYIVEKGRLOEDEAR | 120 |
| Qy | 119 | RIFOQIISGVVEYCHRRNVVHRDLKPENLLDSKYNVKLADFGISNVMHGHLKTS CGSP | 178 |
| Db | 121 | KFQÖIISGVVEYCHRRNVVHRDLKPENLLDSKMNVKIADFGISNMRDGHFLKTS CGSP | 180 |
| Qy | 179 | NYAAPEVISGKLYAGPEVDWVSCGILLYALCGTLPFDDENIPNLFKKIKGIGYTLPSHL | 238 |
| Db | 181 | NYAAPEVISGKLYAGPEVDWVSCGILLYALCGTLPFDDENIPNLFKKIKGIGYTLPSHL | 240 |
| Qy | 239 | SALARDLIPRMLVNEBPMKRITIREIREHQWFQIRLPRYLAVPEPDTQÖAKMIDEDTLRD | 298 |
| Db | 241 | SAGARDLIPRMLIVDPMKRMTIPEIRMHPMFQAHLPRYLAVPEPDTMÖAKKIDEDILÖE | 300 |
| Qy | 299 | VYVMGFNKNHVCESLCSRLONEATVAYYLLLDNRFRAATSGYLGADYÖESMDRNLNÖLASS | 358 |
| Db | 301 | VYKRGFDRNSLVASLCNRVÖNEGTVAAYYLLLENÖFRASSGYMGAEFÖETMEYGYHÖINSS | 360 |
| Qy | 359 | ESSSSGTRNYVPGSSDPHSSGLRPHYYPVERKMWALGLÖSRAHPREITMEVLKALÖELNVRW | 418 |
| Db | 361 | EVLLP-CWÖHLPGIMDFÖQYÖGAR-QÖPVERKMWALGLÖSRAHPREITMEVLKALÖGLNVRW | 418 |
| Qy | 419 | KNNGHYNVKCRWCPGPFPEVNDTLDA SNS---FLG-DSTIMDNDANGRLPTVIKFEFÖL | 473 |
| Db | 419 | KKIGPYNMKCÖWVPGVFGHHEGM-SNNSIHIOFPGDDSTVIENGVT--IPNAVKFEVÖL | 475 |
| Qy | 474 | YKTKDÖKYLDMÖRVTLGPÖLLFLDFCAAFITKLRVL | 509 |
| Db | 476 | YKTRREKYLLDÖRVÖGPGÖFLFLDLCAAFIÄÖLRVL | 511 |

RESULT 8

serine/threonine-specific protein kinase (EC 2.7.1.-) AKIN11 [validated] - Arabidopsis thaliana (mouse-ear cress)
N;Alternate names: SNF1 protein kinase omolog AKIN11
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 03-Nov-2000
C;Accession: T52633
R;Bhalerao, R.P.; Salchert, K.; Bako, L.; Okresz, L.; Szabados, L.; Muranaka, T.; Machida, K.; Proc. Natl. Acad. Sci. U.S.A. 96, 5322-7, 1999

A/Title: Regulatory interaction of PRL1 WD protein with Arabidopsis SNF1-like protein ki
A/Reference number: Z25116; MUID:99238528; PMID:10220464
A/Accession: T52633
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-512 <BHA>
A/Cross-references: EMBL:X99279; PIDN:CAA67671.1
A/Experimental source: cultivar Columbia
C/Genetics:
A/Gene: AKIN11
C/Function:
A/Description: EC 2.7.1.-; serine/threonine-specific protein kinase AKIN11 [validated, M
C/Superfamily: AMP-activated protein kinase; protein kinase homology
C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Query Match 70.7%; Score 1903.5; DB 2; Length 512;
Best Local Similarity 70.7%; Pred. No. 2.5e-74;
Matches 362; Conservative 58; Mismatches 89; Indels 3; Gaps 1;

QY 1 MDGSSK--GSGHSEALRNVLGRTLGIGTGKVKIAEHKLTGHRVAIKINCRQMRME 57
Db 1 MDHSSNRFGNNGVESTLPNYKLTGLIGSGFKVAIAHVVTGKVAIKLNRRKIKNME 60
QY 58 MEEKAKREFKILKLFHPIHRIIRLYEVIYPTDIYVMEYCKYSGELFDYIVEKRLQDEDA 117
Db 61 MEEKVRREIKILRLFMHPHIIROYEVIETSDIYVMEYKSGELFDYIVEKRLQDEDA 120
QY 118 RRIFOQIISGVEYCHRNWVVRDLKPENLILDSKYNVKLADFGLSNVMDGHFLKTS CGS 177
Db 121 RNFFOQIISGVEYCHRNWVVRDLKPENLILDSRCNIKADFGLSNVMRDGHFLKTS CGS 180
QY 178 PNYAAPEVISGKLYAGEVDVWSCGVLIALCGTLPPDDENIPNLFKKIKGGIYTLPSH 237
Db 181 PNYAAPEVISGKLYAGEVDVWSCGVLIALCGTLPPDDENIPNLFKKIKGGIYTLPSH 240
QY 238 LSAIARDLIPRLVVEPMKRITIREIREHQQFQIRLPYLA VPPDPTTQAKMIDEDTLR 297
Db 241 LSSEARDLIPRLIYDPRKRTITPEIRQHRWFQTHLPYLA VSPDPTVEQAKINEIIVQ 300
QY 298 DVVNMGFNKNHVCESLCSRLQNEATVAYLLLDNRPRA TSGYL GADYQESMDRNLQLAS 357
Db 301 EVVNMGFDRNQVLESIRNRTQNDATVYLLLDNRFVRPSGYLSEFQETDTS GSNPMRT 360
QY 358 SSSSSGTRNYPGSSDPHSSGRLPYYPVERKALGLQSRAPREIMVEVLKALQELNVR 417
Db 361 PEAGASPVGHWIPAHVDHYGLGARSQVPVDRKALGLQSHAHPREIMNEVLKALQELNVC 420
QY 418 WKNGHYNVKCRWCPCGPPEVNDTLDASNSFLG DSTIMDNDANGRLPTVIKKEFQLYXTK 477
Db 421 WKIGHYNMKCRWVPGIADGQNTMVNNQLHFRDESSIIEDDCA MTSPTVIKELQLYKAR 480
QY 478 DDKYLLDMQRTVGPQLFLDFCAFLTKLRVL 509
Db 481 EEKYLDDIQRVNGPQFLFLDLCAFLTELRLVI 512

RESULT 9

S59941
serine/threonine-specific protein kinase (EC 2.7.1.-) BKIN2 - barley (fragment)
C/Species: Hordeum vulgare (barley)
C/Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 26-Feb-1999
C/Accession: S59941
R/Hanappel, U.; Vicente-Carabajosa, J.; Barker, J.H.A.; Shewry, P.R.; Halford, N.G.
Plant Mol. Biol. 27, 1235-1240, 1995
A/Title: Differential expression of two barley SNF1-related protein kinase genes.
A/Reference number: S59941; MUID:95284374; PMID:7766906
A/Accession: S59941
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-473 <HAN>
A/Cross-references: EMBL:X82548
C/Genetics:

A/Gene: BKIN2
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C/Superfamily: AMP-activated protein kinase; protein kinase homology
C/Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F;1-244/Domain: protein kinase homology (fragment) <KIN>
F;21,40,115,117/Active site: Lys, Glu, Asp, Lys #status predicted
F;120,124/Binding site: magnesium (Asn, Asp) #status predicted

Query Match 70.6%; Score 1900; DB 1; Length 473;
Best Local Similarity 75.9%; Pred. No. 3.3e-74;
Matches 365; Conservative 45; Mismatches 61; Indels 10; Gaps 4;

QY 26 GTFGKVKIAEHKLTGHRVAIKINCRQMRNMEEKAKREFKILKLFHPIHRIIRLYEVIY 85
Db 1 GSGFKVKIAEHILTGHKVAIKILNRRKIKSMEMEKKREIKILRLFMHPHIIIRLYEVID 60
QY 86 TPTDIYVMEYCKYSGELFDYIVEKRLQDEBARRIFOQIISGVEYCHRNWVVRDLKPE N 145
Db 61 TPADIYVMEYKSGELFDYIVEKRLQDEBARRFQOIISGVEYCHRNWVVRDLKPE N 120
QY 146 LILDSKYNVKLADFGLSNVMDGHFLKTS CGSPNYAAPEVISGKLYAGEVDVWSCGVL 205
Db 121 LILDSKYNVKLADFGLSNVMRDGHFLKTS CGRPNYAAPEVISGKLYAGEVDVWSCGVL 180
QY 206 YALLCGTLPPDDENIPNLFKKIKGGIYTLPSHLSA IARDLIPRLVVEPMKRITIREIRE 265
Db 181 YALLCGTLPPDDENIPNLFKKIKGGIYTLPSHLSPLARDLIPRLVVEPMKRITIREIRE 240
QY 266 HQWFQIRLPYLA VPPDPTTQAKMIDEDTLRDVNMGFNKNHVCESLCSRLQNEATVAY 325
Db 241 HSMFKARLPYLA VPPDPTAQOVKKLDEDTLNDVIKMGFDKNQLTESLQKRLQNEATVAY 300
QY 326 YLLDNRFRA TSGYL GADYQESMDRNLNLQLA -SSSSSSGTRNY -VPGSSDPHSSGRLPY 383
Db 301 YLLDNKLRITSGYLGA BYQESMDSSFSQISPE TPSSASAEARQYSGPG-----FGLRQH 354
QY 384 YPERKVALGLQSRAPREIMVEVLKALQELNVRWKNGHYNVKCRWCPCGPPEVNDTLDA 443
Db 355 PAERKVALGLQSRAPREIITEVLKALQELNVCWKKIGHYNMKCRWSPGFFE--NMHN 412
QY 444 SNSFLG DSTIMDNDANGRLPTVIKKEFQLYTKDDKYLLDMQRTVGPQLFLDFCAFL 503
Db 413 NNGFVESAIIEADGLGDKSTHIVKFEIQLYKTRGD KYLLDLQRVSGPQLFLDLCSAFL 472
QY 504 T 504
Db 473 T 473

RESULT 10

T07788
probable serine/threonine-specific protein kinase (EC 2.7.1.-) SNF1 - potato
N/Alternate names: StubSNF1 protein
C/Species: Solanum tuberosum (potato)
C/Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jan-2000
C/Accession: T07788
R/Lakatos, L.; Banfalvi, Z.
submitted to the EMBL Data Library, January 1997
A/Reference number: Z16133
A/Accession: T07788
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-512 <LAK>
A/Cross-references: EMBL:U83797; NID:g1935915; PIDN:AAB52224.1; PID:g1935916
C/Genetics:
A/Gene: SNF1
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C/Superfamily: AMP-activated protein kinase; protein kinase homology
C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;17-271/Domain: protein kinase homology <KIN>

Best Local Similarity 46.1%; Pred. No. 3e-42;
Matches 239; Conservative 85; Mismatches 109; Indels 86; Gaps 12;

[illegible]

RESULT 13

[hydroxymethylglutaryl-CoA reductase (NADPH2)] kinase (EC 2.7.1.109) - rat
N/Contains: [acetyl-CoA carboxylase] kinase (EC 2.7.1.128); [hydroxymethylglutaryl-CoA reductase]
C/Species: Rattus norvegicus (Norway rat)
C/Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 03-Jun-2002
C/Accession: A53621; S53729
R/Carling, D.; Aguan, K.; Woods, A.; Verhoeven, A.J.M.; Beri, R.K.; Brennan, C.H.; Sidebottom, J. Biol. Chem. 269, 11442-11448, 1994
A/Title: Mammalian AMP-activated protein kinase is homologous to yeast and plant protein kinases
A/Reference number: A53621; MUID:94209324; PMID:7908907
A/Accession: A53621
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-552 <CAR>
A/Cross-references: GB:Z29486; NID:g488375; PIDN:CAA82620.1; PID:g488376
R/Gao, G.; Widmer, J.; Stapleton, D.; Teh, T.; Cox, T.; Kemp, B.E.; Witters, L.A. Biochim. Biophys. Acta 1266, 73-82, 1995
A/Title: Catalytic subunits of the porcine and rat 5'-AMP-activated protein kinase are members of the protein kinase C family
A/Reference number: S53729; MUID:95234757; PMID:7718624
A/Accession: S53729
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-354,'S',356-461,'D',463-552 <GAO>
A/Cross-references: GB:U12149; NID:g862472; PIDN:AAA85033.1; PID:g862473
C/Function:
A/Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate
C/Superfamily: AMP-activated protein kinase; protein kinase homology
C/Keywords: ATP; magnesium; phosphotransferase; serine/threonine-specific protein kinase
F/14-268/Domain: protein kinase homology <KIN>
F/22-30/Region: protein kinase ATP-binding motif
F/45,64,139,141/Active site: Lys, Glu, Asp, Lys #status predicted
F/144,148/Binding site: magnesium (Asn, Asp) #status predicted

| | | | | |
|----------------------------|-------|--------------------|------------|-------------|
| Query Match | 42.5% | Score 1144; | DB 1; | Length 552; |
| Best Local Similarity | 45.9% | Pred. No. 4.4e-42; | | |
| Matches: 238; Conservative | 86; | Mismatches 109; | Indels 86; | Gaps 12; |

[illegible]

RESULT 14

SNF-related kinase [imported] - Guillardia theta nucleomorph
C/Species: nucleomorph Guillardia theta
A/Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
C/Accession: B90100
R/Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reiter,
Nature 410, 1091-1096, 2001
A/Title: The highly reduced genome of an enslaved algal nucleus.
A/Reference number: A99082; MUID:11323671; PMID:11323671
A/Accession: B90100
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-472 <DOU>
A/Cross-references: GB:AF165818; NID:g13794554; PIDN:AAK39929.1; GSPDB:GN00150
C/Genetics:
A/Gene: kin(enf1)
A/Map position: 1
A/Genome: nucleomorph
C/Superfamily: AMP-activated protein kinase; protein kinase homology
C/Keywords: nucleomorph

| | | | | |
|---------------------------|--------|--------------------|------------|-------------|
| Query Match | 42.2%; | Score 1137; | DB 2; | Length 472; |
| Best Local Similarity | 46.6%; | Pred. No. 7.7e-42; | | |
| Matches 233; Conservative | 89; | Mismatches 112; | Indels 66; | Gaps 12; |

```
Oy      17 YNLGRTLGIGTFGKVKIAEHKLTHGRVAIKIINCROMRNMEMEKKAREFKILKLFIHPh 76  
        |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||  
Db      12 YLGLKTlGVGSFGKVKLTGEHHLGGQKAVAKILNRKKIKALMEEEKVYKREICILKLFMHPh 71
```

QY 77 IIRLYEVITYPTDIYVMEYCKYGLFDYIYVEKRLQEDEARRIFOQITSGVEYCHRMV 136
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | |
DB 72 IIRLYEVIETPTDIFVYTEYITGGELEFDYIVERGLNEDESRKFFQOMSGIHEYCHNHMV 131
QY 137 VHRDLKPENLILD SKYVNLADFGLSNVMDGHFLKTS CGSPNYAAPEVISGKLYAGPEV 196
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | |
DB 132 VHRDLKPENLILD AHLNVKIADFGLSNIMKDGNFLKTS CGSPNYAAPEVINGKSYLGPEV 191
QY 197 DVWSCGVILYALLCGTLPEDDENIPNLFKKIKGGIYTLPSHLAALARDLIPRMLVPEPMK 256
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | |
DB 192 DVWSCGVIMYALLCGSLPEDDENIPNLFKKIKSGIYILPGYLSDSLSDMLAKMLITNPLL 251
QY 257 RITIREIREHWFQIRLPRYLAVP--PPDTTQQA KM-IDEDTLRDVYVNMGF-NKNHVCES 312
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | |
DB 252 RITINEIRDPWFENSLPKYLSFPTFKKNFVIOKKLINIDNILELVSNKTFLSKKYIKLG 311
QY 313 LCSRLQNEATVAYYLL-----LDNRFRA TSGYLGADYQESMDRNLNQLASSESS 361
: | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | |
DB 312 IMKHERNSTAITIYHLIRESITPFDMITVDNSY-----IRDIYKKE-- 351
QY 362 SSGTRNYVPGSSD-PHSSGLRPPYPERKWA LQLOS-RAHPREIMVEVLKALQELNVRWK 419
| : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | :
DB 352 ----NVIKKSNEKEHNTSLHQA F-----LGIESPRENLKDI LNEIQRAIKTFRSKTH 399
QY 420 KNGHYNVKCRWCPGPEVNDTL DASN SFLGDSITMDNDANGRLPTVIKFEFQLYKTKDD 479
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 400 NLNHFSV-----IIVINTNSLFETFKYKKKEIILRTTIL---IQIFK-RSM 442
QY 480 KYLLDMQRVTGPQLFLDFC 499
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 443 KYLLIDLQKINGDSFFFLSTC 462

RESULT 15

T07660
probable serine/threonine-specific protein kinase (EC 2.7.1.1-) PKIN1 - potato (fragment)
N;Alternate names: SNF1-related protein kinase
C;Species: Solanum tuberosum (potato)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 21-Jul-2000
C;Accession: T07660
R;Man, A.L.; Purcell, P.C.; Hannappel, U.; Halford, N.G.
Plant Mol. Biol. 34, 31-43, 1997
A;Title: Potato SNF1-related protein kinase: molecular cloning, expression analysis and
A;Reference number: Z16075; MUID:97320459; PMID:9177310
A;Accession: T07660
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-348 <MAN>
A;Cross-references: EMBL:X95996; NID:g1216284; PIDN:CAA65243.1; PID:g1216285
A;Experimental source: cv. Desiree; developing tuber
C;Genetics:
A;Gene: PKIN1
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
C;Superfamily: AMP-activated protein kinase; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

Query Match 40.7%; Score 1096; DB 2; Length 348;
Best local Similarity 60.4%; Pred. No. 3.2e-40;
Matches 215; Conservative 48; Mismatches 75; Indels 18; Gaps 5;

QY 157 ADFGLSNVMDGHFLKTS CGSPNYAAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPPD 216
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | |
DB 1 ADFGLGNIMRDGHFLKTS CGSPNYAAPEVVSGLYAGPEVDVWSCGVILYALLCGTLPPD 60
QY 217 DENIPNLFKKIKGGIYTLPSHLAALARDLIPRMLVVEPMKRITIREIREHWFQIRLPRY 276
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | |
DB 61 DENIPNLFKKIKSGVYTLPSHLAALARDLIPRMLIVDPMKRISVPDIRQHWFKIHLPRY 120
QY 277 LAVPPDPTTQQA KMIDEDTLRDVYVNMGFNKNHVCESLCSRLQNEATVAYYLLLDNRFRA T 336
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | |
DB 121 LAVPPVARQHLKLDDEILQVSRMGLDRDQLDLSLQKRIQDDATVAYYLLYDNRSMAS 180

QY 337 SGYLGADYQESMDRNLNQLASSESSSGTRNYVPGSSDPHSSGLRPPYPERKWA LQLOS 396
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | |
DB 181 SGYLGDEFQESVD CYS PGLFPNLDLQISTGNVSEES-----LRPFRKEKMLVGLQ S 234
QY 397 RAHPREIMVEVLKALQELNVRWKNGHYNVKCRWCPGF--PEVNDTL DASN SFLGDS TI 453
| : | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 235 PANPKEIMNQVLGTLLELNVRWKKIGHYNMKCLWCHDLHLHSMANNHNDDDHFI SNATA 294
QY 454 MDNDANGRL---PTVIKFEFQLYKTKDKYLLDMQRVTGPQLFLDFCAAFJTKL 506
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 295 IST-----HLQPQPTV-KFEMQLYKTEDEKYL LDLQRISGPQFLFLDFCAGFIRQL 344

Search completed: July 7, 2004, 17:57:09
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:51:24 ; Search time 17 Seconds
(without alignments)
1559.042 Million cell updates/sec

Title: US-09-857-522B-4
Perfect score: 2693
Sequence: 1 MDGSSKSGSHSEALRNYNLG.....GPQLFLDFCAFLTKRLVL 509

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|--------------|--------------------|
| 1 | 2062.5 | 76.6 | 502 | 1 RKI1_SECCE | Q02723 secale cere |
| 2 | 1969.5 | 73.1 | 535 | 1 KI10_ARATH | Q38997 arabidopsis |
| 3 | 1148 | 42.6 | 552 | 1 AAK2_HUMAN | P54646 homo sapien |
| 4 | 1144 | 42.5 | 552 | 1 AAK2_RAT | Q09137 rattus norv |
| 5 | 1119 | 41.6 | 548 | 1 AAK1_RAT | P54645 rattus norv |
| 6 | 1115 | 41.4 | 550 | 1 AAK1_HUMAN | Q13131 homo sapien |
| 7 | 1016.5 | 37.7 | 620 | 1 SNF1_CANAL | P52497 candida alb |
| 8 | 1013.5 | 37.6 | 633 | 1 SNF1_YEAST | P06782 saccharomyc |
| 9 | 1010.5 | 37.5 | 619 | 1 SNF1_CANTR | O94168 candida tro |
| 10 | 1002.5 | 37.2 | 611 | 1 SNF1_CANGA | Q00372 candida gla |
| 11 | 981.5 | 36.4 | 576 | 1 SNF1_SCHPO | O74536 schizosacch |
| 12 | 894.5 | 33.2 | 622 | 1 YNA3_CAEEL | P45894 caenorhabdi |
| 13 | 737.5 | 27.4 | 752 | 1 MRK4_HUMAN | Q96134 homo sapien |
| 14 | 737.5 | 27.4 | 786 | 1 SNIL_HUMAN | P57059 homo sapien |
| 15 | 731.5 | 27.2 | 776 | 1 SNIL_RAT | Q91145 rattus norv |
| 16 | 731 | 27.1 | 779 | 1 SNIL_MOUSE | Q60670 mus musculu |
| 17 | 724.5 | 26.9 | 776 | 1 MRK3_HUMAN | P27448 homo sapien |
| 18 | 709.5 | 26.3 | 794 | 1 KI11_HUMAN | Q8tdc3 homo sapien |
| 19 | 708 | 26.3 | 736 | 1 ST29_HUMAN | Q8iwq3 homo sapien |
| 20 | 696.5 | 25.9 | 774 | 1 MRK2_MOUSE | Q05112 mus musculu |
| 21 | 676.5 | 25.1 | 1037 | 1 KCC4_YEAST | P25389 saccharomyc |
| 22 | 659.5 | 24.5 | 1142 | 1 GIN4_YEAST | Q12263 saccharomyc |
| 23 | 659 | 24.5 | 661 | 1 ARK5_HUMAN | O60285 homo sapien |
| 24 | 644.5 | 23.9 | 1518 | 1 KKK1_YEAST | P34244 saccharomyc |
| 25 | 626 | 23.2 | 1147 | 1 KIN2_YEAST | P13186 saccharomyc |
| 26 | 605 | 22.5 | 1064 | 1 KIN1_YEAST | P13185 saccharomyc |
| 27 | 602.5 | 22.4 | 891 | 1 KIN1_SCHPO | P23987 schizosacch |
| 28 | 570.5 | 21.2 | 775 | 1 CDR2_SCHPO | P87050 schizosacch |
| 29 | 560.5 | 20.8 | 714 | 1 HUNK_MOUSE | O88866 mus musculu |
| 30 | 548.5 | 20.4 | 714 | 1 HUNK_HUMAN | P57058 homo sapien |
| 31 | 533.5 | 19.8 | 353 | 1 ASK2_ARATH | P43292 arabidopsis |
| 32 | 532 | 19.8 | 800 | 1 KIN4_YEAST | Q01919 saccharomyc |
| 33 | 530 | 19.7 | 363 | 1 ASK1_ARATH | P43291 arabidopsis |

| | | | | | |
|----|-------|------|-----|---------------|--------------------|
| 34 | 527.5 | 19.6 | 593 | 1 CDR1_SCHPO | P07334 schizosacch |
| 35 | 513.5 | 19.1 | 295 | 1 KMLC_DICDI | P25323 dictyosteli |
| 36 | 505 | 18.8 | 364 | 1 ST2A_MOUSE | Q61241 mus musculu |
| 37 | 503 | 18.7 | 332 | 1 AAIP_WHEAT | Q02066 triticum ae |
| 38 | 489.5 | 18.2 | 580 | 1 SRK1_SCHPO | O94547 schizosacch |
| 39 | 488 | 18.1 | 367 | 1 ST2A_HUMAN | Q9bxa7 homo sapien |
| 40 | 482.5 | 17.9 | 424 | 1 KPSH_HUMAN | P11801 homo sapien |
| 41 | 481 | 17.9 | 460 | 1 CDS1_SCHPO | Q09170 schizosacch |
| 42 | 475 | 17.6 | 358 | 1 ST2B_HUMAN | Q96pf2 homo sapien |
| 43 | 473.5 | 17.6 | 370 | 1 DAK2_MOUSE | Q8vdf3 mus musculu |
| 44 | 473.5 | 17.6 | 432 | 1 STKB_XENTLA | Q91604 xenopus lae |
| 45 | 472 | 17.5 | 454 | 1 DAK3_HUMAN | O43293 homo sapien |

ALIGNMENTS

RESULT 1
RKI1_SECCE ID RKI1_SECCE STANDARD; PRT; 502 AA.
AC Q02723;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Carbon catabolite derepressing protein kinase (EC 2.7.1.-).
GN RKI1.
OS Secale cereale (Rye).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Secale.
OX NCBI_TaxID=4550;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Endosperm;
RX MEDLINE=92020901; PubMed=1924320;
RA Alderson A., Sabelli P.A., Dickinson J.R., Cole D., Richardson M.,
RA Kreis M., Shewry P.R., Halford N.G.;
RT "Complementation of snf1, a mutation affecting global regulation of
RT carbon metabolism in yeast, by a plant protein kinase cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:8602-8605(1991).
CC -!- FUNCTION: ESSENTIAL FOR RELEASE FROM GLUCOSE REPRESSION.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -!- SIMILARITY: Contains 1 UBA domain.
CC
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CC
CC -----
CC EMBL; M74113; AAA33921.1; -.
CC PIR; A41361; A41361.
CC
CC HSSP; P00518; 1PHK.
CC
CC InterPro; IPR001772; Kinase Cterm.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_kinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC InterPro; IPR000449; UBA_domain.
CC Pfam; PF02149; KAI; 1.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF00627; UBA; 1.
CC PRINTS; PR00109; TYRKINASE.
CC PRODOM; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS50030; UBA; 1.
CC Transferase; Serine/threonine-protein kinase; Phosphorylation;
KW


```
KW  ATP-binding; Carbohydrate metabolism.
FT  DOMAIN 14 269 PROTEIN KINASE.
FT  DOMAIN 290 330 UBA.
FT  NP BIND 20 28 ATP (BY SIMILARITY).
FT  BINDING 43 43 ATP (BY SIMILARITY).
FT  ACT_SITE 140 140 BY SIMILARITY.
FT  MOD_RES 173 173 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ  SEQUENCE 502 AA; 57711 MW; 0C9AF827F8989927 CRC64;

Query Match 76.6%; Score 2062.5; DB 1; Length 502;
Best Local Similarity 77.9%; Pred. No. 2.7e-138;
Matches 401; Conservative 37; Mismatches 58; Indels 19; Gaps 6;

QY 1 MDGSSKSGSHSEALRNVLGRTLGIGTFGKVIAEHKLTGHRVAIKINGROMMEME 60
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Db 1 MDG---GGEHSEALKNYLGLKILGVTFKAVITAEHKTRHKVAIKVLRQMAPEMEE 57

QY 61 KAKREFKILKF---IHPHILRLYEVIYPTDIYVVMVEYCKYGELEFDYIVKGRLOEDEA 117
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 58 KAKREIKILRLFDILIHPIIRVYEVIYTPKDFIVMEYCCQNGDLIDYLEKRLQEDEA 117

QY 118 RRIFOIISGVEYCHRNWVVRDLKPEENLLDSKYNVKLADFGLSNVMDHGHFLKTS 177
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 118 RRTFOIISAVEYCHRNKVVHRDLKPEENLLDSKYNVKLADFGLSNVMDHGHFLKTS 177

QY 178 PNYAAPEVISGKLYAGPEVDWVSCGVLVYALLCGTLPEFDENIPNLFKKIKGIYTLPSH 237
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 178 LNYAAPEVISGKLYAGPEVDWVSCGVLVYALLCGAVPFDDNIPNLFKKIKGIYTLPIY 237

QY 238 LSLALARDLIPRLVVEPMKRITIREIREHQQFQIRLPRYLAVPPPTTQQAQIMDEDTLR 297
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 238 LSDLVRDLISRLIVDPMKRITIGEIRKHSWFQNRPLRYLAVPPPDMMQQAQIMDEDTLR 297

QY 298 DVVNMGFKNHVCESLCSRLQNEATVAYLLLDNRRFRATSGYLGAHYQESMDRNLNLQ 357
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 298 DVVKLGVDKDHVCESLCSRLQNEATVAYLLLDNRRFRATSGYLGAHYQEQPM----- 348

QY 358 SESSSGSTRNVPGSDPSSGLRPYYPVERKMAIGL-QSRAHPREIMVEVLKALQELNV 416
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 349 -ESASPSTRSYLPGSNDSCGSLRPYRVERKMAIGLQOSRAPRAIMIEVLKALKEINV 407

QY 417 RWKKNQH-VNVCRCWCPGPEVND-TLDASNSFLGDSITIMDNDANGRLPYIYKEEFQ 474
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 408 CWKKNGDCYNMKCRWCPCGPRVSDMLLDANHSFVDCAIKDNGDANSRLPAVIKEIQLY 467

QY 475 KTKDDKYLDMQRTVGPQLFLDFCAAFITKLRVL 509
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 468 KTKDDKYLDMQRTVGPQLFLDFCAAFITKLRVL 502

RESULT 2
KI10_ARATH STANDARD; PRT; 535 AA.
AC Q38997; O04728; Q39076; Q8RWD2;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE SNF1-related protein kinase KIN10 (EC 2.7.1.-) (AKIN10).
GN KI10 OR SKIN10 OR AT3G01090 OR T4P13.22.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=93013041; PubMed=1339373;
RA le Guen L., Thomas M., Bianchi M., Halford N.G., Kreis M.;
RT "Structure and expression of a gene from Arabidopsis thaliana
RT encoding a protein related to SNF1 protein kinase.";
RL Gene 120:249-254 (1992).
RN [2]
RP --SEQUENCE FROM N.A. (ISOFORM 2).
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RC STRAIN=cv. Columbia;
RA Lessard P., Kreis M., Thomas M.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansgorge W., Unsel'd M.,
RA Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdemenech P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Catolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Clement J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laurie M., Berger-Llauro C., Purnelle B., Maury D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Caesacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pal G., Miltscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Prieuss D., Lin X., Niernan W.C., Salzberg S.L., White O., Venter J.C.,
RA Frazer C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:820-822 (2000).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=cv. Columbia;
RX MEDLINE=22954850; PubMed=14593172;
RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
RA Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
RA Arakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,
RA Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
RA Hayashizaki Y., Johnson-Hopson C., Heuan V.W., Iida K., Karnes M.,
RA Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
RA Yuan S., Shinzaki K., Davis R.W., Theologis A., Ecker J.R.;
RT "Empirical analysis of transcriptional activity in the Arabidopsis
RT genome.";
RL Science 302:842-846 (2003).
RN [5]
RP PARTIAL SEQUENCE FROM N.A. (ISOFORM 2).
RC STRAIN=cv. Columbia;
RX MEDLINE=95115691; PubMed=7816049;
RA le Guen L., Thomas M., Kreis M.;
RT "Gene density and organization in a small region of the Arabidopsis
RT thaliana genome.";
RL Mol. Gen. Genet. 245:390-396 (1994).
CC -!- FUNCTION: May play an important role in a signal transduction
CC cascade regulating gene expression and carbohydrate metabolism in
CC higher plants.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q38997-1; Sequence=Displayed;
CC Note=No experimental confirmation available;
CC Name=2;
CC IsoId=Q38997-2; Sequence=VSP_009001;
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CC -1- TISSUE SPECIFICITY: Expressed in roots, shoots and leaves.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -1- SIMILARITY: Contains 1 UBA domain.

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DR EMBL; M93023; AAA32736.1; -.
DR EMBL; X79707; CAA56146.1; -.
DR EMBL; AC008261; AAF26165.1; -.
DR EMBL; AY093170; AAM13169.1; -.
DR EMBL; BT010386; AAQ56829.1; -.
DR EMBL; X94757; CAA64384.1; -.
DR PIR; JC1446; JC1446.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR001772; Kinase Cterm.
DR InterPro; IPR000719; Prot Kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAl; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Alternative splicing.
FT DOMAIN 42 294 PROTEIN KINASE.
FT NP BIND 48 56 ATP (BY SIMILARITY).
FT DOMAIN 315 355 UBA.
FT ACT SITE 165 165 BY SIMILARITY.
FT BINDING 71 71 ATP (BY SIMILARITY).
FT MOD RES 198 198 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT VARSPLIC 1 23 Missing (in isoform 2).
FT /FTId=VSP_009001.
SQ SEQUENCE 535 AA; 61181 MW; FFFC3832323FD8317 CRC64;

Query Match 73.1%; Score 1969.5; DB 1; Length 535;
Best Local Similarity 72.8%; Pred. No. 1.1e-131;
Matches 377; Conservative 52; Mismatches 74; Indels 15; Gaps 4;

QY 1 MDGSSKG--SGHSEALRNYNLGRITGIGTFGKYKIAEHKLTGHRVAIKINCRQMRNMEM 58
DB 24 MDGSGTSGRSGVESILPNYKLGRTLGISFGYKIAEHALTGHKVAIKILNRKIKMEM 83
QY 59 EEKAKREFKILKLFTHPHIIRLYEVITYPTDIYVVMVEYCKYGELEFDYIEKGRLOEDEAR 118
DB 84 EEKVRREIKILKLFEMPHIIRLYEVITYPTDIYVMEYVNSGELFDYIEKGRLOEDEAR 143
QY 119 RIFQOIISGVYCHRMNVVHRDLKPNLLDSKYNVKLADFGLSNVMDGHFLKTS CGSP 178
DB 144 NFFQOIISGVYCHRMNVVHRDLKPNLLDSKCNVKIADFGLSNIMRDGHFLKTS CGSP 203
QY 179 NYAAPEVISGKLYAGPEVDVWSCGVLVYALCGTLPFDENIPNLFKKIKGIGIYTLPSHL 238
DB 204 NYAAPEVISGKLYAGPEVDVWSCGVLVYALCGTLPFDENIPNLFKKIKGIGIYTLPSHL 263
QY 239 SALARDLIPRLVVEPMKRITIREIREHOWFOIRLPRYLAVPPPDPTQOAKMIDEDTLRD 298
DB 264 SPGARDLIPRLVVEPMKRITIREIREHOWFOIRLPRYLAVPPPDPTQOAKMIDEDTLRD 323

QY 299 VVMGFNKNHVCESLCSRLONEATVAYYLLIDNRFRTATSGYLGADYQESMDRLNOLASS 358
DB 324 VINMGFDRNHLIESLRNRTQNDGVTYYLLIDNRFRTASSGYLGAEFOETME-GTPRMHPA 382
QY 359 ESSSSGTRNYVPGSSDPHSSGLRPYPYVERKWAIGLQSRAPREIMVEVLKALQELNVRW 418
DB 383 ESVASPVSHRLPGIMELYQGVGLRSQYPERKWAIGLQSRAPREIMTEVLKALQDLNVCW 442
QY 419 KKNGHYNNKCRWCPGEPVEVNDTLDA-----SNSFLGDSTIMDNDANGRLPTVIKFEF 471
DB 443 KKIGHYNNKCRWV-----NSSADGMLNSMHDNNYFGDESSIENEAIVKSPNVVKFEI 497
QY 472 QLYTKDKKYLDMQRTVTPQLFLDFCAFLTKLRVL 509
DB 498 QLYKTRDDKYLIDLQRVQGPQFLFLDLCAFLAQLRVL 535

RESULT 3
AAK2 HUMAN
ID AAK2_HUMAN STANDARD; PRT; 552 AA.
AC P54646; Q9H1E8; Q9UD43;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 5'-AMP-activated protein kinase, catalytic alpha-2 chain (EC 2.7.1.-)
DE (AMPK alpha-2 chain).
GN PKAA2 OR AMPK2 OR AMPK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95047501; PubMed=7959015;
RA Aguan K., Scott J., See C.G., Sarkar N.H.;
RT "Characterization and chromosomal localization of the human homologue
RT of a rat AMP-activated protein kinase-encoding gene: a major
RT regulator of lipid metabolism in mammals.";
RL Gene 149:345-350(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=95080410; PubMed=7988703;
RA Berti R.K., Marley A.E., See C.G., Sopwith W.F., Aguan K., Carling D.,
RA Scott J., Carey F.;
RT "Molecular cloning, expression and chromosomal localisation of human
RT AMP-activated protein kinase.";
RL FEBS Lett. 356:117-121(1994).
RN [3]
RP SEQUENCE OF 33-552 FROM N.A.
RA Cobley V.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Responsible for the regulation of fatty acid synthesis
CC by phosphorylation of acetyl-CoA carboxylase. It also regulates
CC cholesterol synthesis via phosphorylation and inactivation of
CC hormone-sensitive lipase and hydroxymethylglutaryl-CoA reductase.
CC Appears to act as a metabolic stress-sensing protein kinase
CC switching off biosynthetic pathways when cellular ATP levels are
CC depleted and when 5'-AMP rises in response to fuel limitation
CC and/or hypoxia. This is a catalytic subunit.
CC -1- SUBUNIT: Heterotrimer of a catalytic subunit, a beta and a gamma
CC non-catalytic subunits.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.

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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U06454; AAA64745.1; -.
DR EMBL; AL035705; CAC17574.1; -.
DR PIR; S51025; S51025.
DR HSSP; Q63450; 1A06.
DR Genew; HGNC:9377; PRKAA2.
DR MIM; 600497; -.
DR GO; GO:0004672; F:protein kinase activity; TAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR001245; Tyr_kinase.
DR Pfam; PF00069; kinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Cholesterol biosynthesis; Fatty acid biosynthesis; Transferase;
KW Serine/threonine-protein kinase; ATP-binding; Phosphorylation;
KW Multigene family.
FT DOMAIN 16 268 PROTEIN_KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CONFLICT 180 180 A -> T (IN REF. 1).
FT CONFLICT 271 271 D -> G (IN REF. 1).
FT CONFLICT 403 404 HL -> RQ (IN REF. 1).
SQ SEQUENCE 552 AA; 62319 MW; C46AAFC1D5104975 CRC64;

Query Match 42.6%; Score 1148; DB 1; Length 552;
Best Local Similarity 46.1%; Pred. No. 1.e-73;
Matches 239; Conservative 85; Mismatches 109; Indels 86; Gaps 12;

QY 2 DGSSKSGHSEALRNVLGRTLGITFGKVKIAEKLITGHVAIKIINCRQRMNMEMBEK 61
DB 8 DGRVK-IGH-----YVLGDTLVGVTFGKVKIGEHQLTGHKVAVKIILNRQKIRSLDVVK 60
QY 62 AKREFKILKFIHPHILRLYEVIYPTDIYVVMYCKYGLFDYIVEKGRLODEARRIF 121
DB 61 IKREIQNLKLFRIHPHILRLYQVISTPTDFVMVEYVSGELFDYICKHGRVEEMEARLIF 120
QY 122 QQIISGEVYCHRNWVVRDLKPENLILDSKNVVKLADFGLSNVMDHGHFLRTSCGSPNYA 181
DB 121 QQILSAVDYCHRHVVRDLKPENLILDAHNAKIADFGLSNMMSDGEFLRTSCGSPNYA 180
QY 182 APEVISGKLYAGPEVDVWSCGVTLYALLCGTLPPDDENIPNLFKKIKGITYLPSHLSAL 241
DB 181 APEVISGRLYAGPEVDWSCGVTLYALLCGTLPPDEHVPPLFKKIRGVFYIPEYLNRS 240
QY 242 ARDLIPRLVVEPMKRTITREIREHWFQIRLPRYLAVPRPDTQQAQMIDEDTLRDV- 300
DB 241 VATLLMMLQVDPKRAITIKDIRHEWFKQDLPSTLF--PEDPSYDANVIDDEAVKEVCE 298
QY 301 NMGFKNHVCESLCS-RLQNEATVAYLLLDNRFRAITSGYLGADYQESMDRNLNQ----- 354
DB 299 KFECTESEVWNSLYSGDPQDLAVAYHLIIDNR-----RIMNQASEFY 341
QY 355 LASSESSSS--GTRNVVPGSSDPSHSSGLRPY-----PVE-----RK 389
DB 342 LASSPSSGSFMDSAMHIPPGLKHPERMPPLADSPKARCPDLALNTTKPKSLAVKAK 401
QY 390 WALGLQSRAPREIMVEVLKALQELNVRWKNGHYNVKCRWCPCGFPEVNDTLASNSFLG 449
DB 402 WHLGIRSQSKPYDIMEVYRAMKQDLFEWKVVNAVYHLVR-----RKNPVTG 448
QY 450 DSTIMDNDANGRLPTVIKFEFQLYTKDKDKYLLDMQRY 488
DB 450 DSTIMDNDANGRLPTVIKFEFQLYTKDKDKYLLDMQRY 488
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DB 449 N-----YVKMSLQLYLVNRSYLLDFKSI 472

RESULT 4
AAK2_RAT
ID_AAK2_RAT STANDARD; PRT; 552 AA.
AC Q09137;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 5'-AMP-activated protein kinase, catalytic alpha-2 chain (EC 2.7.1.-)
DE (AMPK alpha-2 chain).
GN PRKAA2 OR AMPK2 OR AMPK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94209324; Pubmed=7908907;
RA Carlung D., Aguan K., Woods A., Verhoeven A.J.M., Beri R.K.,
RA Brennan C.H., Sidebottom C., Davison M.D., Scott J.;
RT "Mammalian AMP-activated protein kinase is homologous to yeast and
RT plant protein kinases involved in the regulation of carbon
RT metabolism.";
RL J. Biol. Chem. 269:11442-11448(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95234757; Pubmed=7718624;
RA Gao G., Widmer J., Stapleton D., Teh T., Cox T., Kemp B.E.,
RA Witters L.A.;
RT "Catalytic subunits of the porcine and rat 5'-AMP-activated protein
RT kinase are members of the SNF1 protein kinase family.";
RL Blochim. Biophys. Acta 1266:73-82(1995).
CC -1- FUNCTION: Responsible for the regulation of fatty acid synthesis
CC by phosphorylation of acetyl-CoA carboxylase. It also regulates
CC cholesterol synthesis via phosphorylation and inactivation of
CC hormone-sensitive lipase and hydroxymethylglutaryl-CoA reductase.
CC Appears to act as a metabolic stress-sensing protein kinase
CC switching off biosynthetic pathways when cellular ATP levels are
CC depleted and when 5'-AMP rises in response to fuel limitation
CC and/or hypoxia. This is a catalytic subunit.
CC -1- SUBUNIT: Heterotrimer of a catalytic subunit, a beta and a gamma
CC non-catalytic subunits.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q09137-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q09137-2; Sequence=VSP_004949, VSP_004950;
CC Note=Lacks the sequence parts essential for kinase activity and
CC is therefore inactive;
CC -1- TISSUE SPECIFICITY: Skeletal muscle, lower levels in liver, heart
CC and kidney.
CC -1- INDUCTION: By AMP.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z29486; CAA82620.1; -.
DR EMBL; U12149; AAA85033.1; -.
DR PIR; A53621; A53621.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.
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DR InterPro; IPR008271; Ser thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Cholesterol biosynthesis; Fatty acid biosynthesis; Transferase;
KW Serine/threonine-protein kinase; ATP-binding; Phosphorylation;
KW Alternative splicing; Multigene family.
FT DOMAIN 16 268 PROTEIN_KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT VARSPPLIC 32 388 Missing (in isoform Short).
FT VARSPPLIC 392 552 /FTid=VSP_004949.
FT VARSPPLIC 392 552 Missing (in isoform Short).
FT CONFLICT 355 355 /FTid=VSP_004950.
FT CONFLICT 462 462 M -> S (IN REF. 2).
FT CONFLICT 462 462 N -> D (IN REF. 2).
SQ SEQUENCE 552 AA; 62257 MW; 2829E07F674D89B1 CRC64;

Query Match 42.5%; Score 1144; DB 1; Length 552;
Best Local Similarity 45.9%; Pred. No. 2.1e-73;
Matches 238; Conservative 86; Mismatches 109; Indels 86; Gaps 12;

QY 2 DGSSKSGHSEALRYNVLGRTLGIGTFGKVKIAEHKLTGHRVAIKIINCROMNMEMEEK 61
DB 8 DGRVK-IGH-----YVLGDTLGVGTFGKVGKIGHQLTGHKVAVKILNRQKIRSLDVVK 60
QY 62 AKREFKILKFIHPHILRLYEVIYPTDIYVVMEXCKYGELEFDYIVEKGRLODEARRIF 121
DB 61 IKREIQNLKLFRRHPHILKLYQVISTPTDFVMWEYVSGELFDYICKHGRVEVEARRLF 120
QY 122 QQIISGVEYCHRNMYVHRDLKPENLLDSKYNVKLADFGLSNMVMDGHFLKTSGSPNYA 181
DB 121 QQILSAVDYCHRNMYVHRDLKPENVLDAQNMAKIADFGLSNMMSDGEFLRISGSPNYA 180
QY 182 APEVISGKLYAGPEVDVWVSCGVIYALLCGTLPFDENIPNLFKKIKGIGIYTLPSHLSAL 241
DB 181 APEVISGRLYAGPEVDIWSGVIYALLCGTLPFDEHVPFLFKIRGGVPIYIPEYLNRS 240
QY 242 ARDLIPRLVVEPMKRTITREIREHQWFQIRLPYLAVPDPDTQQAQMDEDTLRDVV- 300
DB 241 IATLMLMLQVDPKRAITIKDIRHEWFKQDLPSTYLF--PEDPSYDANVIDDEAVKEVCE 298
QY 301 NMGFNKNHVCESLCS-RLQNEATVAYLLLDNRPRAATSGYLGADYQESMDRNINQ----- 354
DB 299 KFECTESEVMNSLYSGDPQDLAVAYHLIIDNR-----RIMNQASEFY 341
QY 355 LASSSESSS---GTRNYVPGSSSDPHSSGLRPYY-----PVE-----RK 389
DB 342 LASSPPTGSFMDMAMHIIPEGKLPHERMPPLIADSPKARCPDLALNTTKPKSLAVKAK 401
QY 390 WALGLQSRAPREINVEVLKALQELNVKKNKNGHYNVKCRWCGRGFEVNDTLASNSFLG 449
DB 402 WHLGIRSQSKPYDIMAETVRAMKQDLDFEWKVNAVYHLVR-----RKNPVTG 448
QY 450 DSTIMDNDANGRLPTVIKFEFQLYTKDKKYLDMQRV 488
DB 449 N-----YVKMSLQLLYLVNRSYLLDFKSI 472
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RESULT 5
AAK1_RAT STANDARD; PRT; 548 AA.
AC P54645;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
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```
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 5'-AMP-activated protein kinase, catalytic alpha-1 chain (EC 2.7.1.-)
DE (AMPK alpha-1 chain).
GN PRKAA1 OR AMPK1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Hypothalamus, and Liver;
RX MEDLINE=96132781; PubMed=8557660;
RA Stapleton D., Mitchell K.I., Gao G., Widmer J., Mitchell B.J.,
RA Teh T., House C.M., Fernandez C.S., Cox T., Witters L.A.,
RA Kemp B.E.;
RL "Mammalian AMP-activated protein kinase subfamily.";
RL J. Biol. Chem. 271:611-614(1996).
RN [2]
RP PARTIAL SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Hypothalamus, and Liver;
RX MEDLINE=95050763; PubMed=7961907;
RA Stapleton D., Gao G., Mitchell B.J., Widmer J., Mitchell K.,
RA Teh T., House C.M., Witters L.A., Kemp B.E.;
RT "Mammalian 5'-AMP-activated protein kinase non-catalytic subunits are
RT homologs of proteins that interact with yeast Snf1 protein kinase.";
RL J. Biol. Chem. 269:29343-29346(1994).
CC -1- FUNCTION: Responsible for the regulation of fatty acid synthesis
CC by phosphorylation of acetyl-CoA carboxylase. It also regulates
CC cholesterol synthesis via phosphorylation and inactivation of
CC hormone-sensitive lipase and hydroxymethylglutaryl-CoA reductase.
CC Appears to act as a metabolic stress-sensing protein kinase
CC switching off biosynthetic pathways when cellular ATP levels are
CC depleted and when 5'-AMP rises in response to fuel limitation
CC and/or hypoxia. This is a catalytic subunit.
CC -1- SUBUNIT: Heterotrimer of a catalytic subunit, a beta and a gamma
CC non-catalytic subunits.
CC -1- TISSUE SPECIFICITY: Low expression in kidney, liver, lung, heart
CC and brain.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -----
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CC -----
DR EMBL; U40819; AAC52355.1; -.
DR HSSP; Q63450; 1A06.
DR GO; GO:0005622; C:intracellular; ISS.
DR GO; GO:0008189; F:apoptosis inhibitor activity; ISS.
DR GO; GO:0004691; F:AMP-dependent protein kinase activity; ISS.
DR GO; GO:0042557; F:eukaryotic elongation factor-2 kinase activ. . .; NAS.
DR GO; GO:0000187; P:activation of MAPK; ISS.
DR GO; GO:0046318; P:negative regulation of glucosylceramide bio. . .; ISS.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; NAS.
DR GO; GO:0045768; P:positive regulation of anti-apoptosis; ISS.
DR GO; GO:0045542; P:positive regulation of cholesterol biosynth. . .; ISS.
DR GO; GO:0046321; P:positive regulation of fatty acid oxidation; NAS.
DR GO; GO:0045722; P:positive regulation of gluconeogenesis; NAS.
DR GO; GO:0046326; P:positive regulation of glucose import; NAS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
DR GO; GO:0001666; P:response to hypoxia; ISS.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
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DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Cholesterol biosynthesis; Fatty acid biosynthesis; Transferase;
KW Serine/threonine-protein kinase; ATP-binding; Phosphorylation;
KW Multigene family.
FT DOMAIN 16 268 PROTEIN KINASE.
FT NP_BIND 22 30 ATP (BY SIMILARITY).
FT BINDING 45 45 ATP (BY SIMILARITY).
FT ACT_SITE 139 139 BY SIMILARITY.
FT MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (POTENTIAL).
SQ SEQUENCE 548 AA; 62599 MW; 5CCA3281C195F867 CRC64;

Query Match 41.6%; Score 1119; DB 1; Length 548;
Best Local Similarity 45.6%; Pred. No. 1.2e-71;
Matches 233; Conservative 85; Mismatches 117; Indels 76; Gaps 11;

QY 2 DGSSKSGHSEALRNVLGRTLGIGFGKVKIAEHKLTGHRVAIKINCRQRMNMEMEEK 61
DB 8 DGRVK-IGH-----YLGDTLGVGTGFKVKGKHELTHKVAVKILNRQKRSIDVVGK 60
QY 62 AKREFKILKFIHPHILRLYEVIYPTDITYVVMYCKYGELEFDYIVEKRLQEDEARIF 121
DB 61 IRREIQNLKLFHPHILKLYQVISTPSDFVMWEYVSGGELFDYICKNGRLDEKESRRLF 120
QY 122 QQIISGVEYCHRNMYVHRDLKPENLLDISKYNAKLADFGLSNVMDHGHFLTS CGSPNYA 181
DB 121 QQILSGVDYCHRMVVRHDLKPENLLDAMHNAKIADFGLSNMMSDGEFLRTSCGSPNYA 180
QY 182 APEVISGLYAGPEVDWVSCGVILYALCGTLPPDDENIPNLFKKIKGIYTLPSHLSAL 241
DB 181 APEVISGRLYAGPEVDWVSSGVILYALCGTLPPDDHVPPTLFFKICDGFYTPQYLNP 240
QY 242 ARDLIPRMLVVEPMKRTITREIREHWFQIRLPYLAVPPTDTPQAKMIDEDTLR---- 297
DB 241 VISLLKMLQVDPMKRATIKDIREHEWFKQDLPKYLF--PEDPSYSTMTIDDEALKEVCE 298
QY 298 -----DVVNMGENKNHVCESLCSRLQNEATVAYLLDNR--FRATSGYLGA DYQES 347
DB 299 KFECSSEEVLSCLYNRNH-----QDPLAVAYHLIIDNRIRIMEAKDFYLA TSPDS 349
QY 348 M--DRNLNQ-----LASSSSSSGTRNYPGSSDPHSSGRLRPYPVERKALGLQSR 397
DB 350 FLDDHHLTRPHERVPEPLVAETPRARHTLDELNPQSKH-QGVR-----KAKWHLGIRSQ 403
QY 398 AHPREIMEVVLKALQELNVKKNKGHYNVKCRWCPGPPEVNDTLDASNSPLGSDTIMDND 457
DB 404 SRPNDIMAEVCRAIKQLDYEWKVNPYYLRV----- 435
QY 458 DANGRLPTVIKFEFQLYTKDKYLLDMQRV 488
DB 436 RKNPVTSTFSKMSLQLYQVDSRTYLLDFRSI 466
RESULT 6
AAK1_HUMAN STANDARD; PRT; 550 AA.
ID AAK1_HUMAN
AC Q13131; O00286; Q9UNQ4;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE 5'-AMP-activated protein kinase, catalytic alpha-1 chain (EC 2.7.1.-)
DB (AMPK alpha-1 chain).
GN PRKAA1 OR AMPK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Yano K.;
RT "Nucleotide sequence of cDNA for human AMP-activated protein kinase

RT alpha-1.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20499367; PubMed=11042152;
RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
RT "Cloning and functional analysis of cDNAs with open reading frames for
RT 300 previously undefined genes expressed in CD34+ hematopoietic
RT stem/progenitor cells.";
RL Genome Res. 10:1546-1560 (2000).
RN [3]
RP SEQUENCE OF 27-200 FROM N.A.
RC TISSUE=Intestine;
RA Taboada E.N., Hickey D.A.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 294-550 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96132781; PubMed=8557660;
RA Stapleton D., Mitchell K.I., Gao G., Widmer J., Michell B.J.,
RA Teh T., House C.M., Fernandez C.S., Cox T., Witters L.A.,
RA Kemp B.E.;
RT "Mammalian AMP-activated protein kinase subfamily.";
RL J. Biol. Chem. 271:611-614 (1996).
CC -1- FUNCTION: Responsible for the regulation of fatty acid synthesis
CC by phosphorylation of acetyl-CoA carboxylase. It also regulates
CC cholesterol synthesis via phosphorylation and inactivation of
CC hormone-sensitive lipase and hydroxymethylglutaryl-CoA reductase.
CC Appears to act as a metabolic stress-sensing protein kinase
CC switching off biosynthetic pathways when cellular ATP levels are
CC depleted and when 5'-AMP rises in response to fuel limitation
CC and/or hypoxia. This is a catalytic subunit (By similarity).
CC -1- SUBUNIT: Heterotrimer of a catalytic subunit, a beta and a gamma
CC non-catalytic subunits.
CC -1- PTM: Autophosphorylated (By similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB022017; BAA36547.1; -.
DR EMBL; AF100763; AAD43027.1; -.
DR EMBL; U22456; AAG4850.1; -.
DR EMBL; Y12856; CAA73361.1; -.
DR PIR; G01743; G01743.
DR HSSP; Q63450; 1A06.
DR Genew; HGNC:9376; PRKAA1.
DR MIM; 602739; -.
DR GO; GO:0005622; C:intracellular; IC.
DR GO; GO:0008189; F:apoptosis inhibitor activity; NAS.
DR GO; GO:0004691; F:cAMP-dependent protein kinase activity; NAS.
DR GO; GO:0042557; F:eukaryotic elongation factor-2 kinase activ. . .; ISS.
DR GO; GO:0000187; P:activation of MAPK; NAS.
DR GO; GO:0046318; P:negative regulation of glucosylceramide bio. . .; NAS.
DR GO; GO:0017148; P:negative regulation of protein biosynthesis; ISS.
DR GO; GO:0045768; P:positive regulation of anti-apoptosis; NAS.
DR GO; GO:0045542; P:positive regulation of cholesterol biosynth. . .; NAS.
DR GO; GO:0046321; P:positive regulation of fatty acid oxidation; ISS.
DR GO; GO:0045722; P:positive regulation of gluconeogenesis; ISS.
DR GO; GO:0046326; P:positive regulation of glucose import; ISS.
DR GO; GO:0006468; P:protein amino acid phosphorylation; ISS.
DR GO; GO:0001666; P:response to hypoxia; NAS.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.

DR InterPro; IPR002290; Ser thr kinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Cholesterol biosynthesis; Fatty acid biosynthesis; Transferase;
KW Serine/threonine-protein kinase; ATP-binding; Phosphorylation.
FT DOMAIN 18 270 PROTEIN_KINASE.
FT NP_BIND 24 32 ATP (BY SIMILARITY).
FT BINDING 47 47 ATP (BY SIMILARITY).
FT ACT_SITE 141 141 BY SIMILARITY.
FT MOD_RES 174 174 PHOSPHORYLATION (AUTO-) (POTENTIAL).
FT CONFLICT 28 28 T -> A (IN REF. 3).
FT CONFLICT 193 193 A -> V (IN REF. 3).
FT CONFLICT 199 199 I -> L (IN REF. 3).
FT CONFLICT 260 260 S -> T (IN REF. 2).
SQ SEQUENCE 550 AA; 62793 MW; 3316183D744DE325 CRC64;

Query Match 41.4%; Score 1115; DB 1; Length 550;
Best Local Similarity 45.4%; Pred. No. 2.3e-71;
Matches 232; Conservative 86; Mismatches 117; Indels 76; Gaps 11;

QY 2 DGSSKSGHSEALRNVLGRTLGIGTFGKVKIAEHKLTGHRVAIKIINCROMNMEMEEK 61
DB 10 DGRVK-IGH-----YILGDTLGVGTFGKVKGKHELTGKVAVKILNRQKIRSLDVVK 62
QY 62 AKREFKILFIHPHILRIYEVITPTDIYVVMYCKYGELEFDYIVEKRLQDEARRIF 121
DB 63 IRREIQNLKLRHPIHILKLYOVISTPSDIFVMVEYSGELFDYICKNGRLDEKSRRLF 122
QY 122 QQIISGVEYCHRMVVRDLKPENLILDSKYNVKLADGLSNVMHGHFLKTSQSPNYA 181
DB 123 QQILSGVDYCHRMVVRDLKPENLILDAHMAKIDFGLSNMMSDGEFLRTSCSPNYA 182
QY 182 APEVISGKLYAGPEVDVWSCGVLVLLCGTLPEFDENIPNLFKIKGGLYTLPSHLSAL 241
DB 183 APEVISGRLYAGPEVDIWSGVLLYALLCGTLPEFDHVPFLFKICDGIFFYQYLNP 242
QY 242 ARDLIPRLVVEPMKRTIREIREHQMFOIRLPRYLAVPPDPTQOAKMIDEDTLR---- 297
DB 243 VISLLKMLQVDPMKRASIKDIREHEWFKQDLPKYL--PEDPSYSTMIDELAKEVCE 300
QY 298 -----DVNMGNKHNVCESLCSRLQNEATVAYLLDNR--FRATSGYIADYQES 347
DB 301 KEFCESEEVLSCLYNRNH-----QDPLAVAYHLIDNRIRIMEAKDFYLATSPDP 351
QY 348 M--DRNLNQ-----LASESSSSGTRNYPGSSDPHSSGLRPYPYVERKVALGLQSR 397
DB 352 FLDDHHLTRPHERVPPFLVAETPRARHTLDELNPQSKH-QGVR-----KAKWHLGIRSQ 405
QY 398 AHPREIMVEVLKALQELNVKKNNGHYNVKCRWCPRPEVNDTLDASNSFLGDSIMDND 457
DB 406 SRPNDIMAEVCRAIKQLDYEMKVVNPYYLVR----- 437
QY 458 DANGRLPTVIKFEFQLYKTKDKYLLDMQRY 488
DB 438 RKNPVTSTYSKMSLQLYQVDSRTYLLDFRSI 468

RESULT 7
SNF1_CANAL STANDARD; PRT; 620 AA.
AC P52497; Q00309; 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carbon catabolite derepressing protein kinase (EC 2.7.1.-).
OS SNF1.
Candida albicans (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_Taxid=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 32354 / B-311;
RX MEDLINE=98053924; PubMed=9393775;
RA Petter R., Chang Y.C., Kwon-Chung K.J.;
RT "A gene homologous to Saccharomyces cerevisiae SNF1 appears to be
RL Infect. Immun. 65:4909-4917(1997).
RN [2]
RP SEQUENCE OF 7-620 FROM N.A.
RC STRAIN=ATCC 32354 / B-311;
RA Petter R., Kwon-Chung K.J.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Essential for release from glucose repression. It
CC interacts and has functional relationship to the regulatory
CC protein SNF4. Could phosphorylates CAT8 (By similarity).
CC -!- SUBCELLULAR LOCATION: Associated with the nuclear membrane (By
CC similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -----
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CC -----
DR EMBL; L78129; AAB48643.1; -.
DR EMBL; L39263; AAA92456.1; -.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR00719; Prot kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Carbohydrate metabolism; Nuclear protein.
FT DOMAIN 16 29 POLY-HIS.
FT NP_BIND 53 305 PROTEIN_KINASE.
FT BINDING 59 67 ATP (BY SIMILARITY).
FT ACT_SITE 82 82 ATP (BY SIMILARITY).
FT MOD_RES 175 175 BY SIMILARITY.
FT CONFLICT 208 208 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 7 8 PQ -> AR (IN REF. 2).
FT CONFLICT 228 234 AGPEVDV -> SSVQKMI (IN REF. 2).
FT CONFLICT 242 255 YVMLGRLPEFDEF -> GMSCCVVDYHSMTSS (IN
FT CONFLICT 387 387 A -> R (IN REF. 2).
FT CONFLICT 416 416 R -> A (IN REF. 2).
FT CONFLICT 494 494 S -> L (IN REF. 2).
SQ SEQUENCE 620 AA; 70005 MW; 1806652B5061D2B CRC64;

Query Match 37.7%; Score 1016.5; DB 1; Length 620;
Best Local Similarity 41.5%; Pred. No. 2.4e-64;
Matches 225; Conservative 85; Mismatches 133; Indels 99; Gaps 14;

QY 17 YNLGRTLGIGTFGKVKIAEHKLTGHRVAIKIINCROMNMEMEAKREFKILKLFHPH 76
DB 53 YQILKTGEGSFGKVKLAQHLGTGQKVALKIINRKTALAKSDMGFREREISYLRLLRHPH 112
QY 77 IIRLYEVITPTDIYVVMYCKYGELEFDYIVEKRLQDEARRIFQOIISGVEYCHRMV 136
DB 113 IIKLYDVIKSKDEIIMVIEFAG-KELFDYIVQGMPEDEARRFFQOIIAAVEYCHRHKI 171


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Db      338 SPDNDEIDNVLNLSSTMGYEKDEIYESLESSESDTPAFNEIRDAYMLIKENSLIKDMK 397
QY      340 LGADYQESMDRLNQ-----LASS----- 358
Db      398 ANKSVDLDTPLSQSPPTFOQSKSHQSKVDHETAKQHARRMASAITQRTYHQSPFM 457
QY      359 --ESSSSGTRNYPGS-----SDPHSSGLRPYPYVERK--WALGLQSRAPRE 402
Db      458 DQYKEBDSTVSIPLTSLPQIHRAANMLAQSPASKISPLVTKSKTRWHFGIRSRSPPLD 517
QY      403 IMVEVLKALQELNVRWKNKGH---YNVCKRWCPGPEVNDTLASNSFLGDSITMDNDDA 459
Db      518 VMGEIYIALKNLGAENAKPSEEDLWTIKLRW-----KYDIGNKT-----NT 558
QY      460 NGRLPTVIKFEFQLYKTKDKYLLDMQ 486
Db      559 NEKIPDLMKMVIQLFQIETNNYLVDFK 585

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RESULT 9

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SNF1_CANTR
ID SNF1_CANTR STANDARD; PRT; 619 AA.
AC 094168;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Carbon catabolite derepressing protein kinase (EC 2.7.1.-).
GN SNF1.
OS Candida tropicalis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5482;
RN [1]
RP SEQUENCE FROM N.A.
RA Kanai T., Ogawa K., Ueda M., Tanaka A.;
RT "Genetic evaluation of the function of SNF1 in Candida tropicalis.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Essential for release from glucose repression. It
CC interacts and has functional relationship to the regulatory
CC protein SNF4. Could phosphorylates CAT8 (By similarity).
CC -1- SUBCELLULAR LOCATION: Associated with the nuclear membrane (By
CC similarity).
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB024535; BAA75889.1; -.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Carbohydrate metabolism; Nuclear protein.
FT DOMAIN 17 29 POLY-HIS.
FT DOMAIN 52 303 PROTEIN_KINASE.
FT NP_BIND 58 66 ATP (BY SIMILARITY).
FT BINDING 81 81 ATP (BY SIMILARITY).
FT ACT_SITE 174 174 BY SIMILARITY.
FT MOD_RES 207 207 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

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SQ SEQUENCE 619 AA; 70323 MW; 0FCF1FC3DC6706D7 CRC64;

Query Match 37.5%; Score 1010.5; DB 1; Length 619;
 Best Local Similarity 40.0%; Pred. No. 6.4e-64;
 Matches 219; Conservative 91; Mismatches 128; Indels 109; Gaps 12;

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QY      17 YNLGRTLGIGTFGKYIAEHKLJGHRVAIKINCQRMMEMEAKREKILKLFHPH 76
Db      52 YQIKTLGEGSFGKYKLAQHVGTVGQVALKINRKTAKSDMOGRVEREISYLRLLRHPH 111
QY      77 IIRLYEVITPTDIYVVMYCKYKGLFDYIVKGRLOEDEARRIFQQLISGVEYCHRMV 136
Db      112 IIKLYDVIKSKDEIIMVIEFAG-KELFDYIVQKMPEDEARRFQQLIAAVEYCHRAKI 170
QY      137 VHRDLKPENLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNYAPEVISGKLYAGPEV 196
Db      171 VHRDLKPENLLDDQLNVKIADFGLSNMTDGNFLKTS CGSPNYAPEVISGKLYAGPEV 230
QY      197 DWSSGVILYALLCGTLPEDDENIPNLFKKIKGIYTLPSHLAALARDLIPRLVPEPMK 256
Db      231 DWSSGVILYVMLCGRLPFDEIFALFKKISNGVYTLPNYLSPGAKHLLTRMLVNPPLN 290
QY      257 RITIREIREHWFQIRLPRYLAVPPPTTQQAAM-IDEDTLRDV-VNMGFNKNHVCESL- 313
Db      291 RITIHEIMEDENKQDMPDYLLPPDLSKIKTSKIDIDEDVISALSVYMGYDRDEIISVIE 350
QY      314 -----CSRLONEATVAYYLLDNFRATSGYLGADYQESMDRLNQLAS- 357
Db      351 KANREAAAGATPTNQSKSTNEVLDAYLKKNH-----TLVKDLKSKSENIESFLSL 404
QY      358 -----SESSSSGTR-----NYPGS----- 372
Db      405 SPPSSSSFPNPGSTSSAPGVQSLTYQTLATVPDLSTLPNSTIALPTSLPSIHAYMME 464
QY      373 ---SDPHSS--GLRPYPYVERKAWALGLQSRAPREIMVEVLKALQELNVRWKNKGH---Y 424
Db      465 TKVNDPQQQIPAPQPTKLTTRWHFGIRSRSPPLDVMGEIYRALKNLGAENAKPTEBELW 524
QY      425 NVKCRWCPGPEVNDTLASNSFLGDSITMDNDANGRL-----PTVIKFEFQLYKTKKD 479
Db      525 TIRVRW-----KYDSTPQLRVWQRTNLMKMQIQLFQLEPN 559
QY      480 KYLLDMQ 486
Db      560 NYLVDFK 566

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RESULT 10

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SNF1_CANGA
ID SNF1_CANGA STANDARD; PRT; 611 AA.
AC Q00372;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Carbon catabolite derepressing protein kinase (EC 2.7.1.-).
GN SNF1.
OS Candida glabrata (Yeast) (Torulopsis glabrata).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5478;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCCLS84;
RX MEDLINE=97101049; PubMed=8945576;
RA Petter R., Kwon-Chung K.J.;
RT "Disruption of the SNF1 gene abolishes trehalose utilization in the
RT pathogenic yeast Candida glabrata.";
RL Infect. Immun. 64:5269-5273 (1996).
CC -1- FUNCTION: Essential for release from glucose repression. It
CC interacts and has functional relationship to the regulatory
CC protein SNF4. Could phosphorylates CAT8 (By similarity).
CC -1- SUBCELLULAR LOCATION: Associated with the nuclear membrane (By
CC similarity).

```

```
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -----
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CC -----
DR EMBL; L78130; AAB48642.1; -.
DR HSSP; P24941; 1HCL.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW transferase; Serine/threonine-protein kinase; ATP-binding;
KW phosphorylation; Carbohydrate metabolism; Nuclear protein.
FT DOMAIN 6 17 POLY-HIS.
FT DOMAIN 39 290 PROTEIN_KINASE.
FT NP_BIND 45 53 ATP (BY SIMILARITY).
FT BINDING 68 68 ATP (BY SIMILARITY).
FT ACT_SITE 161 161 BY SIMILARITY.
FT MOD_RES 194 194 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 611 AA; 70049 MW; 89E17812A4900CD0 CRC64;

Query Match 37.2%; Score 1002.5; DB 1; Length 611;
Best Local Similarity 40.1%; Pred. No. 2.3e-63;
Matches 224; Conservative 84; Mismatches 150; Indels 101; Gaps 13;

QY 2 DGSSKSGHSEALRNVLGRTLGITFGFKVIAEHKLTGHRVAIKINCRQMNMMEEEK 61
DB 32 DGSRVG-----NYQIVKTLGEGSGFKVLAHYTTGQVALKSINKVLAKSDMQGR 83
QY 62 AKREFKILKFIHPHILRLYEVIYPTDIYVVMCEYKGLFDYIVEKRIQDEARRIF 121
DB 84 IDREISYRLRLRPHITIKLYDVTKSDEIIMVIEYAG-NELFDYIVQRNKSQEARRF 142
QY 122 QQIISGVEYCHRNMYVARDLKPENLLDSKYVVKLADFGLSNMVMDGHFLKTSQGSPTYA 181
DB 143 QQIISAVEYCHRHKIYHRDLKPENLLDEHLNVKLADEGLSNIMTDSNFKTSQGSPTYA 202
QY 182 APEVISGKLYAGPEVDVWVSCGVLVYALLCGTLPPDENINPLFKKIKGIYTLPSHLSAL 241
DB 203 APEVISGKLYAGPEVDVWVSCGVLVYALLCGTLPPDENINPLFKKIKGIYTLPSHLSAL 262
QY 242 ARDLIPRLVVEPMKRTITREIREHWFQIRLPRYLAVPPDPTQO---AKWIDEDTLR 297
DB 263 ASDLIKRMILVNPRLRISIHIMQDEWFKVDIAEYIV--PQDLKQEQEAFNKKSGNEENVE 320
QY 298 DV-----VNMGFNKNHVCESLCSR---LQNEATVAYYLLDNR----- 332
DB 321 EIDDEMVTLSKTMGYDKDEIYEALSESSEDTPAYNEIRNAVYILIKDNKSLIKDMKQDNV 380
QY 333 -----FRATSGYLGAADYQESMDRLNQLASS-----ESSSSG 364
DB 381 TQELDTFLSQSPPTFQONGDGMKASEDQKKHSGRRGLASSVTQRTFHPPFMDQSKBED 440
QY 365 TRNYVPGSSD-----PHSSGLRPYYPVERK--WALGLQSRAPREIMVEVLKA 410
DB 441 STISITSLPQIHRANMLAQGLPAASKISPLVTKSKTRMHFGIRSRSPLDVMGHIIYA 500
QY 411 LQELNVRW---KKNGHVNVKCRWCPCGPPEVNDTLDAANSFLGDSTIMDNDANGRLPTVI 467
DB 501 LKNLGAEWANPSEEDLWTRVRW-----KYDSDESRL-----IEDGVKKIPLML 544
QY 468 KEFQOLYKTKDKDXYLLDMQ 486
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DB 545 KIVIQLFQIETNNYLVDFK 563

RESULT 11
SNF1_SCHPO STANDARD; PRT; 576 AA.
ID SNF1_SCHPO
AC 074536;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE SNF1-like protein kinase (EC 2.7.1.-).
GN SPCC74.03C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymoprez B.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cernutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -!- SIMILARITY: Contains 1 UBA domain.
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CC -----
DR EMBL; AL031543; CAA20833.1; -.
DR PIR; T41587; T41587.
DR HSSP; Q63450; 1A06.
DR GenedB_Spombe; SPCC74.03C; -.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
```


DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW Transferrase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 34 285 PROTEIN KINASE.
FT NP_BIND 304 345 UBA.
FT BINDING 40 48 ATP (BY SIMILARITY).
FT ACT_SITE 63 63 ATP (BY SIMILARITY).
FT ACT_SITE 156 156 BY SIMILARITY.
SQ SEQUENCE 576 AA; 65996 MW; E5857E8F171E7B50 CRC64;

Query Match 36.4%; Score 981.5; DB 1; Length 576;
Best Local Similarity 38.0%; Pred. No. 6.5e-62;
Matches 228; Conservative 78; Mismatches 165; Indels 129; Gaps 12;

QY 1 MDGSSKSGS---HSEALRNVLG----RTLGITFGKVKIAEHKLTGHRVAIKINCR 51
DB 9 MENSTMRNGARVLPPEAISKRHIGPYIIRETLGEGSFGKVLATHYKTQOKVALKFRISQ 68
QY 52 QMRNMEMEAKAREFKLFIHPHIIRLYEVIYTPPTDIYVMEYCKYGEIYVEKGR 111
DB 69 LLKKSDMHMRVEREISYKLRLHPHIKLYDVITTPFDIVMVEIYAG-GELFDYVEKKR 127
QY 112 LQEDEARIFQOIISGVEYCHRMNVHRDLKPENLIDSKYNVLADEGLSNVMDGHFL 171
DB 128 MTEDEGRRFQOITCAIEYCHRHKIVHRDLKPENLIDNLNVKIADFGLSNMTDGNFL 187
QY 172 KTSCGSPNYAAPEVISGKLYAGPEVDWSCGVLIALCGTLPPDDENIPNLFKKIKGGI 231
DB 188 KTSCGSPNYAAPEVINGKLYAGPEVDWSCGIVLYMLVGRLLPFDEFIPLFKKYNVCV 247
QY 232 YTLPSHLSALARDLIPRLVVEPMKRITIREIREHWFQIRLPRYLAVPPPTTQAKMI 291
DB 248 YVMPDFLSPGAQSLIRMLIVADPMQRTITQEIIRDPWFNVNLPDYLR--PMEEVQGSYA 304
QY 292 DEDTLRDVNV-MGFNKNHVCESLCSRLQNEATVAYVLLDNRFRATSGYLADYQESMDR 350
DB 305 DSRIVSKLGEAMGFSEDIYEALRSDENNEVKEAYNLLHENQVIOEKSHLSKSKYDSFL 364
QY 351 NLNQLASSESSSSGTRNVVPGSSDPHSSGLR-----PYYPVE----- 387
DB 365 SVSPAPASEYTESLOKSKQELIDPTLEGPRWTVSDPPTYAKQTIDSNICVLVPTAEKNK 424
QY 388 -----RKWALGLOSRAPREIMVEVLKALQELNVKWK--- 419
DB 425 LEMRTLADASAVDTSGSTRKKSRRNKNHFGVRCRGDAPEILLAVYRALQRAQOFTVPK 484
QY 420 -----KNGHYNVKCRWCPGFPPEVNDTLDASNSFLGSDSTIMDNDANGRLP-----T 465
DB 485 PVNGKYRSDMYTIKSRW-----EIPHCXREGKNT 513
QY 466 VIKFEFQLYKTKDKKYLDMQR-----VTGPQ-----LLFLDFCAFLTKL 506
DB 514 YAYIELQLYEVMPCFMDLVKSNGYKDIYSHPERTADHGMDLKSFPFLDLGAMLVCKL 573

RESULT 12
YNA3_CAEEL STANDARD; PRT; 622 AA.

AC P45894;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative serine/threonine-protein kinase PAR2.3 in chromosome III
DE (EC 2.7.1.-).
GN PAR2.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoea; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;

RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Snowken R.,
RA Sims M., Smaison N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinon-Sproat J.,
RA Wohlman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38 (1994).
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC -----
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CC -----
DR EMBL; U00025; AAA50618.1; -.
DR PIR; S44859; S44859.
DR HSSP; Q63450; 1A06.
DR WormPep; PAR2.3; CE00847.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Hypothetical protein; Transferrase; Serine/threonine-protein kinase;
KW ATP-binding.

FT DOMAIN 24 276 PROTEIN KINASE.
FT NP_BIND 30 38 ATP (BY SIMILARITY).
FT BINDING 53 53 ATP (BY SIMILARITY).
FT ACT_SITE 147 147 BY SIMILARITY.
SQ SEQUENCE 622 AA; 69515 MW; D5FBA1555004B246 CRC64;

Query Match 33.2%; Score 894.5; DB 1; Length 622;
Best Local Similarity 39.1%; Pred. No. 9.9e-56;
Matches 208; Conservative 77; Mismatches 154; Indels 93; Gaps 12;

QY 7 GSGHSEALRNVLGRTLGITFGKVKIAEHKLTGHRVAIKINCRQMRNMEMEAKAREF 66
DB 15 GTGHLK-IGNFVYKETIGKAGFAGVAKRGTHIQGYDVAIKIILNCRGAKIGTVNKTREI 73
QY 67 KILKLFHPHIIRLYEVIYTPPTDIYVMEYCKYGEIYVEKGRLOEDEARIFQOIIS 126
DB 74 DNLQKLTHPHITRLFRVISTPSDIFLVMELVSGELFSYITRKGAIPRESRRYFQIIS 133
QY 127 GVEYCHRMNVHRDLKPENLIDSKYNVLADEGLSNVMDGHFLKTSCGSPNYAAPEVI 186
DB 134 GVSYCHNHMIVHRDLKPENLIDANKNIKLADEGLSNYMTDGLLSTACGSPNYAAPELI 193
QY 187 SGKLYAGPEVDWSCGVLIALCGTLPPDDENIPNLFKKIKGGIYTLPSHLSALARDLI 246
DB 194 SNKLYGPEVDWSCGVLIALCGTLPPDQNVPTLFAKIKSGRYTVYSMEKQADALI 253
QY 247 PRLVVEPMKRITIREIREHWFQIRLPRYLAVPPPTTQAKMIDEDTLRDV----- 299
DB 254 STMLOVDPVKADVKRIVNHWSFRIDLPLYLF---PECENESSIVIDVQVSAEKTPE 310
QY 300 -----VNMGFNKNHVCES-----LCSRLQNEATVAYVLLDNRPRP----- 335
DB 311 KIIFYFIFRHLKFDYKEDVTGALLAEDHHHFLCIAIRLEVNHNKNADESSQKAMEDFW 370

QY 336 -----TSGYLGADYQ-ESMDRLNLQASSSSSGTRNYPGSSDHPHSGLRPY 384
DB 371 EIGKTMKMGSTSLPVGATTKSEKSERNAVKVGFSAVGRKIL-----EGLKK-- 419
QY 385 PVERK---WALGLQSRAPREIMEVLKALQELNVRWKNNGHYNVKCRWCPGFPEVNDTL 441
DB 420 --EQKLTWNLGIRACLDPVETMKHVFSLKSVDMEMKVLSMYHIIVRSKP--TPIN--- 472
QY 442 DASNSFLGSDTIMDNDANGRLPTVIKFEFQLY----KTKDDKYLDMQRYT 489
DB 473 -----PDPVKVSLQLFALDKKENNKGYLLDFKGLT 502
RESULT 13
MRK4_HUMAN
ID_MRK4_HUMAN STANDARD; PRT; 752 AA.
AC Q96LJ4; Q96JG7; Q9BYD8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE MAP/microtubule affinity-regulating kinase 4 (EC 2.7.1.27)
DE (MAP/microtubule affinity-regulating kinase like 1).
GN MARK4 OR MARKL1 OR KIAA1860.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA Diewes G., Mandelkow E.M.;
RT "MARK4, homologue of MARKL, MARK2 and MARK3."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=21226021; PubMed=11326310;
RA Kato T., Satoh S., Okabe H., Kitahara O., Ono K., Kihara C.,
RA Tanaka T., Tsunoda T., Yamaoka Y., Nakamura Y., Furukawa Y.;
RT "Isolation of a novel human gene, MARKL1, homologous to MARK3 and its
RT involvement in hepatocellular carcinogenesis."
RL Neoplasia 3:4-9(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RA Beghini A., Magnani I., Roversi G., Piepoli T., Diterlizzi S.,
RA Pollo B., Conti A.M.F., Cowell J.K., Finocchiaro G., Iarizza L.;
RT "Neutral progenitor-restricted isoform of MARKL1 gene is upregulated by
RT 19q13 amplification in human glioblastoma."
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=21245130; PubMed=11347906;
RA Nagase T., Nakayama M., Nakajima D., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XX.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 8:85-95(2001).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thyroid;
RA Itoigai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Satoh K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;

CC isold=Q96LJ4-1; Sequence=Displayed;
CC Name=2; Synonyms=MARKL1S;
CC isold=Q96LJ4-2; Sequence=VSP 004946;
CC -1- TISSUE SPECIFICITY: Ubiquitous. Isoform 2 is brain-specific.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. MARK
CC subfamily.
CC -1- SIMILARITY: Contains 1 kinase-associated (KAL) domain.
CC -1- SIMILARITY: Contains 1 UBA domain.
CC -----
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CC -----
CC EMBL; AY057448; AAL23683.1; -.
DR EMBL; AB049127; BAB39380.1; -.
DR EMBL; AY120867; AAM55491.1; -.
DR EMBL; AK075272; BAC11510.1; -.
DR EMBL; AB058763; BAB47489.1; ALT_INIT.
DR HSSP; Q63450; 1A06.
DR GeneW; HGNC:13538; MARK4.
DR MIM; 606495; -.
DR InterPro; IPR001772; Kinase_Cterm.
DR InterPro; IPR000719; Prot_Kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF02149; KAL; 1.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00627; UBA; 1.
DR PRINTS; PR00109; TYRKINASE.
DR PRODOM; PD000001; Prot_kinase; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Alternative splicing.
FT DOMAIN 59 310 PROTEIN KINASE.
FT DOMAIN 324 368 UBA.
FT DOMAIN 703 752 KAL.
FT NP_BIND 65 73 ATP (BY SIMILARITY).
FT BINDING 88 88 ATP (BY SIMILARITY).
FT ACT_SITE 181 181 BY SIMILARITY.
FT VARSPLIC 628 752 ADEPERIGPEVTSCHLPWDQETETAPRLLRFPWSVKLTSSR
PPEALMALROATAAARCRROPOPLACIHGAGGPEPL
SHFEVEVCQLPRPGLRGVLFRRVAGTALAFTLVTRISNDL
EL -> TLDPKRONSNRCVSGASLPGSKIRSQTNLRESG
DLRSQVAIYLGIRKKPPPGCSDSPGV (in isoform
2).
FT /FTid=VSP 004946.
FT F -> S (IN REF. 2).
FT CONFLICT 70 70
SQ SEQUENCE 752 AA; 82519 MW; 4B430FFD2B150E7A CRC64;
Query Match 27.4%; Score 737.5; DB 1; Length 752;
Best Local Similarity 42.7%; Pred. No. 1.5e-44;
Matches 163; Conservative 52; Mismatches 122; Indels 45; Gaps 6;
QY 16 NYNLGRTLGIGTFGKVKIAEHKLTGHRVAIKIINCRQMRNMEMEAKREFKILKLFHP 75
DB 58 NYRLRLRTIGKGNPAKVKLARHILTGREVAIKIIDKTOL-NPSSLQKLFREVRIMKGLNHP 116
QY 76 HIIRLYEVIYPTDIYVVMYCKYGELEFDYIVEKGRLOEDEARRIFQOIISGVEYCHRM 135
DB 117 NIVKLFVEVIEKTLVLYVMEYASAGEVDYLVSHGRMKEKEARAKFRQIVSAVHYCHQKN 176
QY 136 VVHRDLKPENLILDSKYNVVLADFGLSNVMDGHFLKTS CGSPNYAABEVISGLYAGPE 195
DB 177 IVHRDLKAENLLDABANIKIADFGFSNFTLGSKLDTF CGSPPYAABELFGKKYDGE 236

QY 196 VDWSCGVLTYALCGTLPEDDENIPNLFKKIKGIYTLPSHLSALARDLIPRMVVEPM 255
DB 237 VDIWSLGVILYTLVSGSLPFDGHNLEKLRERVLRGKYRVPFYMYSTDCESILRRFLVLPNA 296
QY 256 KRITIREIREHOWFOI-----RLPRYLAVPPPTTQQAkWIDEDTLRDVVMNGFNKNHVC 310
DB 297 KRCTLEQIMKDKWINIGVEGELKPY-----TEPEDEFGDTKRIEVMVGMYTKEIK 349
QY 311 ESLCSRLQNEATVAYVYLLDNRFRATSGYLGAQYQESMDRNLNQLA-----SSE 359
DB 350 ESLTSQKNEVTATYLL-----LGRKTEEGDRGAPGLALARVRAPSDTTNGT 397
QY 360 SSSSGTRNYVPGSSDPHSSGLR 381
DB 398 SSSSKGT-----SHSKGOR 410

RESULT 14

SNIL_HUMAN STANDARD; PRT; 786 AA.
AC P57059;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine protein kinase SNF1LK (EC 2.7.1.-).
GN SNF1LK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; Pubmed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
RA Shenthan A., Sasaki T., Shibuya K., Kawasaki K., Asakawa S.,
RA Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
RA Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecher H.,
RA Ramser J., Beck A., Klages S., Hennig S., Rieselsmann L., Dagand E.,
RA Wehmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehmach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21."
RL Nature 405:311-319(2000).
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.
CC SNF1 subfamily.
CC -1- SIMILARITY: Contains 1 UBA domain.
CC -----
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CC -----
DR EMBL; AP001751; BAA95536.1; -.
DR HSSP; P24941; 1A01.
DR Genew; HGNC:11142; SNF1LK.
DR MIM; 605705; -.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_Thr_kin_AS.
DR InterPro; IPR002290; Ser_Thr_kinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR SMART; SM00165; UBA; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 27 281 PROTEIN KINASE.
FT DOMAIN 306 346 UBA.
FT NP_BIND 33 41 ATP (BY SIMILARITY).
FT BINDING 56 56 ATP (BY SIMILARITY).
FT ACT_SITE 149 149 BY SIMILARITY.
SQ SEQUENCE 786 AA; 85252 MW; FB4EE7CAF87CB1A CRC64;

Query Match 27.4%; Score 737.5; DB 1; Length 786;
Best Local Similarity 36.3%; Pred. No. 1.6e-44;
Matches 179; Conservative 75; Mismatches 164; Indels 75; Gaps 12;

QY 2 DGSSKSGHSEALR--NYNLGRTLGIGTGGKYKIAEHKLTGHRVAIKINCRQNMME 59
DB 10 DPAGQGQGQKPLRVGYFDIERTLGKGNFAVVKLARHRTKTQVAIKIIDTRLDSSNL- 68
QY 60 EKAKREFKILKLFTHPHIIRLYEVIYPTDIYVMEYCKYGEIPDYIVEKGRLOEDEARR 119
DB 69 EKIVREVQLMKLHNPHIKLYQVMEYKDMYVTEFAKNGEMFDYLTSGHLSSENEARK 128
QY 120 IFOQIISGVEYCHRNVVHARDLKPENILDSKYNVLA---DFGLSNVMDGHFLKTS CG 176
DB 129 KFWQILSAVEYCHDHIVHRDLKTENLLDGNNDIKLAGTEDFGFGNFYKSGEPLSTWCG 188
QY 177 SPNYAAPEVISGKLYAGPEVDVWSCGVLTYALCGTLPEDDENIPNLFKKIKGIYTLPS 236
DB 189 SPPIAAPEVFEKGEYEGPQDLIWSLGVLYLVCGSLPFDGPNLPTLRQVLEGRFRIPF 248
QY 237 HLSALARDLIPRMVVEPMKRITIREIREHOWFO-----IRLPRYLAVPPPTTQQAkWID 292
DB 249 FMSQDCESLIRRMVVDPARRITIAQIRQHRMWAEPCLPGPACPAFSASHTSNLGDYD 308
QY 293 EDTLRDVMNGFNKNHVCESLCSRLQNEATVAYVYLLDNRFRATSGYLGAQYQESMDRNL 352
DB 309 EQALGIMQTLGVDRQRTVESLQNSSYNHFAIYLLLE-----RL 348
QY 353 NQLASSESSSG--TRNYVPGSSDPHSSGLRPYEVERKVALGLQSR-----AHPREI 403
DB 349 KEYRNAQCARPGAPRQPRRSSD--LSGLE--VPQE-----GLSTDPFRPALLCPQPOTL 399
QY 404 MVEVLKALQEL-----NVRWKKNGHYNVKC-----RWCPGFPE 436
DB 400 VQSVLQAEMLDCELSLQWPLFPVPDASCSSGVFRPRVSPSSLLDTAISBEARQGPGLBE 459
QY 437 VNDTLDAASNPLG 449
DB 460 EQDTQESLPSSTG 472

RESULT 15

SNIL_RAT STANDARD; PRT; 776 AA.
ID SNIL_RAT
AC Q9R1U5; Q9R081;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine protein kinase SNF1LK (EC 2.7.1.-) (Salt-
DE inducible protein kinase) (Protein kinase KID2).
GN SNF1LK OR SIK OR KID2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
RX MEDLINE=99330184; Pubmed=10403390;
RA Wang Z., Takemori H., Halder S.K., Nonaka Y., Okamoto M.;
RT "Cloning of a novel kinase (SIK) of the SNF1/AMPK family from high
RT salt diet-treated rat adrenal."
RT FEBS Lett. 453:135-139(1999).


```
RN [2]
RP SEQUENCE FROM N.A.
RA Feldman J.D., Vician L., Crispino M., Hoe W., Baudry M.,
RA Herschman H.R.
RT "The Kid2 gene encodes a protein kinase induced by depolarization in
RT brain."
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -1- SIMILARITY: Contains 1 UBA domain.
CC -----
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CC -----
DR EMBL; AB020480; BAA82673.1; -.
DR EMBL; AF106937; AAF14191.1; -.
DR HSSP; P24941; 1A01.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_kin_AS.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00069; kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50030; UBA; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 27 278 PROTEIN KINASE.
FT DOMAIN 303 343 UBA. (BY SIMILARITY).
FT NP BIND 33 41 ATP (BY SIMILARITY).
FT BINDING 56 56 ATP (BY SIMILARITY).
FT ACT SITE 149 149 BY SIMILARITY.
FT CONFLICT 473 473 R -> K (IN REF. 2).
SQ SEQUENCE 776 AA; 84908 MW; 7BF745AF28F17E6E CRC64;

Query Match 27.2%; Score 731.5; DB 1; length 776;
Best Local Similarity 45.6%; Pred. No. 4.2e-44;
Matches 151; Conservative 56; Mismatches 115; Indels 9; Gaps 4;

QY 7 GSGHSEALR--NYNLGRTLGIGTFGKVKIAEHKLTGHRVAIKIINCROMNMEMEKAKR 64
Db 15 GGGQQKPLRVGFYDVERTLGKGFVAVKLARHRYTKQVAIKIIDKTRLDSSNL-EKIYR 73

QY 65 EFKILKLFHPIHRIIRLYEVIYPTDIYVVMYCKYGGELFDYIVEKGRLOEDEARRIFQOI 124
Db 74 EVQLMKLLNHPNIILKYQVETKMDLYIVTEPAKNGEMFDYLTSGHLSSENAKKFWOI 133

QY 125 ISGVEYCHRMNVVHRDLKPENLLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNYAAPE 184
Db 134 LSAVEYCHNHIIVHRDLKTENLLDGMMDIKLADFGFNFKPGEPLSTWCGSPPYAAPB 193

QY 185 VTSGKLYAGPEVDVWSCGVILYALLCGTLFPDDENIPNLFKKIKGIIYTLPSHLSALARD 244
Db 194 VFEQKEYEGPQLDIWSLGVLYLVCGSLPFDGPNLPTLRQRLVLEGRFRIPFPMISQDCET 253

QY 245 LIPRLVVEPMKRITITIREIHEQWFOIRLPRYLAVPPDPTTQQAQM-----IDEDTLRDV 299
Db 254 LIRMLVVDPAKRITITIAQIRQHRMQAD-PTLLQDDPAFSMQGYTSNLGDVNEQVLGIM 312

QY 300 VMMGFNKNHVCESLCSRLQNEATVAYYLLD 330
Db 313 QALGIDRQRTVESLQNSSYNHFAIYYLLE 343
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2004, 17:54:00 ; Search time 52 Seconds
(Without alignments)
3046.990 Million cell updates/sec

Title: US-09-857-522B-4
Perfect score: 2693
Sequence: 1 MDGSSKSGHSEALRNYNLG.....GPQLFLDFCAFLTKLRYL 509

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|--------|-------------|-----------|----------------------|-------------------|
| 1 | 2693 | 100.0 | 509 | US-10-183-687-236 | Sequence 236, App |
| 2 | 2693 | 100.0 | 513 | US-10-425-114-58891 | Sequence 58891, A |
| 3 | 2422 | 89.9 | 509 | US-10-183-687-401 | Sequence 401, App |
| 4 | 2422 | 89.9 | 509 | US-10-437-963-152150 | Sequence 152150, |
| 5 | 2411.5 | 89.5 | 508 | US-10-437-963-152149 | Sequence 152149, |
| 6 | 2411.5 | 89.5 | 525 | US-10-425-114-49946 | Sequence 49946, A |
| 7 | 2378 | 88.3 | 531 | US-10-183-687-256 | Sequence 256, App |
| 8 | 1977 | 73.4 | 505 | US-10-183-687-402 | Sequence 402, App |
| 9 | 1977 | 73.4 | 505 | US-10-437-963-183463 | Sequence 183463, |
| 10 | 1974.5 | 73.3 | 514 | US-10-183-687-248 | Sequence 248, App |
| 11 | 1963 | 72.9 | 504 | US-10-183-687-407 | Sequence 407, App |
| 12 | 1958 | 72.7 | 570 | US-10-183-687-240 | Sequence 240, App |
| 13 | 1945 | 72.2 | 549 | US-10-425-114-63632 | Sequence 63632, A |
| 14 | 1939 | 72.0 | 515 | US-10-183-687-252 | Sequence 252, App |
| 15 | 1937 | 71.9 | 545 | US-10-425-114-62429 | Sequence 62429, A |

| | | | | | | |
|----|--------|------|-----|----|----------------------|-------------------|
| 16 | 1931 | 71.7 | 579 | 12 | US-10-183-687-238 | Sequence 238, App |
| 17 | 1922.5 | 71.4 | 482 | 12 | US-10-425-114-52351 | Sequence 52351, A |
| 18 | 1890.5 | 70.2 | 523 | 12 | US-10-183-687-258 | Sequence 258, App |
| 19 | 1881.5 | 69.9 | 514 | 12 | US-10-183-687-408 | Sequence 408, App |
| 20 | 1748 | 64.9 | 530 | 12 | US-10-425-114-47097 | Sequence 47097, A |
| 21 | 1654 | 61.4 | 515 | 12 | US-10-424-599-180405 | Sequence 180405, |
| 22 | 1462.5 | 54.3 | 356 | 12 | US-10-424-599-181075 | Sequence 181075, |
| 23 | 1148 | 42.6 | 552 | 9 | US-09-824-735-4 | Sequence 4, Appli |
| 24 | 1013.5 | 37.6 | 633 | 9 | US-09-824-735-3 | Sequence 3, Appli |
| 25 | 1013.5 | 37.6 | 633 | 9 | US-09-801-368-338 | Sequence 338, App |
| 26 | 1013.5 | 37.6 | 633 | 15 | US-10-369-493-1696 | Sequence 1696, Ap |
| 27 | 898 | 33.3 | 679 | 15 | US-10-369-493-22764 | Sequence 22764, A |
| 28 | 894.5 | 33.2 | 622 | 15 | US-10-369-493-5806 | Sequence 5806, Ap |
| 29 | 881.5 | 32.7 | 420 | 15 | US-10-369-493-3864 | Sequence 3864, Ap |
| 30 | 802 | 29.8 | 438 | 16 | US-10-437-963-196592 | Sequence 196592, |
| 31 | 758 | 28.1 | 268 | 15 | US-10-369-493-13344 | Sequence 13344, A |
| 32 | 749 | 27.8 | 783 | 9 | US-09-815-915-2 | Sequence 2, Appli |
| 33 | 749 | 27.8 | 783 | 14 | US-10-393-316-2 | Sequence 2, Appli |
| 34 | 749 | 27.8 | 826 | 12 | US-10-425-114-54182 | Sequence 54182, A |
| 35 | 746 | 27.7 | 744 | 9 | US-09-919-585-3 | Sequence 3, Appli |
| 36 | 745 | 27.7 | 729 | 14 | US-10-142-356-11 | Sequence 11, Appl |
| 37 | 745 | 27.7 | 729 | 14 | US-10-195-101-33 | Sequence 33, Appl |
| 38 | 745 | 27.7 | 729 | 14 | US-10-161-565-26 | Sequence 26, Appl |
| 39 | 737.5 | 27.4 | 639 | 12 | US-10-016-248-71 | Sequence 71, Appl |
| 40 | 737.5 | 27.4 | 639 | 12 | US-10-016-248-72 | Sequence 72, Appl |
| 41 | 737.5 | 27.4 | 688 | 16 | US-10-276-645-8 | Sequence 8, Appli |
| 42 | 737.5 | 27.4 | 703 | 12 | US-10-016-248-70 | Sequence 70, Appl |
| 43 | 737.5 | 27.4 | 752 | 9 | US-09-835-081-2 | Sequence 2, Appli |
| 44 | 737.5 | 27.4 | 752 | 15 | US-10-258-106-16 | Sequence 16, Appl |
| 45 | 737.5 | 27.4 | 752 | 16 | US-10-276-645-7 | Sequence 7, Appli |

ALIGNMENTS

RESULT 1
US-10-183-687-236
; Sequence 236, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B81458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 236
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Zea mays
US-10-183-687-236

Query Match 100.0%; Score 2693; DB 12; Length 509;
Best Local Similarity 100.0%; Pred. No. 2.9e-227;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDGSSKSGHSEALRNYNLGRITLIGTFGKYIAEHKLTGHRVAIKIINCRQRMMEEE 60

|||||
Db 1 MDGSSKSGHSEALRNYNLGRITLGITFGKVKIAEHKLTGHRVAIKINCRQMRNMEME 60
Qy 61 KAKREFKILKLFIRPHIIRLYEVIYPTDIYVVMCKYGELEFDYIVERKRLQDEARRI 120
Db 61 KAKREFKILKLFIRPHIIRLYEVIYPTDIYVVMCKYGELEFDYIVERKRLQDEARRI 120
Qy 121 FQOIISGVEYCHRNMVVHRDLKPENLLDSKYNVKLADFGLSNMVMDGHFLKTS CGSPNY 180
Db 121 FQOIISGVEYCHRNMVVHRDLKPENLLDSKYNVKLADFGLSNMVMDGHFLKTS CGSPNY 180
Qy 181 AAPEVISGKLYAGPEVDWVSCGVILYALLCGTLPFDENIPNLFKKIKGIYTLPSHLSA 240
Db 181 AAPEVISGKLYAGPEVDWVSCGVILYALLCGTLPFDENIPNLFKKIKGIYTLPSHLSA 240
Qy 241 LARDLIPRMLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQOAKMIDEDTLRDVV 300
Db 241 LARDLIPRMLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQOAKMIDEDTLRDVV 300
Qy 301 NMGFNKNHVCESLCSRLQNEATVAYLLLDNRFRAATSGYLGAADYQESMDRNLNQLASSES 360
Db 301 NMGFNKNHVCESLCSRLQNEATVAYLLLDNRFRAATSGYLGAADYQESMDRNLNQLASSES 360
Qy 361 SSSGTRNYPGSSSDPHSSGLRPPYVERKWKALGLQSRAPREIMVEVLKALQELNVRWK 420
Db 361 SSSGTRNYPGSSSDPHSSGLRPPYVERKWKALGLQSRAPREIMVEVLKALQELNVRWK 420
Qy 421 NGHYNVCKRCWCPGFPEVNDTLDAASNFLGDSITMDNDANGRLPTVIKFEFQLYXTKDDK 480
Db 421 NGHYNVCKRCWCPGFPEVNDTLDAASNFLGDSITMDNDANGRLPTVIKFEFQLYXTKDDK 480
Qy 481 YLLDMQRTGPQLLFLDFCAAFITKLRVL 509
Db 481 YLLDMQRTGPQLLFLDFCAAFITKLRVL 509

RESULT 2
US-10-425-114-58891
; Sequence 58891, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 58891
; LENGTH: 513
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700473306_FLI.pep
US-10-425-114-58891

Query Match 100.0%; Score 2693; DB 12; Length 513;
Best Local Similarity 100.0%; Pred. No. 3e-227;
Matches 509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDGSSKSGHSEALRNYNLGRITLGITFGKVKIAEHKLTGHRVAIKINCRQMRNMEME 60
Db 5 MDGSSKSGHSEALRNYNLGRITLGITFGKVKIAEHKLTGHRVAIKINCRQMRNMEME 64
Qy 61 KAKREFKILKLFIRPHIIRLYEVIYPTDIYVVMCKYGELEFDYIVERKRLQDEARRI 120
Db 65 KAKREFKILKLFIRPHIIRLYEVIYPTDIYVVMCKYGELEFDYIVERKRLQDEARRI 124

Qy 121 FQOIISGVEYCHRNMVVHRDLKPENLLDSKYNVKLADFGLSNMVMDGHFLKTS CGSPNY 180
Db 125 FQOIISGVEYCHRNMVVHRDLKPENLLDSKYNVKLADFGLSNMVMDGHFLKTS CGSPNY 184
Qy 181 AAPEVISGKLYAGPEVDWVSCGVILYALLCGTLPFDENIPNLFKKIKGIYTLPSHLSA 240
Db 185 AAPEVISGKLYAGPEVDWVSCGVILYALLCGTLPFDENIPNLFKKIKGIYTLPSHLSA 244
Qy 241 LARDLIPRMLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQOAKMIDEDTLRDVV 300
Db 245 LARDLIPRMLVVEPMKRITIREIREHWFQIRLPRYLAVPPDPTQOAKMIDEDTLRDVV 304
Qy 301 NMGFNKNHVCESLCSRLQNEATVAYLLLDNRFRAATSGYLGAADYQESMDRNLNQLASSES 360
Db 305 NMGFNKNHVCESLCSRLQNEATVAYLLLDNRFRAATSGYLGAADYQESMDRNLNQLASSES 364
Qy 361 SSSGTRNYPGSSSDPHSSGLRPPYVERKWKALGLQSRAPREIMVEVLKALQELNVRWK 420
Db 365 SSSGTRNYPGSSSDPHSSGLRPPYVERKWKALGLQSRAPREIMVEVLKALQELNVRWK 424
Qy 421 NGHYNVCKRCWCPGFPEVNDTLDAASNFLGDSITMDNDANGRLPTVIKFEFQLYXTKDDK 480
Db 425 NGHYNVCKRCWCPGFPEVNDTLDAASNFLGDSITMDNDANGRLPTVIKFEFQLYXTKDDK 484
Qy 481 YLLDMQRTGPQLLFLDFCAAFITKLRVL 509
Db 485 YLLDMQRTGPQLLFLDFCAAFITKLRVL 513

RESULT 3
US-10-183-687-401
; Sequence 401, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B81458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 401
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: gi 4107001
US-10-183-687-401

Query Match 89.9%; Score 2422; DB 12; Length 509;
Best Local Similarity 88.6%; Pred. No. 1.7e-203;
Matches 451; Conservative 35; Mismatches 23; Indels 0; Gaps 0;
Qy 1 MDGSSKSGHSEALRNYNLGRITLGITFGKVKIAEHKLTGHRVAIKINCRQMRNMEME 60
Db 1 MEGNARGGSHSEALKNYNLGRITLGITFGKVKIAEHKLTGHRVAIKILNRQMRNMEME 60

| | | | |
|----|-----|--|-----|
| QY | 61 | KAKREFKILKLFIFHHIIRLYEVIYPTDIYVMMEYCKYGELEFDYIVEKRLQJDEBARRI | 120 |
| Db | 61 | KAKREIKILRLFIHPIHIRLYEVIYPTDIYVMMEYCKYGELEFDYIVEKRLQJDEBARRI | 120 |
| QY | 121 | FQOIISGVEYCHRNWVVRHDLKPENLLDSKXNVKLADFGLSNVMDGHILKTS CGSPNY | 180 |
| Db | 121 | FQOIISGVEYCHRNWVVRHDLKPENLLDSKXNVKLADFGLSNVMDGHILKTS CGSPNY | 180 |
| QY | 181 | AAPEVISGKLYAGPEVDWVSCGVILYALLCGTLPEDDENIPNLFKKIKGGIYTLPSHLSA | 240 |
| Db | 181 | AAPEVISGKLYAGPEVDWVSCGVILYALLCGTLPEDDENIPNLFKKIKGGIYTLPSHLSA | 240 |
| QY | 241 | LARDLIPRMLVVEPMKRITIREIREHQMFOIRLPRYLAVPPDDTTOQAKMIDEDTLRDVV | 300 |
| Db | 241 | LARDLIPRMLVVDPMKRITIREIREHQMFOIRLPRYLAVPPDDTTOQAKMIDEDTLQDVV | 300 |
| QY | 301 | NMGFNKNHVCESLCSRLONEATVAYLLLDNRFRAATSGYLADYQESMDRNLNQLASSES | 360 |
| Db | 301 | NLGXEKDHVCESLRNRLQNEATVAYLLLDNRFRAATSGYLADYQESLERNLNRFASSSES | 360 |
| QY | 361 | SSSGTRNVVPGSSSDPHSSGLRPPYVPERKMWALGLOSRAHPREIMVEVLKALQELNVRWKK | 420 |
| Db | 361 | AASNTRHYLLPGSSSDPHASGLRPHYVPERKMWALGLOSRAQPREIMIEVLKALIEDLNVCMKK | 420 |
| QY | 421 | NGHYNVKCRWCPGFPEVNDTLDASNSFLGSDSTIMDNDANGRLPTVYKKEFPQLYKTKDK | 480 |
| Db | 421 | NGQYNMKCRWSVGYPQATDMLDVNHSFVDDSTIMDNGDVNGRLPAVYKKEFQLYKSRDEK | 480 |
| QY | 481 | YLLDMQRVVTGPQLLFLDFFCAAFITKLRVL | 509 |
| Db | 481 | YLLDMQRVVTGPQLLFLDFFCAAFITKLRVL | 509 |

```

RESULT 4
US-10-437-963-152150
; Sequence 152150, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152150
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52229C.1.pep
US-10-437-963-152150

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| | Query Match | 89.9% | Score 2422; | DB 16; | length 509; |
|----|---|------------------|---------------------|-----------|-------------|
| | Best Local Similarity | 88.6%; | Pred. No. 1.7e-203; | | |
| | Matches 451; | Conservative 35; | Mismatches 23; | Indels 0; | Gaps 0; |
| QY | 1 MDGSSKSGSHSEALRNYNLGRITGIGTFGVKIAEHKLTHGRVAIKIINCRQRMNMEMEE | 60 | | | |
| | ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | | | | |
| Dd | 1 MEGNARGGGHSEALKKNYNLCRTLIGISFGVKIAEHLTGHRVAIKILNRQRMRNMEMEE | 60 | | | |
| QY | 61 KAKREFKILKLFIIHPHIIRLYEVIYTPTDIYVMEYCKYGELFDYIVEKGRLQDEARRI | 120 | | | |
| | ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: | | | | |
| Dd | 61 KAKREIKILRLFIIHPHIIIRLYEVITYPTDIYVMEYCKFGEFLDYIVEKGRLQDEARRI | 120 | | | |

| | | | |
|----|-----|---|-----|
| QY | 121 | FOOIISGVEYCHRRNMVVRHDLKPENLILLDSKYNVKLADFGLSNVMDHGHLKTS CGSPNY | 180 |
| Db | 121 | FOOIISGVEYCHRRNMVVRHDLKPENLILLDSKYNVKLADFGLSNVMDHGHLKTS CGSPNY | 180 |
| QY | 181 | AAPEVISGKLYAGPEVDWMSGVILYALLCGTLPEDDENIPNLFKKIKGGIYTLPSHLSA | 240 |
| Db | 181 | AAPEVISGKLYAGPEVDWMSGVILYALLCGTLPEDDENIPNLFKKIKGGIYTLPSHLSA | 240 |
| QY | 241 | LARDLIPRLVVEPMKRITITREIREHQWFQIRLPRYLAVPPBDTTOQAKMIDEDTLRDVY | 300 |
| Db | 241 | LARDLIPRLVVDPMKRITITREIREHQWFQIRLPRYLAVPPBDTAQQAKMIDEDTLQDVY | 300 |
| QY | 301 | NMGFNKNHVCESLCSRLONEATVAYLLLDNRFRATSGYIGADYQESMDRNLNQLASSES | 360 |
| Db | 301 | NMGVEKDHVCESLRNRLONEATVAYLLLDNRFRATSGYIGADYQESLERNLNRFASSSES | 360 |
| QY | 361 | SSSGTRNVVPGSSDPHSSGLRPYYVERKMAI GLQSRAPREIMVEVLKALQELNVRWKK | 420 |
| Db | 361 | ASSNTRHYLLPGSSDPHASGLRPHYVERKMAI GLQSRAPREIMIEVLKALDELNVCMKK | 420 |
| QY | 421 | NGHYNVKCRWCPGFPEVNDTLDASNSFLGDSITMDNDANGRLPTVIKFEFQLYTKDKDK | 480 |
| Db | 421 | NGQYNMKCRWMSGVYFQATMDLVDVHNSFVDDSIIMDNGDVNGRLPAVIKFEIQLYKS RDEK | 480 |
| QY | 481 | YLLDMQRTVGPOLLFLDFCAAFITKLRLV | 509 |
| Db | 481 | YLLDMQRTVGPOLLFLDFCAAFITKLRLV | 509 |

```

RESULT 5
US-10-437-963-152149
; Sequence 152149, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 152149
; LENGTH: 508
;
; TYPE: PRT
; ORGANISM: Oryza sativa
;
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52228C.1.pep
US-10-437-963-152149

```

[illegible]

||||| 181 AAPEVISGKLYAGPEVDWSCGVLTYALLCGTLFPDDENIPNLFKKIKGGIYTLPSHLSA 240
QY 241 LARDLIPRMLVVEPMKRITIREIREHQMFOIRLPRYLAVPPDPTQQAAMIDEDTLRDV 300
Db 241 LARDLIPRMLVVEPMKRITIREIREHQMFOIRLPRYLAVPPDPTQQAAMIDEDTLQDV 300
QY 301 NMGFNKNHVCESLCSRLQNEATVAYLLLDNRFRAATSGYLQADYQESMDRNLNQLASSES 360
Db 301 NLGYGKDHVCESLRNRLQNEATVAYLLLDNRFRAATSGYLQADYQESLERNFNRFASSES 360
QY 361 SSSGTRNYPGSSDPHSSGLRPYPYVERKMWALGLQRAHPREIMVEVLKALQELNVRWK 420
Db 361 ASSNTRHYLPGSSDPHASGLRPHYVERKMWALGLQRAQPREIMIEVLKALQDLNVSWK 420
QY 421 NGHYNVKCRWCPGPEVNDTLDAASNFLGDSITMDNDANGRLPTVIKFEFQLYXTKDX 480
Db 421 NGQYNMKCRMSVG-TQATDMLDVNNSFVDSIIMDNGDVNGRLPAVIKEIQLYKTRDEX 479
QY 481 YLLDMQRYTGPQLLFLDFCAAFITKLRVL 509
Db 480 YLLDMQRYTGPQLLFLDFCADFLTCLRVL 508

RESULT 6
US-10-425-114-49946
; Sequence 49946, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49946
; LENGTH: 525
; TYPE: PRT
; ORGANISM: Oryza sativa nipponbare
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3477-009-G7_FLI.pep
US-10-425-114-49946

Query Match 89.5%; Score 2411.5; DB 12; Length 525;
Best Local Similarity 89.0%; Pred. No. 1.5e-202;
Matches 453; Conservative 29; Mismatches 26; Indels 1; Gaps 1;
QY 1 MDGSSKSGSHSEALRNYNLGRITLGITFGKVIAEHKLTGHRVAIKIINCRQRMNMEME 60
Db 18 MDGNAGKGSHSEALKYVNLGRTLGISFGKVIAEHKLTGHRVAIKILNRQRMNMEME 77
QY 61 KAKREFKILKFIHPHIIRLYEVIYPTDIYVMEYCKYGEIYVEKRLQDEARRI 120
Db 78 KAKREIKILRLFIHPHIIRLYEVIYPTDIYVMEYCKYGEIYVEKRLQDEARRI 137
QY 121 FQOIISGVEYCHRNMYVHARDLKPENLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNY 180
Db 138 FQOIISGVEYCHRNMYVHARDLKPENLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNY 197
QY 181 AAPEVISGKLYAGPEVDWSCGVLTYALLCGTLFPDDENIPNLFKKIKGGIYTLPSHLSA 240
Db 198 AAPEVISGKLYAGPEVDWSCGVLTYALLCGTLFPDDENIPNLFKKIKGGIYTLPSHLSA 257
QY 241 LARDLIPRMLVVEPMKRITIREIREHQMFOIRLPRYLAVPPDPTQQAAMIDEDTLRDV 300
Db 258 LARDLIPRMLVVEPMKRITIREIREHQMFOIRLPRYLAVPPDPTQQAAMIDEDTLQDV 317

QY 301 NMGFNKNHVCESLCSRLQNEATVAYLLLDNRFRAATSGYLQADYQESMDRNLNQLASSES 360
Db 318 NLGYGKDHVCESLRNRLQNEATVAYLLLDNRFRAATSGYLQADYQESLERNFNRFASSES 377
QY 361 SSSGTRNYPGSSDPHSSGLRPYPYVERKMWALGLQRAHPREIMVEVLKALQELNVRWK 420
Db 378 ASSNTRHYLPGSSDPHASGLRPHYVERKMWALGLQRAQPREIMIEVLKALQDLNVSWK 437
QY 421 NGHYNVKCRWCPGPEVNDTLDAASNFLGDSITMDNDANGRLPTVIKFEFQLYXTKDX 480
Db 438 NGQYNMKCRMSVG-TQATDMLDVNNSFVDSIIMDNGDVNGRLPAVIKEIQLYKTRDEX 496
QY 481 YLLDMQRYTGPQLLFLDFCAAFITKLRVL 509
Db 497 YLLDMQRYTGPQLLFLDFCADFLTCLRVL 525

RESULT 7
US-10-183-687-256
; Sequence 256, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B81458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 256
; LENGTH: 531
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-183-687-256

Query Match 88.3%; Score 2378; DB 12; Length 531;
Best Local Similarity 86.8%; Pred. No. 1.3e-199;
Matches 442; Conservative 34; Mismatches 33; Indels 0; Gaps 0;
QY 1 MDGSSKSGSHSEALRNYNLGRITLGITFGKVIAEHKLTGHRVAIKIINCRQRMNMEME 60
Db 23 MEGNTRGGHSDALKYVNLGRTLGITFGKVIAEHKLTGHRVAIKILNRQRMNMEME 82
QY 61 KAKREFKILKFIHPHIIRLYEVIYPTDIYVMEYCKYGEIYVEKRLQDEARRI 120
Db 83 KAKREIKILRLFIHPHIIRLYEVIYPTDIYVMEYCKYGEIYVEKRLQDEARRI 142
QY 121 FQOIISGVEYCHRNMYVHARDLKPENLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNY 180
Db 143 FQOIISGVEYCHRNMYVHARDLKPENLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNY 202
QY 181 AAPEVISGKLYAGPEVDWSCGVLTYALLCGTLFPDDENIPNLFKKIKGGIYTLPSHLSA 240
Db 203 AAPEVISGKLYAGPEVDWSCGVLTYALLCGTLFPDDENIPNLFKKIKGGIYTLPSHLSA 262
QY 241 LARDLIPRMLVVEPMKRITIREIREHQMFOIRLPRYLAVPPDPTQQAAMIDEDTLRDV 300
Db 263 LARDLIPRMLVVEPMKRITIREIREHQMFOIRLPRYLAVPPDPTQQAAMIDEDTLKEIV 322

[illegible]

```

RESULT 8
US-10-183-687-402
; Sequence 402, Application US/10183687
; Publication No. US20030204870A1
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Allen, William B.
APPLICANT: Cahoon, Rebecca
APPLICANT: Epelbaum, Sabine
APPLICANT: Famodu, Omolayo O.
APPLICANT: Harvell, Leslie T.
APPLICANT: Jones, Todd
APPLICANT: Kinney, Tony
APPLICANT: Klein, Ted
APPLICANT: Li, Changjiang
APPLICANT: Oliveira, Igor Cunha
APPLICANT: Sakai, Hajime
APPLICANT: Shen, Bo
APPLICANT: Tarczyński, Mitchell C.
FILE OF INVENTION: Alteration Of Oil Traits In Plants
FILE REFERENCE: BB1458 US NA
CURRENT APPLICATION NUMBER: US/10/183,687
CURRENT FILING DATE: 2002-06-27
PRIOR APPLICATION NUMBER: 60/301,913
PRIOR FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 532
SOFTWARE: Microsoft Office 97
SEQ ID NO 402
;
; LENGTH: 505
;
; TYPE: PRT
;
; ORGANISM: Oryza sativa
;
; FEATURE:
;
; NAME/KEY: misc_feature
;
; LOCATION:
;
; OTHER INFORMATION: gi 4107009
US-10-183-687-402

```

| | Query Match | 73.4% | Score 1977; | DB 12; | Length 505; |
|----|--|------------------|---------------------|-----------|-------------|
| | Best Local Similarity | 74.1%; | Pred. No. 1.8e-164; | | |
| | Matches 377; | Conservative 52; | Mismatches 76; | Indels 4; | Gaps 2, |
| Qy | 1 MDGSSKSGHSEALRNYNLGRITIGTGFVKIAEHKLTHGRVAIKIINCRORMMEMEE | 60 | | | |
| Dd | 1 MEGAGR--DGNPLGGYRIGKTILGIGSFGKVKIAEHLTGHRVAIKILNRRAIKSMEMEE | 57 | | | |
| Qy | 61 KAKREFKILKFIFPHIIRLEVIYTPTDIYVMEYCKYGELDYIVEKGRLQEDEARRI | 120 | | | |
| Dd | 58 KYKREIKILRLFMHPIIRLEVIDTPADIYVMEYKSGELDYIVEKGRLQEEEARRF | 117 | | | |
| Qy | 121 FQQIISGVVEYCHRRNMVVHBDLKPENLLDSKYNVKLADEFGLSNVMHDGHFLKTS | 180 | | | |
| Dd | 118 FQQIISGVVEYCHRRNMVVHBDLKPENLLDSKCNVKIADFGLSNVMRDGHFLKTS | 177 | | | |
| Qy | 181 AAPEVISGKLYAGPEVDWSCGVLTYALLCGTLPFDDENIPNLFKKIKGIYTLPSHTSA | 240 | | | |

| | | | |
|----|-----|---|-----|
| Db | 178 | AAPEVISGKLYAGPEVDVWSCGVILLYALLCGTLPFDDENIPNLFKIKIGGIYTLPSHLS | 237 |
| Qy | 241 | LARDLIPRLVVEPMKRITIREIREHQMFOIRLPRYLAVPPDITTOAKMIDEDTLRDV | 300 |
| Db | 238 | LARDLIPRLVDPMKRITIREIREHQMFTVGLPRYLAVPPDITTOAKMDDETLDV | 297 |
| Qy | 301 | NMGFNKNHVCESLCSRLQNEATVAYLLLDNRFRATSGYLGADYQESMDRNLQLASSES | 360 |
| Db | 298 | NMGFDKNQOLIESLHKRLQNEATVAYLLLDNRRLRTTSGYLGAEFHESMESSLAQVTPAET | 357 |
| Qy | 361 | SSSGTRNYVPSSSDPHSSGRLPYPERK ¹ KWALGLQSRAPPREIMVEVLKALQELNVRWKK | 420 |
| Db | 358 | PNSATDHRQHGHMESPFGELRHHPAADRKWALGLQSRAPPREIITEVLKALQELNVCWKK | 417 |
| Qy | 421 | NGHYNVKCRWCPGFPEVNDTLDASNSFLGDSTIMDNDANGRLPTVIKPEFOLYKTKDK | 480 |
| Db | 418 | IGHYNMKCRWSPSPFSHESMHNHNGFGAESAIIETDDSEKSTHTV-KFEIQLYKTRDEK | 476 |
| Qy | 481 | YLLDMQ ² RV ² TGPQLLFLDFCAFLTKLRVL | 509 |
| Db | 477 | YLLDLQ ² RVSGPQLLFLDLCSAFLTQLRVL | 505 |

```

RESULT 9
US-10-437-963-183463
; Sequence 183463, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 183463
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_80552C.1.pep
US-10-437-963-183463

```

| | Query Match | 73.4%; | Score 1977; | DB 16; | Length 505; | |
|----|--|------------------|---------------------|-----------|-------------|--|
| | Best Local Similarity | 74.1%; | Pred. No. 1.8e-164; | | | |
| | Matches 377; | Conservative 52; | Mismatches 76; | Indels 4; | Gaps 2 | |
| Qy | 1 MDGSSKSGSHSEALRNYNLGRTLGITGFQVKIAEHKLGTGRVAIKIINCRÖRMNMEMEE | 60 | | | | |
| Db | 1 MEGAGR---DGNPLGGYRIKLTIGISFGKVKIAEHLTGHKVAKILNRRAIKSMEMEE | 57 | | | | |
| Qy | 61 KAKREFKI.LFIHPHILRLYEVIYTPTDIYVMVEYCKYGELFDYIVEKGRLQEDEARRI | 120 | | | | |
| Db | 58 KVKREIKILRLFEMPHILRLYEVIDTPADIYVMEYVKSGLFDYIVEKGRLQEEEARRF | 117 | | | | |
| Qy | 121 FQÖIIISGV EYCHRRNVVHRDLKPENLLDSKNVNVLADFGLSNMVMDGHFLKTS CGSPNY | 180 | | | | |
| Db | 118 FQÖIIISGV EYCHRRNVVHRDLKPENLLDSKCNVKIADFGLSNMVRDGHFLKTS CGSPNY | 177 | | | | |
| Qy | 181 AAPEVISGKLYAGPEVDVWSCGVL YALLCGTLPDDENIPNLFKKIKGGIYTLPSHLSA | 240 | | | | |
| Db | 178 AAPEVISGKLYAGPEVDVWSCGVL YALLCGTLPDDENIPNLFKKIKGGIYTLPSHLSP | 237 | | | | |
| Qy | 241 LARDLIPRMLVVEPMKRITIREIREHÖWFÖIRLPRYLAVPPDTTQÖAKMIDEDTLRDVV | 300 | | | | |
| Db | 238 LARDLIPRMLVVEPMKRITIREIREHÖWFTVGLPRYLAVPPDTAQÖVKLLDDETLLNDVI | 297 | | | | |

| | | | |
|----|-----|---|-----|
| QY | 301 | NMGENKNHVCESLCSRLÖNEATVAYLLLDNFRPATSGYLGDADYÖESMDRNLNQLASSES | 360 |
| Db | 298 | NMGFDKQÖLIESLHKRLÖNEATVAYLLLDNRILRTTSGYLGAEFHESMESSLAÖYTPAET | 357 |
| QY | 361 | SSGCTENVVPGGSDPHSSGLRPYYPVERKALGLÖSRAHPREIMEVLKALOELNVWKK | 420 |
| Db | 358 | PNSATDHRÖGHMESPGFGLRHHPAADRKVALGLÖSRAHPREIITEVLKALOELNVCKKK | 417 |
| QY | 421 | NGHYNVKRCWCPGFPEVNNDTLDASNSFLGDSTIMDNDDANGRLPTVIKFEFÖLYKTOKDK | 480 |
| Db | 418 | IGHYNMKCROWSPSFPESHESMMHNHGFGAESAIETDDSEKSTHTV-KFEIQLYXTRDEK | 476 |
| QY | 481 | YLLDMÖRVGTGPÖLLFLDFCAAFITKLRYL | 509 |
| Db | 477 | YLLDLÖRVSGPÖLLFLDLCSAFLTÖQLRYL | 505 |

```

RESULT 10
US-10-183-687-248
; Sequence 248, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: BBI458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 248
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Glycine max
US-10-183-687-248

```

| | | | | |
|-----------------------|--------------|-------------------|----------------|-------------|
| Query Match | 73.3%; | Score 1974.5; | DB 12; | Length 514; |
| Best Local Similarity | 74.0%; | Pred. No. 3e-164; | | |
| Matches 382; | Conservative | 49; | Mismatches 76; | Indels 9; |
| | | | | Gaps 3; |

[illegible]

```

Db      241  SPGARDLIPGMLVVDPMRRMTIPEIRQHPWFQARLPRYLLAVPPBDTMOQAKKIDEEILOE 300

Qy      299  VVNMGFNKNHVCESLCSRLONEATVAYLLLDNRFRTSGYLGADYQESMDRNLNQLASS 358
        301  VYKMGFDRNQLVESTLGNRIQNEGTVAYLLLDNRFRVSSGYLGAEFQETMDSGFMHSS 360

Qy      359  ESSSSGTRNYVPGSSDPHSSGLRPYYVERKMWALGLQSRAPREIMVEVLKALQELNVRW 418
        361  ELASSVVGNRFPGYMEYPGVGSROQFVERKMWALGLQSRAPREIMTEVLKALQELNVCW 420

Qy      419  KKNQHYNVKCRWCPCGFP-----EVNDTLDASNSFLGDSTIMDNNDANGRLPTVIKFEFOL 473
        421  KKI GHYNMKCRWVAGIPGHHEGMVNNNVHNSHHYFGDDSNIIENDAVS--TSNVKFEVQL 478

Qy      474  YKTKDDKYLLDMQRVTPGPOLLFLDFCAAFLLTKLRVL 509
        479  YKTBREKYLLDLQRVQGPQFLFLDLCAAFLLAQLRVL 514

```

```

RESULT 11
US-10-183-687-407
; Sequence 407, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B1458 US MA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 407
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Cucumis sativus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: gi 1743009
US-10-183-687-407

```

| | | | | |
|-----------------------|------------------|-------------------|-----------|-------------|
| Query Match | 72.9%; | Score 1963; | DB 12; | Length 504; |
| Best Local Similarity | 74.8%; | Pred. No. 3e-163; | | |
| Matches 374; | Conservative 53; | Mismatches 65; | Indels 8; | Gaps 4; |

[illegible]

```
Db 187 VDWSCGVILYALLCGTLPEDDENI PNLFKIKGIGYTLPSHLSSGARELIPSM LVDEM 246
QY 256 KRITIREIHOWFOIRLPRYLAVPPDPTQOAKMIDEDTLRDVNMGFKNHVCESLCS 315
Db 247 KRITIREIHOWFOIRLPRYLAVPPDPTQOAKMIDEDTLRDVNMGFKNHVCESLCS 306
QY 316 RLONEATVAYLLLDNRFRTSGYLGAADYQESMDRNLNQLASSESSSGTRNYPGSSDP 375
Db 307 RLONEATVAYLLLDNRFRTSGYLGAADYQESMDRNLNQLASSESSSGTRNYPGSSDP 366
QY 376 HSSGLRPYPVERKWAIGOSRAHPREIMVEVLKALQELNVKKNNGHYNVKCRWCPGFP 435
Db 367 QGMGLRAQFVERKWAIGOSRAHPREIMTEVLKALRELNVKKNNGHYNVKCRWCPGFP 426
QY 436 -----EVNDTLDA SFLGD-STIMDNDANGRLPTVIKFEFQLYKTKDKYLLDMQRT 489
Db 427 GHHEGMINNPVH-SNHYFGDKSTIIENDGV-VKSPNVIKFEVQLYKTREEKYLLDLQRVQ 484
QY 490 GPQLLFLDFCAFLTCLRVL 509
Db 485 GPQLLFLDFCAFLTCLRVL 504
```

RESULT 12

```
US-10-183-687-240
; Sequence 240, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B01458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 240
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Zea mays
US-10-183-687-240
```

```
Query Match 72.7%; Score 1958; DB 12; Length 570;
Best Local Similarity 74.8%; Pred. No. 9.7e-163;
Matches 382; Conservative 48; Mismatches 67; Indels 14; Gaps 6;
QY 1 MDGSSKSGSHSEALRNYNLGRITIGTGFVKVIAEHKLTGHRVAIKIINCRQMRNMEME 60
Db 72 MEGAGK--DGNPLRNRYRIKTLGIGSFGKVKIAEHISTGHKVAIKILNRRKIRGMEEMB 128
QY 61 KAKREFKILKLFHPHIIIRLYEVITYPTDIYVVMYCKYGE LFDYIVEKGRLOEDEARRI 120
Db 129 KVKREIKILRLFMHPHIIIRLYEVIDTPADIYVVMYCKYGE LFDYIVEKGRLOEDEARRI 188
QY 121 FQOIISGVEYCHRNWVVRDLKPE NLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNY 180
Db 189 FQOIISGVEYCHRNWVVRDLKPE NLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNY 248
```

```
QY 181 AAPEVISGLYAGPEVDVWSCGVILYALLCGTLPEDDENI PNLFKIKGIGYTLPSHLISA 240
Db 249 AAPEVISGLYAGPEVDVWSCGVILYALLCGTLPEDDENI PNLFKIKGIGYTLPSHLISG 308
QY 241 LARDLIPRLVPEPMKRITIREIHOWFOIRLPRYLAVPPDPTQOAKMIDEDTLRDVY 300
Db 309 AARDLIPRLVPEPMKRITIREIHOWFOIRLPRYLAVPPDPTQOAKMIDEDTLRDVY 368
QY 301 NMGFKNHVCESLCSRLONEATVAYLLLDNRFRTSGYLGAADYQESMDRNLNQLASSE- 359
Db 369 GMGYDKNLVLESIOKRLONEATVAYLLLDNRLRTTSGYLGAECQEA MDSFSNIASYET 428
QY 360 -SSSSGTRNYPGSSDPHSSGLRPYPVERKWAIGOSRAHPREIMVEVLKALQELNVW 418
Db 429 PSSARGNRQOIFMES---PVGLRPHLPAERKWAIGOSRAHPKEIMSEVLKALQELNVW 485
QY 419 KKNGHYNVKCRWCPGPEVNDTLDA SFLGDSTIMDNDANGRLPTVIKFEFQLYKTKD 478
Db 486 KKGHYNVKCRWSPGPEPA---QIHNNHNFSA GS--IETDSLSERL-SLIKFEIQLYKTRD 539
QY 479 DKYLLDMQRTVGPQLLFLDFCAFLTCLRVL 509
Db 540 EKYLLDLQRVSGPQLLFLDFCAFLTCLRVL 570
```

RESULT 13

```
US-10-425-114-63632
; Sequence 63632, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63632
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE089A07_FLI.pep
US-10-425-114-63632
```

```
Query Match 72.2%; Score 1945; DB 12; Length 549;
Best Local Similarity 73.3%; Pred. No. 1.3e-161;
Matches 373; Conservative 54; Mismatches 76; Indels 6; Gaps 3;
QY 1 MDGSSKSGSHSEALRNYNLGRITIGTGFVKVIAEHKLTGHRVAIKIINCRQMRNMEME 60
Db 47 MEGAGR--DANPLSGYRIKTLGIGSFGKVKIAEHILTGHKVAIKILNRRKIRSMDEE 103
QY 61 KAKREFKILKLFHPHIIIRLYEVITYPTDIYVVMYCKYGE LFDYIVEKGRLOEDEARRI 120
Db 104 KVKREIKILRLFMHPHIIIRLYEVIDTPADIYVVMYCKYGE LFDYIVEKGRLOEDEARRI 163
QY 121 FQOIISGVEYCHRNWVVRDLKPE NLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNY 180
Db 164 FQOIISGVEYCHRNWVVRDLKPE NLLDSKYNVKLADFGLSNVMDGHFLKTS CGSPNY 223
QY 181 AAPEVISGLYAGPEVDVWSCGVILYALLCGTLPEDDENI PNLFKIKGIGYTLPSHLISA 240
Db 224 AAPEVISGLYAGPEVDVWSCGVILYALLCGTLPEDDENI PNLFKIKGIGYTLPSHLISP 283
QY 241 LARDLIPRLVPEPMKRITIREIHOWFOIRLPRYLAVPPDPTQOAKMIDEDTLRDVY 300
Db 284 SARDLIPRLVPEPMKRITIREIHOWFOIRLPRYLAVPPDPTQOAKMIDEDTLRDVY 343
```

```
QY      301 NMGFENKNHVCESLCSRLONEATVAYYLILDNFRPATSGYLGADYOESMDRNLNQLASSES   360
        |||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      344 KMGFDKNOIIESLONRLONEATVAYYLLIDNRLRTTSGYLGSEFOESMDSFSQVI-AET    402

QY      361 SSSGTENVYPGSSDPHSSGLRPYYPVERKALGLQSRAPREIMVEVLKALOELNVRWKK     420
        :||:||||:|||||::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      403 PLSATELRQHGFSESPGSGLRQHFHAERKVALGLQSRAPREIISEVLKALOELNVWKK       462

QY      421 NGHYNVKCRWCPCGFPEVNDTLDASNSFLGDSTIMDNDANGRLPTVIKFEEFOLYKTKDK    480
        |||::|||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|||||
Db      463 IGHYNMKCRWSPGCLE--SMHMNSDSFSAEAIIEITDVFMEEKSTPTVKFEILOLYKTRDEK  520

QY      481 YLLDMQRVTGPOLLFLDFCAAFLTKLRYL   509
        |||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      521 YLLDLQRVSGSHLLFLDLCSAFLTQLRYL   549
```

RESULT 14
US-10-183

```

; Sequence 252, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B1458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 252
; LENGTH: 515
; TYPE: PRT
; ORGANISM: Glycine max
US-10-183-687-252

```

| | | | | |
|-----------------------|------------------|---------------------|------------|-------------|
| Query Match | 72.0%; | Score 1939; | DB 12; | length 515; |
| Best Local Similarity | 72.1%; | Pred. No. 3.9e-161; | | |
| Matches 373; | Conservative 58; | Mismatches 76; | Indels 10; | Gaps 4; |

```

QY      1 MDGSS-KGSCHS--EALRNYNLGRTLIGTFEGKYKIAEHKLTGHRVAIKINCROMNME 57
      || : : | | | | | | | | | | | | | | | | : : ||
Db      1 MDRSTGRGGGGSVDMFLRNYKLGKTLGIGSFEGKYIAEHVRTGHKVAIKILNRHKIKNME 60
QY      58 MEEKAKREEFKILKLFIPHIIRLYEVIYTPPTDIYVMEYCKYGE LFDYIVEKGRLOEDEA 117
      ||| : | | | : | | | : | | | | | | | | | | | | |
Db      61 MEEKVREIKILRLFMHHIIRLYEVETPTDIYVMEYKSGELFDYIVEKGRLOEDEA 120
QY      118 RRIFOQIISGVEYCHRRNVVHRDLKPENLLDSKYNVKLADFGLSNVMDHGHFLKTS CGS 177
      | | | | | | | | | | | | | | | | : : | | | | | | |
Db      121 RHFFOQIISGVEYCHRRNVVHRDLKPENLLDSKFNKIADFGLSNIMRDGHFLKTS CGS 180
QY      178 PNYAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPPDDENIPNLFKKIKGITYLPSH 237
      | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 PNYAPEVISGKLYAGPEVDVWSCGVILYALLCGTLPPDDENIPNLFKKIKGITYLPSH 240
QY      238 L$ALARDLIPRLVPEPMKRITIREIREH$WFQIRLPRYLA VPPDDTTQ$AKMIDEDTLR 297
      || | | | | | | | | : | | | : | | | : | | | | | | | | : | :

```

| | | | |
|----|-----|--|-----|
| Db | 241 | LSFGARDLI PRMLVDDPMKRMTIPEIRQHPWFQVHLPRYLAVPPBDTLQQAKKIDEIILQ | 300 |
| QY | 298 | DVVMGFMKNHVCESLCSRLONEATVAYLLLLDNRFRATSGYLGADYQESMDRNLQOLAS | 357 |
| Db | 301 | EVMVMGFDRNLQVLESLNRIQNEGIVTYLLLLDNRFRVSSGYLGAEFQETMDSGFNMHS | 360 |
| QY | 358 | SESSSSGTRNVYPGSSDPHSSGLRPYTVVERKMWALGLQSRAPHPREIMVEVLKALQELNVR | 417 |
| Db | 361 | GEVASPVGHHSTGYMDYQGVGMKQOFVERKMWALGLQSRAPQPREIMTEVLKALQELNVC | 420 |
| QY | 418 | WKKNGHYNNVKCRWCPCGFP-----EYNDITLDASNSFLGDSITIMDNDANGRLPTVIKFEFQ | 472 |
| Db | 421 | WKKIIGHYNNMKCRWAVAGTAGHHEGMINNSLSHNHYFGNDSGI IENEAVS--KSNVVKFEVQ | 478 |
| QY | 473 | LYTKTDKYLILDMQRYVTGPOLLFLDFCAAFLTIKLRVL | 509 |
| Db | 479 | LYKTREEKYLILDLQRVQGFQFLFLDLCAAFLSQLRVL | 515 |

RESULT 15

```

US-10-425-114 62429
; Sequence 62429, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425, 114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62429
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700204782_FLI.pep
US-10-425-114-62429

```

| | | | | |
|-----------------------|------------------|---------------------|------------|-------------|
| Query Match | 71.9%; | Score 1937; | DB 12; | Length 545; |
| Best Local Similarity | 72.8%; | Pred. No. 6.3e-161; | | |
| Matches 374; | Conservative 56; | Mismatches 68; | Indels 16; | Gaps 5; |

[illegible]

| | | | |
|----|-----|---|-----|
| Db | 400 | TSATEHRQHVFTESPG-----SGLRQHFASERKVALGLQSRAPREIISEVTKALQELN | 453 |
| Qy | 416 | VRWKGNHYNVCKRCWCPGFPEVNDTLDASNSFLGDSITMDNDANGRLPTVIAKFEFQLYK | 475 |
| Db | 454 | VYWKKIGHYNNMKCRNSPGCLE--SMANCDGFSAESAI IETDDLIAKSTRIVKFEIQLYK | 511 |
| Qy | 476 | TKDDKYLLDMQRTVTFPQLLFLDFCAAFLTCLRVL | 509 |
| Db | 512 | TRDEKYLLDLQRVSGPQLLFLDLCSAFLTQLRVL | 545 |

Search completed: July 7, 2004, 17:58:14
Job time : 54 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 9, 2004, 11:24:34 ; Search time 629 Seconds
(without alignments)
3437.731 Million cell updates/sec

```

Title: US-09-857-522B-4
Perfect score: 2693
Sequence: 1 MDGSSKSGSHSEALRNYNG.....GPQLLFDFCAFLTKLRVL 509

```

| Scoring table: | | |
|----------------|----------|-------------|
| | BLOSUM62 | |
| Xgapop | 10.0 | Xgapext 0.5 |
| Ygapop | 10.0 | Ygapext 0.5 |
| Fgapop | 6.0 | Fgapext 7.0 |
| Delop | 6.0 | Delext 7.0 |

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

Command line parameters:

```

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO_spool/US09857522/runat_07072004_161356_1862/app_query.fasta.1.647
-DB=N_Geneseq_29Jan04 -QFMT=fastlap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09857522 @CGN 1 1 470 @runat_07072004_161356_1862 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGADEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGADEXT=0.5 -DELOP=6 -DELEXT=7

```

```
Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result | § | | | | Description | |
|--------|--------|-------------|--------|----|-------------|--------------------|
| No. | Score | Query Match | Length | DB | ID | |
| 1 | 2693 | 100.0 | 1948 | 3 | AAa52768 | AAa52768 Corn puta |
| 2 | 2693 | 100.0 | 1948 | 7 | ACC00743 | ACC00743 Zea mays |
| 3 | 2378 | 88.3 | 1899 | 7 | ACC00753 | ACC00753 Trilicium |
| 4 | 1974.5 | 73.3 | 2123 | 3 | AAa52772 | AAa52772 Soybean p |
| 5 | 1974.5 | 73.3 | 2123 | 7 | ACC00749 | ACC00749 Glycine m |
| 6 | 1969.5 | 73.1 | 1539 | 6 | ABZ14852 | Abz14852 Arabidops |
| 7 | 1942 | 72.1 | 2052 | 7 | ACC00745 | ACC00745 Zea mays |
| 8 | 1939 | 72.0 | 2543 | 3 | AAa52774 | Aaa52774 Soybean p |

| | | | | | | |
|----|--------|------|------|---|----------|--------------------|
| 9 | 1939 | 72.0 | 2543 | 7 | ACC00751 | ACC00751 Glycine m |
| 10 | 1937.5 | 71.9 | 1929 | 4 | AAF62011 | Aaf62011 Tomato Le |
| 11 | 1931 | 71.7 | 2107 | 3 | AAA52769 | Aaa52769 Corn puta |
| 12 | 1931 | 71.7 | 2107 | 7 | ACC00744 | Acc00744 Zea mays |
| 13 | 1923 | 71.4 | 1536 | 2 | AAQ47789 | Aaq47789 SHP gene |
| 14 | 1903.5 | 70.7 | 1539 | 6 | ABZ12357 | Abz12357 Arabidops |
| 15 | 1903.5 | 70.7 | 1792 | 3 | AAC44825 | Aac44825 Arabidops |
| 16 | 1899.5 | 70.5 | 1825 | 6 | AAL46639 | Aal46639 A thalian |
| 17 | 1891.5 | 70.2 | 1825 | 6 | AAL46642 | Aal46642 A thalian |
| 18 | 1890.5 | 70.2 | 2006 | 3 | AAA52777 | Aaa52777 Wheat put |
| 19 | 1890.5 | 70.2 | 2006 | 7 | ACC00754 | Acc00754 Triticum |
| 20 | 1869.5 | 69.4 | 1539 | 6 | AAI71048 | Aai71048 Arabidops |
| 21 | 1545.5 | 57.4 | 1485 | 3 | AAC46066 | Aac46066 Arabidops |
| 22 | 1537 | 57.1 | 3550 | 6 | AAL46640 | Aal46640 A thalian |
| 23 | 1529 | 56.8 | 3550 | 6 | AAL46641 | Aal46641 A thalian |
| 24 | 1267 | 47.0 | 944 | 9 | ADC75707 | Adc75707 DNA homol |
| 25 | 1187.5 | 44.1 | 817 | 3 | AAA52776 | Aaa52776 Wheat put |
| 26 | 1148 | 42.6 | 1783 | 2 | AAQ76198 | Aaq76198 cDNA of h |
| 27 | 1144 | 42.5 | 2761 | 2 | AAQ76197 | Aaq76197 cDNA of r |
| 28 | 1139 | 42.3 | 3079 | 4 | AAS60973 | Aas60973 Human can |
| 29 | 1119 | 41.6 | 1647 | 9 | ADB52890 | Adb52890 Primary r |
| 30 | 1115 | 41.4 | 1647 | 2 | AAT85925 | Aat85925 Mammalian |
| 31 | 1109 | 41.2 | 2663 | 4 | ABL05573 | Abi05573 Drosophil |
| 32 | 1101.5 | 40.9 | 1698 | 9 | ADB61362 | Adb61362 Clone of |
| 33 | 1013.5 | 37.6 | 1902 | 7 | ACC60983 | Acc60983 Gene sequ |
| 34 | 1004.5 | 37.3 | 5277 | 9 | ABL05572 | Abi05572 Drosophil |
| 35 | 971 | 36.1 | 915 | 4 | ADC07761 | Adc07761 Rice DNA |
| 36 | 817.5 | 30.4 | 986 | 6 | ABN98495 | Abn98495 Arabidops |
| 37 | 773 | 28.7 | 2000 | 9 | ADC08538 | Adc08538 Rice DNA |
| 38 | 749 | 27.8 | 2352 | 4 | AAI66823 | Aai66823 Human pro |
| 39 | 749 | 27.8 | 2968 | 4 | AAI66822 | Aai66822 Human pro |
| 40 | 749 | 27.8 | 4699 | 5 | AAH76213 | Aah76213 Human kin |
| 41 | 746 | 27.7 | 2193 | 7 | AAD51406 | Aad51406 Human mic |
| 42 | 746 | 27.7 | 2271 | 6 | AAD30396 | Aad30396 Human PAR |
| 43 | 745 | 27.7 | 2632 | 3 | AAx82952 | Aax82952 Human ker |
| 44 | 745 | 27.7 | 2190 | 4 | AAF44654 | Aaf44654 Novel pro |
| 45 | 745 | 27.7 | 2698 | 2 | AAV03002 | Aav03002 Human Twe |

ALIGNMENTS

```

RESULT 1
AAAS2768
ID   AAAS2768 standard; cDNA; 1948 BP.
XX
AC   AAAS2768;
XX
DT   03-JAN-2001 (first entry)
XX
DE   Corn putative catabolite repression protein SNF1 coding sequence #2.
XX
KW   Corn; carbon catabolite repression; sucrose non-fermenting protein 1;
XX   SNF1; plant growth; ss.
XX
OS   Zea mays.
XX
FH   Key Location/Qualifiers
FT   CDS 173..1702
FT   FT /*tag= a
FT   FT /product= "SNF1"
XX
PN   WO200036115-A2.
XX
PD   22-JUN-2000.
XX
PF   15-DEC-1999; 99WO-US029824.
XX
PR   16-DEC-1998; 98US-0112563P.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ;
PI   Miao G;

```


XX MPI; 2000-431593/37.
DR P-PSDB; AAB03416.

XX New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
PT involved in carbon catabolite repression in plants and seeds, useful for
PT controlling carbon and nitrogen partitioning pathways during plant growth
PT and development.

XX Claim 2; Page 34-35; 59pp; English.

CC The present sequence is a putative sucrose non-fermenting protein SNF1
CC coding sequence from corn. The sequence was isolated by searching a corn
CC cassel shoot cDNA library for sequences similar to those encoding SNF1 in
CC Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The
CC protein is involved in carbon catabolite repression, and so the gene and
CC protein can be used in plants to control the nitrogen and carbon
CC partitioning pathways during plant growth and development. They can also
CC be used to alter the accumulation of carbohydrates, lipids and proteins
CC during plant growth

XX Sequence 1948 BP; 572 A; 380 C; 461 G; 535 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1 38e-264 Length: 1948
Score: 2693.00 Matches: 509
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-857-522B-4 (1-509) x AAAS2768 (1-1948)

QY 1 MetAspGlySerSerIySGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
DB 173 ATGATGGAAGTACGTAAGGAGTGGCATCTGAAGCATTAAAGAACTAACACTGGGA 232
QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
DB 233 AGAAGCTTAGGTATCGTACATTGGAAAAGTGAAGATTGCAGAGCATTAAGCTTACTGA 292
QY 41 HisArgValAlaIleLysIleIleAsnGlySerGlnMetArgAsnMetGluMetGlu 60
DB 293 CATAGGGTTGCTATTAAGATCATCAACTGCCGCCAATGAGAAATATGAAATGGAAGAG 352
QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
DB 353 AAAGCAAGAGAGAAATCAAGATATTGAAGTTGTTCAFTCACCCCATATCATTCGGCTT 412
QY 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly 100
DB 413 TATGAGTCATATACACACCTACAGATATATGTTGTGATGGAATATTGTAAGTATGGC 472
QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
DB 473 GAGTTATTGATTAATGTTGTGAGAAAGCAGATTACAGAAAGATGAAGCTCGTCGAATC 532
QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAsp 140
DB 533 TTCCAGCAGATCATATCTGGCGTCGATACTGCCATAGAAACATGGTTGCCACCGTGAC 592
QY 141 LeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
DB 593 CTAAAGCCGGAACCTTGTACTTGATTCAAGTATTAATGTAACCTTGCCGATTTTGGT 652
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
DB 653 CTGAGCAATGTCATGATGATGCGCATTTTCTGAAGACTAGCTGTGGAGTCCGAATAT 712
QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSer 200
DB 713 GCTGCTCCAGAGGTATATCTGTGAATACTATATCTGGAACCTGAGGTGATGTATGAGT 772

QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
DB 773 TGTGGGGATCTTTATGCTCTTCTTTGTGGAACTCTTCCATTGATGATGAGAATATT 832
QY 221 ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
DB 833 CCCAATCTGTCAAAAAAATTAAGGAGGTATCTACACACTTCCAAGTCATTGTCTGCT 892
QY 241 LeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIleThrIle 260
DB 893 TTGGCCAGGATTTGATCCACGAACTGCTGTGTGAGCCCTTGAAGAATCACAAATT 952
QY 261 ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
DB 953 AGGGAATTCGGGAGCATCAATGGTCCAGATTGCCCTTCCAGTTACTTGCGAGTGCC 1012
QY 281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal 300
DB 1013 CCACCAGATACGACACACAAAGCCAAATGATTGATGAAGATACACTTCGAGATGTGTT 1072
QY 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
DB 1073 AATATGGATTTAACAAGAACCATGTGTGTAATCACTGTGACAGACACTTCAAAATGAG 1132
QY 321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
DB 1133 GCAACTGTTCATATTATTACTATTGGAACAATCGGTTTAGAGCAACTAGTGCTATCTT 1192
QY 341 GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer 360
DB 1193 GGGCAGATTATCAAGATCAATGAGACAGAAATTAATCAGCTGGCGTCATCTGAATCA 1252
QY 361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
DB 1253 TCTAGTTCTGTGTAAGGAAATTATGTTCCAGGAAGCAGTGATCTCATAGCAGTGTTG 1312
QY 381 ArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAlaHisPro 400
DB 1313 CGGCATATTATCTCTGTGAAGAAATGCGCGCTTGACCTTGACTCTCGGGCCACCTT 1372
QY 401 ArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrpLysLys 420
DB 1373 CGTGAATATAGTTGAGGCTTTAAAGCACTTCAAGAAATTAAAGTCAGATGGAAGAG 1432
QY 421 AsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsnAspThr 440
DB 1433 AATGGGCACCTACAAAGTGAATGAGTGTGCCAGGGTTTCTGAACTTAATGACACAG 1492
QY 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
DB 1493 TTAGATGCCGACAACAGCTTCTTGTGAGACTCTACCATCATGATGAATGATGATTAAT 1552
QY 461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLysAspAspLys 480
DB 1553 GGGAGGCTTACTACTGTGATCAAGTTGAATTCCAGCTTTACAGACGAGACGACAAG 1612
QY 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
DB 1613 TACCTCTTAGATATGACAGAGATTACTGGAACCTCAGCTGCTTCTTGACTTGTGCG 1672
QY 501 AlaPheLeuThrLysLeuArgValLeu 509
DB 1673 GCCTTCTTACCAAGCTTAGGGTTCTA 1699

RESULT 2
ACC00743 ID ACC00743 standard; cDNA; 1948 BP.
XX ACC00743;
AC ACC00743;
DT 16-MAY-2003 (first entry)
XX Zea mays oil trait related cDNA sequence SEQ ID NO:235.
DE

XX Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CKC-like transcription factor; antisense inhibition; co-suppression;
KW transgenic plant; gene; ss.
XX
OS Zea mays.
XX WO2003002751-A2.
XX
XX 09-JAN-2003.
XX
XX 27-JUN-2002; 2002WO-US020152.
XX
XX 29-JUN-2001; 2001US-0301913P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.
XX
XX Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT,
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B,
PI Tarczynski MC;
XX
XX WPI; 2003-201509/19.
XX P-PSDB; ABR40708.
XX
XX Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
XX Claim 18; Page 272-273; 542pp; English.

XX The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention

XX Sequence 1948 BP; 572 A; 380 C; 461 G; 535 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.38e-264 Length: 1948
Score: 2693.00 Matches: 509
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-857-522B-4 (1-509) x ACC00743 (1-1948)

QY 1 MetAspGlySerSerlysglyserglyhisserglualaleuArgAsnTyrAsnleugly 20
DB 173 ATGATGGAAGTAGTAAGGAGGTGGCATCTGAAGCATTAAGGAAGCACTGGGA 232
QY 21 ArgThrleuglylleglythrphneglylysvallysilealaglunhislyseuthrgly 40
DB 233 AGAAGCTTAGGTATCGGTACATTTGGAAAAGTGAAGATGACAGACATTAAGCTTACTGA 292
QY 41 HisArgValAlaIlelysilileleasnCybArgGlnMetArgAsnMetGlnMetGluGlu 60

DB 293 CATAGGGTTGCTATTAAGATCATCACTGCCGCCAATGAGAAATATGAAATGGAAGAG 352
QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
DB 353 AAAGCAAAGAGAGATTCAGATATGAGTTGTTCATTCAACCCCAATCATTCGGCTT 412
QY 81 TyrGluValIleTyrThrProThrAspIleTyrValIleMetGluTyrCysLysTyrGly 100
DB 413 TATGAGGTATATACACACCTACAGATATATATGTGTGATGGAATATTTAAGTATGGC 472
QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
DB 473 GAGTTATTTGATTACATTGTTGAGAAAGGAGATTACAGGAAGATGAAGCTTCGTAATC 532
QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp 140
DB 533 TTCAGCAGATCATATCTGGCGTGAATACTGCCATGAAAACATGGTTGCCACCGTGAC 592
QY 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
DB 593 CTAAAGCCGGAACCTGTTACTTGATTCAAGTAAATGTAATAAACTTCGGGATTTTGGT 652
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
DB 653 CTGAGCAATGTCTATCATGATGAGCCATTTTCTGAAGACTAGCTGTGGAGTCCGAACAT 712
QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
DB 713 GCTGCTCCAGAGGTATATATCTGTTAAACTATATGCTGGAACCTGAGGTGATATGAGAGT 772
QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
DB 773 TGTGGGGTATCTTTATGCTCTTCTTGTGGAACTCTTCATTGTGATGAGAAATAT 832
QY 221 ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
DB 833 CCCAATCTGTTCAAAAAAATTAAAGGAGGTATCTACACACTTCCAAGTCAATTTGCTGCT 892
QY 241 LeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIleThrIle 260
DB 893 TTGGCCAGGATTTGATCCACGATGCTGTGTGAGCCTATGAGAGAAATCACAAATT 952
QY 261 ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
DB 953 AGGGAATTCGGAGCATCAATGTGTTCCAGATTGCCCTTCCACGTTACTTGGCAGTGCT 1012
QY 281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal 300
DB 1013 CCACGAGATACGACACAACAAGCCAAATGATGTGAGAAAGATACACTTCGAGATGTGTT 1072
QY 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
DB 1073 AATATGGATTTAAACAAGAACCATGTGTGCAATCACTGTGCAGCAGCACTTCAAAATGAG 1132
QY 321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
DB 1133 GCAACTGTGCATATATTTACTATGTGACAAATCGGTTAGAGCAACTAGTGGCTATCTT 1192
QY 341 GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer 360
DB 1193 GGGGAGATTATCAAGAATCAATGAGACAGAAATTTAAATCAGCTGGCGCTCATCTGAATCA 1252
QY 361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
DB 1253 TCTAGTTCTGTGTAAGGAATATGTTTCCAGGAAGCAAGTATCTCATAGCAAGTGTG 1312
QY 381 ArgProTyrTyrProValGluArgLysTyrAlaLeuGlyLeuGlnSerArgAlaHisPro 400
DB 1313 CGGCCATATATCTGTTGAAGAAATGCGCGCTTGACACTTCAGTCTCGGCCACCCCT 1372
QY 401 ArgGluIleMetValGluValLeuLysValLeuGlnGluLeuAsnValArgTyrLysLys 420
DB 1373 CGTGAATATATGCTGAGGCTTTAAAGCACTTCAAGAAATTAACGTCAGATGGAAGAAG 1432

QY 421 AsnglyHisTyraSnVallysCySarqTTPCySProglYpHeProgluValAsnAspThr 440
Db 1433 AATGGGCACTACAAGTGAATGCAGATGGTCCAGGGTTCTCGAAGTTAATGACACG 1492
QY 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
Db 1493 TTAGATGCCAGCAACAGCTTTCTGTGACTCTACCATCATGATATGATGATCTAAT 1552
QY 461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrlsThryAspAspLys 480
Db 1553 GGAGAGCTACTACTGTGATCAAGTTGAATTCAGCTTTACAAGACGAGACGACAAAG 1612
QY 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
Db 1613 TACCTCTAGATATGCAGAGAGTAGTACTGACCTCAGCTGCTCTTCTGACTTCTGTGCG 1672
QY 501 AlaPheLeuThrLysLeuArgValLeu 509
Db 1673 GCCTTCCTTACCAGCTTAGGGTTCTA 1699

RESULT 3
ACC00753
ID ACC00753 standard; cDNA; 1899 BP.
XX ACC00753;
XX
XX
DT 16-MAY-2003 (first entry)
XX
DE Triticum aestivum oil trait related cDNA sequence SEQ ID NO:255.
XX
XX Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW LIP5-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CKC-like transcription factor; antisense inhibition; co-suppression;
transgenic plant; gene; ss.
XX
XX Triticum aestivum.
OS
XX
PN WO2003002751-A2.
XX
PD 09-JAN-2003.
XX
PF 27-JUN-2002; 2002WO-US020152.
XX
PR 29-JUN-2001; 2001US-0301913P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX (PION-) PIONEER HI-BRED INT INC.
XX
PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczyński MC;
XX
XX WPI; 2003-201509/19.
DR P-PSDB; ABR40718.
XX
XX Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
XX Claim 18; Page 296; 542pp; English.
XX
XX The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP5-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense

CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention

XX
SQ Sequence 1899 BP; 572 A; 364 C; 462 G; 501 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 1.93e-232 | Length: | 1899 |
| Score: | 2378.00 | Matches: | 442 |
| Percent Similarity: | 93.52% | Conservative: | 34 |
| Best Local Similarity: | 86.84% | Mismatches: | 33 |
| Query Match: | 88.30% | Indels: | 0 |
| DB: | 7 | Gaps: | 0 |

US-09-857-522B-4 (1-509) x ACC00753 (1-1899)

QY 1 MetAspGlySerSerLysGlySerGlyHisSerGluAlaLeuArgAsnTyraSnLeuGly 20
Db 67 ATGAAGGGAACACTAGAGAGAGGTGGCATTTCTGACGCATTAAAGAACTACAATGTGGGC 126
QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
Db 127 AGAACAATTAGGTATAGGCACATTTGGAAAAGTGAGATTGCAGACATAAGCATACAGGG 186
QY 41 HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGlu 60
Db 187 CATAAAGTGTATAAAGATTCTGAACCGTCGTCAATGAGAACTAGAAATGAGAGAG 246
QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
Db 247 AAAGCAAGAGAGAGATCAAGATATTGAGTTGTTTCATCCACCCTCATATCATCCGGCTT 306
QY 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrgly 100
Db 307 TATGAGGTCAATTACACACCCTACAGATATATTGTTGTGATGGAAATATTGCCAAGTATGCT 366
QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
Db 367 GAGCTATTGCATGTCATTGTTGAGAAAGCGGCTTACAGGAAGATGAGGCTCGTGAATC 426
QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp 140
Db 427 TTCACAGCAGTTATATCTGTTGTAATACTGCCACAGAAACATGCTGCTCATCGTAT 486
QY 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyraSnValLysLeuAlaAspPheGly 160
Db 487 CTAAGCCAGAGAACTGTTACTTGATTCGAATACATGTAAGTGAAGTGGAGCTTGGG 546
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
Db 547 TTAAGTAATGTCATGCATGATGGCCATTTCGAAGACTAGCTGCGGAGTCCAAACTAT 606
QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
Db 607 GCTGCACCAAGAGTTATCTCAGGTAATTATACGCTGGAACCTGAGTTGATGTTGAGC 666
QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
Db 667 TGGGGGTGATCTTATGCTCTTCTTGTGGCACTCTTCATTGATGATGACAAATATT 726
QY 221 ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
Db 727 CCCAACTGTTCAAAAAGATAAAGGGAGCATCTATATCTTCCAGTCAATTATCTGCT 786
QY 241 leuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIleThrIle 260
Db 787 CTTGCAAGGATTTGATCCCAAGATGCTGTTGTGATCCTATGAGAATCACAAATT 846
QY 261 ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280

||||| 847 CGTGAATTCGAGAACCCCATGTTTCAGAAATCGCCTTCCTCGCTACCTGGCAGTGCCCT 906
QY 281 ProProAspThrThrGlnGlnAlaIleAlaIleAspGluAspThrLeuArgAspValVal 300
DB 907 CCACCAGACACGGCGCAGCAAGCCAAATGATGATGAGATACACTTAAGAGATTGTC 966
QY 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
DB 967 AACCTGGATATGATTAAGACCATGTGTGTAATCATTTGTGCATAGAGCTGCAAAATGAG 1026
QY 321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
DB 1027 GCAACTGTTCATATTACTTACTCTTGACAATCGGTTCCGGCCACTAGTGGCTATTG 1086
QY 341 GLYAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer 360
DB 1087 GGGGCTGACTATCTACATCAATGGGTAGGAGTTTAATCAGTTTACTTCAATGGAAATCA 1146
QY 361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
DB 1147 GCAAGCCCAAGTACCAAGCAGATATCTCCAGCAAGCAATGATTCTCAAGGCGAGTGCTTG 1206
QY 381 ArgProTyrTyrProValGluArgLysTyrAlaLeuGlyLeuGlnSerArgAlaHisPro 400
DB 1207 CGGCCATATTACCCCGTTGAAAGAAATGGGCTTTGGGCTCCAGTCTCGAGTCAACCT 1266
QY 401 ArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTyrLysLys 420
DB 1267 CGTGAGATATGATCGAGGTTCTAAAGGCACCTCAAGAAATTAATGTCTGCTGGAAGAAG 1326
QY 421 AsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsnAspThr 440
DB 1327 AATGACACTACAACAATGAATGACAGTGTGTCCTGGGCTTCTCAGGTCAAGATATG 1386
QY 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
DB 1387 TTAGATGCCAACCAACAGCTTTGTGATGACTCTACCATCATGATTAACGGCCATGCTAAT 1446
QY 461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLysAspAspLys 480
DB 1447 GGGAGGCTACCTGCCGTGATCAAGTTGAATCCAGCTTTACAAGACCAAGATGACAAG 1506
QY 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
DB 1507 TACCTGCTAGATATGACAGAGAGTACTGACCTCAGCTCCTCTCTGGAATTTTGCGCG 1566
QY 501 AlaPheLeuThrLysLeuArgValLeu 509
DB 1567 GCCTTCCTTACCAACCTTAGGGTCTTA 1593

RESULT 4
AAA52772
ID AAA52772 standard; cDNA; 2123 BP.
XX

AC AAA52772;
XX
DT 03-JAN-2001 (first entry)
XX

DE Soybean putative catabolite repression protein SNF1 coding sequence #2.
XX
KW Soybean; carbon catabolite repression; sucrose non-fermenting protein 1;
XX SNF1; plant growth; ss.
OS
XX Glycine max.
XX

FT Key Location/Qualifiers
FT CDS 123..1667
FT /*tag= a
FT /product= "SNF1"
XX

PN WO2000036115-A2.
XX

PD 22-JUN-2000.
XX
PF 15-DEC-1999; 99WO-US029824.
XX
PR 16-DEC-1998; 98US-0112563P.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ;
PI Miao G;
XX
DR WPI; 2000-431593/37.
DR P-PSDB; AAB03420.
XX
PT New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
PT involved in carbon catabolite repression in plants and seeds, useful for
PT controlling carbon and nitrogen partitioning pathways during plant growth
PT and development.
XX
PS Claim 2; Page 42-43; 59pp; English.
XX
CC The present sequence is a putative sucrose non-fermenting protein SNF1
CC coding sequence from the soybean. The sequence was isolated by searching
CC a pod cDNA library for sequences similar to those known to encode SNF1 in
CC Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The
CC protein is involved in carbon catabolite repression, and so the gene and
CC protein can be used in plants to control the nitrogen and carbon
CC partitioning pathways during plant growth and development. They can also
CC be used to alter the accumulation of carbohydrates, lipids and proteins
CC during plant growth
XX
SQ Sequence 2123 BP; 593 A; 395 C; 477 G; 658 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 3.59e-191 Length: 2123
Score: 1974.50 Matches: 382
Percent Similarity: 83.53% Conservative: 49
Best Local Similarity: 74.03% Mismatches: 76
Query Match: 73.32% Indels: 9
DB: 3 Gaps: 3
US-09-857-522B-4 (1-509) x AAA52772 (1-2123)
QY 1 MetAspGlySerSer-----LysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsn 18
DB 123 ATGATGAGACCAAGCTGGCCGAGGTGGTGGCTTGACATGTTTCTACCAATATATAA 182
QY 19 LeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeu 38
DB 183 TTGGGAAAACACTCGGATTGGATCTTTGGCAAGGTGAAAATTGCAGAACATGTGTTG 242
QY 39 ThrGlyHisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMet 58
DB 243 ACTGGCCATTAAGGTTGCGATCAAGATCTTAAACGACGCAAGATTAAGAACATGAAATG 302
QY 59 GluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIle 78
DB 303 GAAGAAAAGTGAGAAAGAGAAATCAAAATTTAAGATTGTTCAATGATCCTCACATTATT 362
QY 79 ArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLys 98
DB 363 CGACTTTATGAAGTCATAGAACTCCAACTGACATATATGTTGATGAGATGTGAAG 422
QY 99 TyrGlyLysLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArg 118
DB 423 TCTGAGAGCTTTTCGATTACATAGTAGAAGAGGTAGCTTGCGAAGATGAAGCTCGT 482
QY 119 ArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHis 138
DB 483 AATTTTTCAGACAGATTAATCTCTGGGCTGAGTACTGTCAACAGGAATATGTGTTTCA 542
QY 139 ArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAlaAsp 158

Db 543 AGAGATTGAAGCCTGAGAATTACTTTGGACTCCAAATGTAATGTCAGATTGCTGAT 602

Qy 159 PheGlyLeuSerAsnValMethHisAspGlyHisPheLeuLysThrSerCysGlySerPro 178
|||||
:::|
Db 603 TTTGGCTGAGCAACATCATGCGTGATGGTCACTTCTTAAACAAGTTGTGAAGCCCT 662

Qy 179 AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspVal 198
|||||
|||||
Db 663 AACTATGACGCTCCTGAGGTTATCTCTGGAAATGTATGCTGACCTGAAGTGATGTC 722

Qy 199 TrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGlu 218
|||||
|||||
Db 723 TGGAGCTGTGGTGAATTTTATATAGCCCTTCTTGTGGCACCCTTCTTGTGATGATGAA 782

Qy 219 AsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeu 238
|||||
|||||
Db 783 AATATTCCAAATCTCTTCAAGAAATAAGGGTGGATTTACACTCTTCCCACTCATCTA 842

Qy 239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIle 258
|||||
|||||
Db 843 TCACCCGGTGTAGAGATTGATACAGAGGATGCTTGTGGTACCTTAAGAGAGAAATG 902

Qy 259 ThrIleArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAla 278
|||||
|||||
Db 903 ACCATACCTGAGATCCGTCAACACCCATGGTTCCAAGCTCGACTTCACGTTATTAGCT 962

Qy 279 ValProProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAsp 298
|||||
|||||
Db 963 GTGCCACCACGACGATACATGCAACAGGCCAAAGAATGATGAGAGATCCCTTCAGGAA 1022

Qy 299 ValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGln 318
|||||
|||||
Db 1023 GTGTGAAATAATGGATTGACAGGAATCAATGCTGAATCTCTTGGGAACAGATACAA 1082

Qy 319 AsnGluAlaThrValAlaIleTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGly 338
|||||
|||||
Db 1083 AATGAGGGTACTGTGCATACTATTGTTATTGACAAACCGATTCTGTTTCCAGTGGC 1142

Qy 339 TyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
|||||
|||||
Db 1143 TATCTTGAGCTGATTTCAAGAGACCATGATTCGGTTTAAATCAATGCAATTCAGT 1202

Qy 359 GluSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
|||||
|||||
Db 1203 GAACCTGCTTCTTCACTGTTGTGAAACCGCTTCCAGGCTACATGAAATATCCAGAGTA 1262

Qy 379 GlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAla 398
|||||
:::|
Db 1263 GGATCGAGGCAACAGTCCCTGTGAAAGAAATGGGCCCTTGCGCTCACTCCGAGCC 1322

Qy 399 HisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrp 418
|||||
|||||
Db 1323 CATCCTCGTGAATATATGACTGAGGTTCTTAAAGCTTTCAGAATTAATGTTTGTGG 1382

Qy 419 LysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPhePro----- 435
|||||
|||||
Db 1383 AAGAAGATTGGTCACTACAACATGAAGTGAAGTGGGTGCTGGCATTCCTGGTCACCAC 1442

Qy 436 -----GluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThrIle 453
|||||
|||||
Db 1443 GAAGGAATGTTAAACAATAATGTGCATAGTAATCACTTGTGAGATGATTCCAACATT 1502

Qy 454 MetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGlnLeu 473
:::|
:::|
Db 1503 ATTGAGATGATGCTGTTCT-----ACTTCAATGTGTCAAGTTTGAAGTCAGCTT 1556

Qy 474 TyrIysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGlnLeu 493
|||||
|||||
Db 1557 TACAAACCCCGGAAGAAAGATATCTGCTTCAAAAGGTGCAGGGTCCACAGTTT 1616

Qy 494 LeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
|||||
|||||
Db 1617 CTTTCTTGATCTATGTGCTGCTTCTTCCATGACAGCTTCGTGTCCTC 1664

RESULT 5
ACCC00749
ID ACC00749 standard; cDNA; 2123 BP.
XX
XX ACC00749;
AC
XX 16-MAY-2003 (first entry)
DT
XX
DE Glycine max oil trait related cDNA sequence SEQ ID NO:247.
XX
XX Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CKC-like transcription factor; antisense inhibition; co-suppression;
KW transgenic plant; gene; ss.
XX
OS Glycine max.
XX
XX
PN MO2003002751-A2.
XX
XX 09-JAN-2003.
PD
XX
XX 27-JUN-2002; 2002MO-US020152.
PF
XX
XX 29-JUN-2001; 2001US-0301913P.
PR
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
XX Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczynski MC;
XX
XX WPI; 2003-201509/19.
DR P-PSDB; ABR40714.
DR
XX
XX

PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
XX
PS Claim 18; Page 286-287; 542pp; English.

XX
CC The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity, and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 2123 BP; 593 A; 395 C; 477 G; 658 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 3.59e-191 Length: 2123
Score: 1974.50 Matches: 382
Percent Similarity: 83.53% Conservative: 49
Best Local Similarity: 74.03% Mismatches: 76
Query Match: 73.32% Indels: 9
DB: 7 Gaps: 3

US-09-857-522B-4 (1-509) x ACC00749 (1-2123)

QY 1 MetAspGlySerSer-----LysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsn 18
Db 123 ATGATGACACGAGTGGCCGAGGTGTGCTGCTGGACATGTTCTTACCAAAATTATATAA 182
QY 19 LeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeu 38
Db 183 TTGGAAAAAACACTCGGATTGGATCTTTTGGCAAGGTGAATAATGCAGAACATGTGTG 242
QY 39 ThrGlyHisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMet 58
Db 243 ACTGCCCATAGAGTTGCCATCAAGATCCTTAACCGACGCAAGATTAAGAACATGGAATG 302
QY 59 GluGlyLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIle 78
Db 303 GAAGAAAAAGTGAAGAGAAATCAAAATTTAAGATTGTTCATGCATCCTCACATTATT 362
QY 79 ArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLys 98
Db 363 CGACTTATGAAGTCATAGAAATCCCAACTGACATATATGTTCATGAGTATGTGAAG 422
QY 99 TyrGlyGlyLeuPheAspTyrIleValGlyLysGlyArgLeuGlnGluAspGluAlaArg 118
Db 423 TCTGAGAGCTTTTGCATTAACATAGAGAAGGGTAGGTTGCAGAGAATGAGTCCGT 482
QY 119 ArgIlePheGlnGlnIleIleSerGlyValGlyTyrCysHisArgAsnMetValHis 138
Db 483 AATTTTTTTCAGCAGATATCTCTGGGGTGAAGTACTGTCAACAGAAATATGGTGTTCAT 542
QY 139 ArgAspLeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAsp 158
Db 543 AGAGATTGAAGCCTGAGAAATTACTTTTGACCTCCAAATGTATGTCAAGATTGCTGAT 602
QY 159 PheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerPro 178
Db 603 TTTGGCTTGAGCAACATCATGCGTATGTGTCACCTTCTTAAACAAGTTGTGAAGCCCT 662
QY 179 AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspVal 198
Db 663 AACTATGAGCTCTGAGGTATCTCTGGAAATGTATGCTGAGCCTGAAGTGAATGTC 722
QY 199 TrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspGlu 218
Db 723 TGGAGCTGTGTGTAATTTATATATGCCCTTCTTTGGCAACCCTTTCCTTTGATGATA 782
QY 219 AsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeu 238
Db 783 AATATTCCAATCTTTCAGAAATAAAGGGTGGATTTAACACTCTTCCACATCATCTA 842
QY 239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIle 258
Db 843 TCACCCGGTCTAGAGATTGTATACAGAGGATGCTTGTGTGACCCCTATGAGAGAATG 902
QY 259 ThrIleArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAla 278
Db 903 ACCATACCTGAGATCCGTCAACACCATGTGTCCAGCTGCACTCCACGTTATTAGCT 962
QY 279 ValProProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAsp 298
Db 963 GTGCCACACCAAGATACATGCAACAGGCCAAAGATGTATGAGAGATCCTTCAGGAA 1022
QY 299 ValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGln 318
Db 1023 GTGTGAATAATGGATTGACAGGAATCAATGTGTTGAATCTCTTGGGAACAGATACAA 1082
QY 319 AsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGly 338
Db 1083 AATGAGGGTACTGTGCATACTATTGTATTGTGCAACCGATTTCGTGTTCCAGTGGC 1142
QY 339 TyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
Db 1143 TATCTTGAGCTGAGTTTCAAGAGACCATGATCCGGTTTAAATCAAAATGATTCAGT 1202
QY 359 GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerSerAspProHisSerSer 378

Db 1203 GAACTTGCTTCTTACATGTTGTTGGAAACCGCTTTCCAGGCTACATGGAATATCCAGAGTA 1262
QY 379 GlyLeuArgProTyrTyrProValGluArgLysTyrAlaLeuGlyLeuGlnSerArgAla 398
Db 1263 GGATCGAGGCAACAGTTCCTGTTGAAAGGAATGGGCCCTTGGGCTTCACTCGAGCC 1322
QY 399 HisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrp 418
Db 1323 CATCCTCGTGAATTAATGACTGAGGTTCTTAAAGCTTTGCAAGAATTAATGTTGTTGG 1382
QY 419 LysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPhePro----- 435
Db 1383 AAGAAGATTGGTCACTACAACATGAAGTGTAGGTGGGTTGCTGGCATTCCTGTCAACAC 1442
QY 436 -----GluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThrIle 453
Db 1443 GAAGGAATGGTTAACAAATAATGTGCATAGTAATCACTTTGGAGATGATTCACAACATT 1502
QY 454 MetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGlnPheGlnLeu 473
Db 1503 ATTGAAATGATGCTGTTCT------ACTTCAAAATGTGTGTCAAAGTTGAAGTCAAGCTT 1556
QY 474 TyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGlnLeu 493
Db 1557 TACAACACCCGGGAAGAAAGTATCTGCTGATCTTCAAAAGGTGACAGGTCCACAGTTT 1616
QY 494 LeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
Db 1617 CTTTCTTGATCATATGTGCTGCTTTCCTGACAGCTTCGTGTCCTC 1664

RESULT 6

ABZ14852
ID ABZ14852 standard; DNA; 1539 BP.

AC ABZ14852;

DT 21-JAN-2003 (first entry)

DE Arabidopsis thaliana stress regulated gene SEQ ID NO 2657.

KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

OS Arabidopsis thaliana.

PN WO200216655-A2.

XX 28-FEB-2002.

PF 24-AUG-2001; 2001WO-US026685.

XX 24-AUG-2000; 2000US-0227866P.

PR 26-JAN-2001; 2001US-0264647P.

PR 22-JUN-2001; 2001US-0300111P.

PA (SCRI) SCRIPPS RES INST.

PI (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

DR WPI; 2002-304127/34.

PT Identifying a stress condition to which a plant cell has been exposed and
producing plants with increased tolerance to these abiotic stresses.

XX Claim 144; SEQ ID NO 2657; 577pp + Sequence Listing; English.

CC The invention relates to identifying a stress condition to which a plant
cell has been exposed, comprising: (a) contacting nucleic acid

CC representative of expressed polynucleotides in the plant cell with an
array or probes representative of the plant cell genome; and (b)

CC detecting a profile of expressed polynucleotides in the plant cell
characteristic of a stress response. The method is useful in the

CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office

XX SQ Sequence 1539 BP; 432 A; 313 C; 381 G; 413 T; 0 U; 0 Other;

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 7.33e-191 | Length: | 1539 |
| Score: | 1969.50 | Matches: | 377 |
| Percent Similarity: | 82.82% | Conservative: | 52 |
| Best Local Similarity: | 72.78% | Mismatches: | 74 |
| Query Match: | 73.13% | Indels: | 15 |
| DB: | 6 | Gaps: | 4 |

US-09-857-522B-4 (1-509) x AB214852 (1-1539)

QY 1 MetAspGlySerSerIysGly-----SerGlyHisSerGluAlaLeuArgAsnTyrAsn 18
DB 1 ATGGATGATCAGGCACAGCAGCAGTAGAAGTGGGGTAGAATCGATTCTACCAATTACAAG 60
QY 19 LeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeu 38
DB 61 CTGGGAGAACTCTTGCTATTGTTGCTTCTTGAGGGTGAAGATAGCTGACGATGCATTG 120
QY 39 ThrGlyHisArgValAlaIleLysIleIleAsnGlyArgGlnMetArgAsnMetGluMet 58
DB 121 ACAGACATAGGTTGCTATCAAGATCCCTCAATCGTCGCAAAATCAAGACATGAGATG 180
QY 59 GluGlyLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIle 78
DB 181 GAGGAGAAAGTAGAGAGAGATCAAAATCTTGAGACTATTATGATCATCTCACATCATC 240
QY 79 ArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLys 98
DB 241 CGTCTCTATGAGGTATAGAGACTCCACAGATATTATCTGTGATGAGATGTGAGAC 300
QY 99 TyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnIleAspGluAlaArg 118
DB 301 TCTGGTGAAGCTATTGACTATATTGTTGAGAGGGTAGATTGACAGAGGATGAGCGAGG 360
QY 119 ArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHis 138
DB 361 AACTTTTTCAGCAGATATATATCAGAGAGTGAATCTGCCATCGAAACATGGTGTTCAC 420
QY 139 ArgAspLeuLysProGluAsnLeuLeuLysSerLysTyrAsnValLysLeuAlaAsp 158
DB 421 AGAGACCTCAAGCCTGAAAACTTGCTTTGGACTCTAAATGCAATGTAAAGATTGCTGAT 480
QY 159 PheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerPro 178
DB 481 TTTGGCCTGAGCAACATATATGCGAGATGTCATTTTGAAGACAAGTTGTGAAGTCCA 540
QY 179 AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspVal 198
DB 541 AATTATGCCGCTCCAGAGTAATTTCGGGCAAGTATATGCTGGCCCTGAAGTAGATGTC 600
QY 199 TrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGlu 218
DB 601 TGGAGCTGTGTGTGATACTTAACGCTCTTCTCTGTGGGACGCTTCCATTGATGATGAA 660
QY 219 AsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeu 238
DB 661 AACATTCCCAACCTTTTAAAGATAAAGGAGGAGATATACACATTACCTAGCCATTTA 720
QY 239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIle 258
DB 721 TCTCCTGTGCTAGAGATTGATCCCCCGAGATGCTTGTAGTGAACCCCATGAACGAGTA 780
QY 259 ThrIleArgGluIleArgGluHisGlnThrPheGlnIleArgLeuProArgTyrLeuAla 278

DB 781 ACCATCCCTGAGATCCGGCAACACCCTTGTTCCAAAGCTCATCTTCCGAGGTATTAGCT 840
QY 279 ValProProAspThrThrGlnAlaLysMetIleAspGluAspThrLeuArgAsp 298
DB 841 GTTCTCTCCAGATATCTGTGCAAGCAAGCAAAAGATTGACGAGAGATTCTCAAGAA 900
QY 299 ValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGln 318
DB 901 GTTATCAATATGGATTGTGACAGAAACCACTCATCGAATCGCTCCGCAACCGAACCCAG 960
QY 319 AsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGly 338
DB 961 AATGATGGCACTGTGACGACTACTATCTGATACTGGACAATCGTTCCGTGCTAGTGT 1020
QY 339 TyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
DB 1021 TATCTCGGGGCTGAGTTTCAAGAGACCATGGAA--GGTACTCCCCGTATGCATCCAGCA 1077
QY 359 GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
DB 1078 GAAAGCGTTGCTTCACTGTTAGCCATCGGCTTCCAGGACTGATGGAATATCAAGAGATT 1137
QY 379 GlyLeuArgProTyrTyrProValGluArgLysTyrAlaLeuGlyLeuGlnSerArgAla 398
DB 1138 GGCTTGAGATCTCAATACCCCTGTGAGAGAAATAGGGCTCTTGACTTCACTCTCGGGCT 1197
QY 399 HisProArgGluIleMetValGluValLeuLysAlaLeuGlnLeuAsnValArgTyr 418
DB 1198 CATCCCCGTAATAATAGACGGAAGTCTGAAAAGCCCTGCAAGATTGAAATGATGTTGG 1257
QY 419 LysLysAsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsn 438
DB 1258 AAGAAGATAGGGCACTACAACATGAAGTGCAGATGGTTCCT-----AAC 1302
QY 439 AspThrLeuAspAla-----SerAsnSerPheLeuGlyAspSer 451
DB 1303 AGCAGCCGAGATGGTATGCTCAAGTAACTCGATGCACAGATAACAATACTTTGGAGACGAG 1362
QY 452 ThrIleMetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPhe 471
DB 1363 TCCAGCATATAAGAAACGAAGCAGCTGTTAAGTCGCCCAATGTTGTCAAGTTGAAATT 1422
QY 472 GlnLeuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyPro 491
DB 1423 CAGTTGTATAAACTCGGAGCAGCAAGTATCTACTGATTGACAGAGATCAAGGTCTCCT 1482
QY 492 GlnLeuLeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
DB 1483 CAGTCTTGTCTTGATCTGTGTGCTGCTTTCTTGCTCAGCTCGAGTCTC 1536
RESULT 7
ID ACC00745
AC ACC00745 standard; cDNA; 2052 BP.
XX
DT 16-MAY-2003 (first entry)
XX
DE Zea mays oil trait related cDNA sequence SEQ ID NO:239.
XX
KW Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW Lipid-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CKC-like transcription factor; antisense inhibition; co-suppression;
transgenic plant; gene; ss.
XX
OS Zea mays.
XX
PN W02003002751-A2.
XX
PD 09-JAN-2003.
XX
PF 27-JUN-2002; 2002WO-US020152.

XX 29-JUN-2001; 2001US-0301913P.
PR
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
PA (PION-) PIONEER HI-BRED INT INC.
XX
PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
PI Jones TJ, Kinney AJ, Klein TW, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczyński MC;
XX
DR WPI; 2003-201509/19.
DR P-PSDB; ABR40710.
XX
XX Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX
PS Claim 18; Page 277-278; 542pp; English.
XX
XX The present invention describes an isolated nucleotide fragment (I)
CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP5-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CKC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (III) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 2052 BP; 563 A; 445 C; 481 G; 563 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 7,11e-188 Length: 2052
Score: 1942.00 Matches: 380
Percent Similarity: 83.56% Conservative: 47
Best Local Similarity: 74.36% Mismatches: 70
Query Match: 72.11% Indels: 14
DB: 7 Gaps: 6
US-09-857-522B-4 (1-509) x ACC00745 (1-2052)
QY 1 MetAspGlySerSerlyGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
DB 216 ATGAGGGGGGCGAGGCAAG-----GATGGCAACCCCGTTGAGGAATTATCGGATTGGC 266
QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
DB 267 AAGACTCTCGGAATTGGCTCATTCGGGAAGGTGAATAATTGGGAGCATATACGACTGGA 326
QY 41 HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGluGlu 60
DB 327 CACAAAGGTGGCAATCAAGATTCTCAACCGCCGTAAATCAGAGGCATGAGATGGAAGAG 386
QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
DB 387 AAAGTTAAAGAGAGATTAAAGATTAGGTTATTATGATCCACATATATATCCGCTC 446
QY 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly 100
DB 447 TATGAGGTATAGACACACCGGCTGATATTATGTTATGAGATGTTAAGTGTGG 506
QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
DB 507 GAATTAATTGATTACATTGTTGAGAAAGGTAGGCTGCACAGAGAGAGAGCTGCCGTTTC 566

QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp 140
DB 567 TTCCAACAGATTATATCCGGGTGTGAATATATGCAAGAAACATGATGTCATCGTGAT 626
QY 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
DB 627 CTAAGACCAGAAACCTCTATTTGATTCGAAATGCAATGTTAAGATTGCGAGTTTGGC 686
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
DB 687 TTAAGTAATGTTATGCGGGATGTCATTTCTGAGACACAAGTTGTGTAGCCCAATTAT 746
QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSer 200
DB 747 GCTGCTCTGAGGTGATATCTGTAACCTATATGCTGACCTGAAGTTGATGTGAGAC 806
QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
DB 807 TGTGGGGTATTCTTTATGCTCTTTATGTGTACTCTGCCATTGATGACGAAACATA 866
QY 221 ProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
DB 867 CCAACCTTTTAAAGAAATAAAGGTGAATATACCTTCCAGCCATTGTCTGCT 926
QY 241 LeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIleThrIle 260
DB 927 GCAGCAAGGATTGATTCCAAAGATGCTAGTTGTCATCTATGAGCGGATCAACATT 986
QY 261 ArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
DB 987 CGTGAATTCGCGAACATGATGTTGTTCAAAATCTTCTCCCGCGCTATTGACTGTGCT 1046
QY 281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal 300
DB 1047 CCTCCAGATAGTGGCGCAACAAGTCAAAAAGGTTGATGAGAAACTCTCCGAGGTTTAA 1106
QY 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
DB 1107 GGTATGGGATATGACAAGAACCTGTGGTGGAATCAATCCAAAAGGCTGCAAAATGAG 1166
QY 321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
DB 1167 GCAACTGTTGCATATTACTTACTCTTGACAAATAGGCTCCGTACCAACCACTGCTATCTT 1226
QY 341 GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGlu-- 359
DB 1227 GGAGCTGAATGTCAAGAAAGCTATGAGCTCTCATCTCAAAACATCGCATATGAAACA 1286
QY 360 ---SerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
DB 1287 CCAAGTTCAGCAGCTGGGAATAGACAGCAAAATATTATGAGAGTCT-----CCAGTT 1337
QY 379 GlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAla 398
DB 1338 GGCTTGAGACCAATCTTCCAGCTGAGAGAAATGGGCTCTTGCTCTTCAGTCTCGAGCA 1397
QY 399 HisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrp 418
DB 1398 CATCCAAAGAAATAATGCTGTGAAGTGTGAAAGCTCTGCAAGAAATTAATGTTTACTGG 1457
QY 419 LysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPheProGluValAsn 438
DB 1458 AAAAAGATAGCTCATATACATGAGATGAGATGAGTCCGTGCTCTCTGCT----- 1511
QY 439 AspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAsp 458
DB 1512 ---CAAATTCATTAACAATCATTAACCTTCACTGACAGGCTCC-----ATTGAAACTGATAGC 1562
QY 459 AlaAsnGlyArgLeuProThrValIleLysPheGlnLeuTyrLysThrLysAsp 478
DB 1563 CTGAGTGAGAGGTTA--AGTTTAATTAAGTTGAATTCAGCTGTACAAACAAGAGAC 1619
QY 479 AspLysTyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPhe 498

Db 1620 GAGAAATACCTCTCGATTGCAAGAGTACGTGGCCACAGCTCTCTTCTGACTTG 1679
Qy 499 CysAlaAlaPheLeuThrLysLeuArgValIeu 509
Db 1680 TGGCGGCGCTTCTTAACCTCAACTGAGAGTTCTT 1712
RESULT 8
AAAS2774
ID AAAS2774 standard; cDNA; 2543 BP.
XX
AC AAAS2774;
XX
DT 03-JAN-2001 (first entry)
XX
DE Soybean putative catabolite repression protein SNF1 coding sequence #4.
XX
KM Soybean; carbon catabolite repression; sucrose non-fermenting protein 1;
XX
KM SNF1; plant growth; ss.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT CDS 73..1620
FT /*tag= a
FT /product= "SNF1"
XX
PN WO200036115-A2.
XX
PD 22-JUN-2000.
XX
PF 15-DEC-1999; 99WO-US029824.
XX
PR 16-DEC-1998; 98US-0112563P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Allen SM, Heppard EP, Sakai H, Weng Z, Helentjaris TG, Macool DJ;
PI Miao G;
XX
DR WPI; 2000-431593/37.
DR P-PSDB; AAB03422.
XX
PT New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
PT involved in carbon catabolite repression in plants and seeds, useful for
PT controlling carbon and nitrogen partitioning pathways during plant growth
PT and development.
XX
PS Claim 2; Page 47-48; 59pp; English.
XX
CC The present sequence is a putative sucrose non-fermenting protein SNF1
CC coding sequence from the soybean. The sequence was isolated by searching
CC a seed cDNA library for sequences similar to those known to encode SNF1
CC in Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa.
CC The protein is involved in carbon catabolite repression, and so the gene
CC and protein can be used in plants to control the nitrogen and carbon
CC partitioning pathways during plant growth and development. They can also
CC be used to alter the accumulation of carbohydrates, lipids and proteins
CC during plant growth
XX
SQ Sequence 2543 BP; 740 A; 477 C; 557 G; 769 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.96e-187 Length: 2543
Score: 1939.00 Matches: 373
Percent Similarity: 83.37% Conservative: 58
Best Local Similarity: 72.15% Mismatches: 76
Query Match: 72.00% Indels: 10
DB: 3 Gaps: 4
US-09-857-522B-4 (1-509) x AAAS2774 (1-2543)
Qy 1 MetAspGlySerSer---LysGlySerGlyHisSer-----GluAlaIeuArgAsnTyr 17

Db 73 ATGACACATCAACTGCGCGGTGGTGGTGGAGTGTGACATGTTTCTCCGAATATAT 132
Qy 18 AsnIeuGlyArgThrIeuGlyIleGlyThrPheGlyLysValIysIleAlaGluHisLys 37
Db 133 AAGTTGGGAAAAACACTCGGCATTTGGCTCTTTGGCAAGGTGAATAATTGTCAGCATGTA 192
Qy 38 LeuThrGlyHisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGlu 57
Db 193 CGAGCTGGTCATAAAGTTGCTATTAAGATCTTAAACCGCCACAGATTAATAAACATGGAA 252
Qy 58 MetGluGlyLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIle 77
Db 253 ATGAAGAAAAAGTTAGAGAGAAATCAAAATTTTAAGATTGTTATGCATCATCATATT 312
Qy 78 IleArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCys 97
Db 313 ATAAGACTATATGAGGTGTAGAAACCCCAACAGACATATATGTTATGAGATATGTG 372
Qy 98 LysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAla 117
Db 373 AAATCTGAGAGCTCTTGATTACATAGAGAAGGTCGGCTCAAGAAGATGAAGCC 432
Qy 118 ArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValVal 137
Db 433 CGTCATTTTTCACGACATATTTCTGCTGTGAGTACTGTCAAGAAATATGTGTGTT 492
Qy 138 HisArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAla 157
Db 493 CATAGAGACTGAAGCCTGAGAATTACTCTTGAACTCAAAATTTTAACATCAAGATTGCT 552
Qy 158 AspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySer 177
Db 553 GATTTGGGTGAGCAACATCATGCGTGAATGCTCACTTCTTAAGACAAAGTTGTGAAGC 612
Qy 178 ProAsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAsp 197
Db 613 CCTAATTATGCGGCTCCAGAGGTATCTCTGAAAATGTATGCTGACACAGAAGTAGAT 672
Qy 198 ValTyrSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAsp 217
Db 673 GTCTGAGAGCTGTGCTGTAATTTTATATGCTCTCTGTGCGACCTCTTCTTTGATGAT 732
Qy 218 GluAsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHis 237
Db 733 GAAACATTTCCAAATCTCTCAAAAAATAAAGGTGGATATACACTTCTTCTAGTCAT 792
Qy 238 LeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArg 257
Db 793 CTATCACCTGGTGTAGAGATTGTATACCAAGATGCTGTGGTGATCCATGAAGAGG 852
Qy 258 IleThrIleArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeu 277
Db 853 ATGACCATACCTGAGATACGCCAACACCATGTTCCAAATTCACTACCGCGTTATTTA 912
Qy 278 AlaValProProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArg 297
Db 913 GCAGTGCACACCAAGATACACTGCAACAGCCAAAAGATTGATGAGAGATTCTTCAG 972
Qy 298 AspValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeu 317
Db 973 GAAGTGGTTATATGGGATTGTGACAGGAATCAATTGGTGAATCTCTTAGCAACAGATA 1032
Qy 318 GlnAsnGluAlaThrValAlaIleTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSer 337
Db 1033 CAAATGAGGGTACTGTAAACATACTATTGTTATTGGACAAACCGTTTCGTTCAGT 1092
Qy 338 GlyTyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSer 357
Db 1093 GGTATCTTGGAGCTGAATTTCAAGAGACATGGAATCTGTTTAAACCGTATGCATTCC 1152
Qy 358 SerGluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerSerProHisSer 377

Db 1153 GGCGAAGTGTCTTCAGTTGTTGGACACACACAGGATATGATTAACAAGG 1212
Qy 378 SerGlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArg 397
Db 1213 GTAGGATGCGGCAACAGTCCCTGTTGAGAGAAATGGGCCCTTGGGCTTCACTCCGA 1272
Qy 398 AlaHisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArg 417
Db 1273 GCCCAACACAGTGAATATACTGAGGTCCCTTAAAGCTCTACAAGAATTAATGTTGT 1332
Qy 418 TrpLysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPhePro----- 435
Db 1333 TGAAGAAGATTGGACACTATAACATGAAGTGCAGATGGGTTGCTGGCACCTGCTGTCAT 1392
Qy 436 -----GluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThr 452
Db 1393 CATGAAGGAATGATTACAATCTCTGCATAGTAATCACTTGGAAATGATTCGCGC 1452
Qy 453 IleMetAspAsnAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGln 472
Db 1453 ATTATTGAAATGAAGCTGTTCT-----AAGTCAATGTGTCAAGTTGAAGTGACG 1506
Qy 473 LeuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGln 492
Db 1507 CTTTACAAAACTCGTAGGAGAATAATATCTGCTGATCTTCAAGGGTCCAGGGCCACAG 1566
Qy 493 LeuLeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
Db 1567 TTTCTTTCTTGATCTGTGCGCTGCTTCCTTCAACAGCTACGTGTTCTC 1617

RESULT 9
ACCC00751
ID ACC00751 standard; cDNA; 2543 BP.

XX AC ACC00751;
XX DT 16-MAY-2003 (first entry)
XX DE Glycine max oil trait related cDNA sequence SEQ ID NO:251.
XX KW Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase;
KW receptor-like protein kinase; mitogen activated protein kinase; oil;
KW LIP15-like transcription factor caleosin; ATP citrate lyase; SNF1;
KW CXC-like transcription factor; antisense inhibition; co-suppression;
KW transgenic plant; gene; ss.
XX OS Glycine max.
XX PN WO2003002751-A2.
XX PD 09-JAN-2003.
XX PF 27-JUN-2002; 2002WO-US020152.
XX PR 29-JUN-2001; 2001US-0301913P.
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PI Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT;
PI Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B;
PI Tarczynski MC;
XX DR WPI; 2003-201509/19.
XX DR P-PSDB; ABR40716.
XX PT Novel nucleotide fragment encoding polypeptides having receptor-like
PT protein kinase activity, caleosin-like activity, useful for altering oil
PT phenotypes in plants such as sunflower, coconut, soybean, wheat and rice.
XX PS Claim 18; Page 291-292; 542pp; English.
XX CC The present invention describes an isolated nucleotide fragment (I)

CC comprising a nucleic acid sequence (NS) chosen from a NS encoding a
CC polypeptide (PP) having receptor-like protein kinase activity, mitogen
CC activated protein (MAP)-kinase activity, LIP15-like transcription factor
CC activity, caleosin-like activity, ATP citrate lyase activity, SNF1-like
CC activity and CXC-like transcription factor activity. Also described: (1)
CC complement (II) of (I); (2) a chimeric construct (III) comprising (I) or
CC (II), operably linked to a regulatory sequence; (3) a plant (IV)
CC comprising (II) in its genome; (4) seeds (V) obtained from (IV); and (5)
CC oil obtained from (V). (I) or its part can be used in antisense
CC inhibition or co-suppression in a transformed plant. (III) is useful for
CC altering the oil phenotype in a plant such as corn, soybean, wheat, rice,
CC canola, Brassica, sorghum, sunflower or coconut. (III) is also useful for
CC creating transgenic plants having altered lipid profiles. (I) can also be
CC used as a hybridisation probe. ACC00626 to ACC00868 and ABR40591 to
CC ABR40879 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 2543 BP; 740 A; 477 C; 557 G; 769 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.96e-187 Length: 2543
Score: 1939.00 Matches: 373
Percent Similarity: 83.37% Conservative: 58
Best Local Similarity: 72.15% Mismatches: 76
Query Match: 72.00% Indels: 10
DB: 7 Gaps: 4

US-09-857-522B-4 (1-509) x ACC00751 (1-2543)

Qy 1 MetAspGlySerSer---LysGlySerGlyHisSer-----GluAlaLeuArgAsnTyr 17
Db 73 ATGACACAGATCACTGCGCGTGTGGTGAAGTGTGACATGTTCTCCGAATATAT 132
Qy 18 AsnLeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLys 37
Db 133 AAGTTGGGAAACACCTCGCATTTGGTCTTTGGCAAGGTGAATAATTGTCGACATGTA 192
Qy 38 LeuThrGlyHisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGlu 57
Db 193 CGAGCTGTCATAAAGTTGCTATAAGATCTTAAACCGCCACACAGATTAAACATGGAA 252
Qy 58 MetGluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIle 77
Db 253 ATGGAAGAAAGTTAGAGAGAAATCAAAATTTAAGATTGTTATGCAATCATCACATT 312
Qy 78 IleArgLeuTyrGluValIleTyrThrProThrAspIleTyrValIleMetGluTyrCys 97
Db 313 ATAAGACTATATGAGGTGTAGAAACCCACACAGACATATATGTTATGAGATATGTG 372
Qy 98 LysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAla 117
Db 373 AAATCTGGAGAGCTCTTGTATTACATAGTAGAAGGGTCCGCTCAAGAGATGAAGCC 432
Qy 118 ArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValVal 137
Db 433 CGTCATTTTTCAGCAGATTAATTCTGCTGTGAGTACTGTCAACGAAATATGTGTGTT 492
Qy 138 HisArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAla 157
Db 493 CATAGAGACTGAAGCCTGAGAATTAACTCTTGGACTCAAAATTTAAACATCAAGATTGCT 552
Qy 158 AspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySer 177
Db 553 GATTTGGGTTGAGCAACATCATGCGGTGATGTCACCTTCTTAAACAAGTTGTGAAGC 612
Qy 178 ProAsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAsp 197
Db 613 CCTAATATGCGGCTCCAGAGGTATCTCTGGAATAATTGTATGCTGACAGAGTAGAT 672
Qy 198 ValTyrSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAsp 217
Db 673 GTCTGGAGCTGTGTGTAATTATATATGCTCTTCTGTGGCACTCTTCTTTGATGAT 732

QY 218 GluAsnIleProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHis 237
|||||
Db 733 GAAAAACATCCCAATCTCTCAAAAAATAAGGGTGGATATACACTCTTCTAGTCAT 792
QY 238 LeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArg 257
|||||
Db 793 CTATCACCTGCTGCTAGAGATTGTGATACCAGAGATGCTGTGTGATCCCATGAAGAG 852
QY 258 IleThrIleArgGluIleArgGluHisGlnIleArgGlnIleArgLeuProArgTyrLeu 277
:::|||||
Db 853 ATGACCATACCTGAGATACGCCAACACCCATGGTCCAGTTCACTTACCCTTATTTA 912
QY 278 AlaValProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArg 297
|||||
Db 913 GCAGTGCACCCACAGATACCTGCACCAAGCCAAAGATTGATGAGAGATTCTTCAG 972
QY 298 AspValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeu 317
:::|||||
Db 973 GAAGTGGTTAATATGGAATTGACAGGAATCAATTGGTTGAATCTCTTAGCAACAGATA 1032
QY 318 GluAsnGluAlaThrValAlaTyrTyrLeuLeuAspAsnArgPheArgAlaThrSer 337
|||||
Db 1033 CAAATGAGGGTACTGTACATATACTATTGTATTGACAACCGGTTTCGTTTCTAGT 1092
QY 338 GlyTyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSer 357
|||||
Db 1093 GGTATCTTGAGCTGAATTCCAAGAGACATGGATTCTGTTTAAACCGTATGCAATTC 1152
QY 358 SerGluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSer 377
|||
Db 1153 GCGGAAGTTGCTTCTCCAGTTGTGACACACACAGGCGTATATGATATCAAGGG 1212
QY 378 SerGlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArg 397
|||
Db 1213 GTAGGAATGCGGCAACAGTCCCTGTTGAGAGAAATGGGCCCTTGGGCTTCACTTCGA 1272
QY 398 AlaHisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArg 417
|||||
Db 1273 GCCCAACACGTCGAATATGACTGAGGTCCTTAAAGCTCTCAACAAGATTAAATGTTTGT 1332
QY 418 TrpLysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPhePro----- 435
|||||
Db 1333 TGGAGAAGATTGGACACATATAACATGAAGTGACAGTGGTGTGCACATGCTGCAT 1392
QY 436 -----GluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThr 452
:::|||||
Db 1393 CATGAAGGAATGATTAAACAATTCTCTGCATAGTAATCACTTACCTTGGAAATGATCCGCGC 1452
QY 453 IleMetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGln 472
|||
Db 1453 ATTATTGAAATGAAGCTGTTCT-----AAGTCAAAATGTGTCAAGTTTGAAGTGCAAG 1506
QY 473 LeuTyrLysThrLysAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGln 492
|||||
Db 1507 CTTTACAAAACTCGTGAGGAGAAATATCTGCTTGATCTTCAAAAGGGTCCAGGGCCACAG 1566
QY 493 LeuLeuPheLeuAspPheCysAlaIlePheLeuThrLysLeuArgValLeu 509
|||||
Db 1567 TTTCTTTTCTTGATCTGTGCGCTGCTTCTTCTTCAAGCTTACGTTCTC 1617
RESULT 10
ID AAF62011 standard; DNA; 1929 BP.
XX AAF62011;
XX 02-MAY-2001 (first entry)
DE Tomato LesNf1 (sucrose nonfermenting yeast homologue) gene.
XX
KW Sucrose non-fermenting; SNF-4; SNF-1; tomato; sugar metabolism; seed;
KW source-sink; fruit; enhanced quality; sugar accumulation; LesNf1;
KW stress resistance; transgenic plant; germination stimulation; ds.

XX OS Lycopersicon esculentum.
XX
PN W0200107570-A1.
XX
PD 01-FEB-2001.
XX
PF 21-JUL-2000; 2000WO-US019981.
XX
PR 21-JUL-1999; 99US-00359161.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Bradford KJ, Peetambar D, Yang H, Cooley M, Downie B, Gee OH;
XX WPI; 2001-168545/17.
XX
PT New sucrose non-fermenting (SNF1) and SNF4 polynucleotides and expression
PT cassettes containing the polynucleotides for modulating source-sink
PT relationships in plants and enhancing yield or quality of harvested plant
PT products.
XX
PS Claim 19; Page 39; 43pp; English.
XX
CC This invention relates to polynucleotide sequences encoding plant sucrose
CC non-fermenting SNF-4 or SNF-1 polypeptides. Specifically included in the
CC invention are tomato LesNF-4 and LesNF-1 polynucleotide sequences. A
CC recombinant expression vector comprising SNF-4 or SNF-1 polynucleotide
CC sequences is useful for modulating sugar metabolism in a plant. The
CC recombinant expression cassette comprising the DNA sequence is useful for
CC modulating source-sink relationships in plants and therefore enhances
CC yield or quality of harvested plant products, such as fruit. SNF-4 and
CC SNF-1 DNA can be used to enhance sink activity or starch or lipid
CC accumulation in seeds. Also they can be used to enhance sugar
CC accumulation in fruits. The expression cassettes can also be used to
CC enhance responsiveness to stress conditions in plants. Enhanced
CC expression of SNF1 and SNF4 polynucleotides or polypeptides is used to
CC alter expression of sugar related genes or to enhance resistance to
CC stress. Inhibition of endogenous SNF1 or SNF4 genes modulates the
CC activity of enzymes associated with sugar metabolism. In seeds,
CC inhibition of SNF4 expression can be used to break dormancy and stimulate
CC germination. The present sequence represents the tomato LesNF-1 gene
XX
SQ Sequence 1929 BP; 546 A; 384 C; 442 G; 557 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1,88e-187 Length: 1929
Score: 1937.50 Matches: 375
Percent Similarity: 85.08% Conservative: 64
Best Local Similarity: 72.67% Mismatches: 68
Query Match: 71.95% Indels: 10
DB: 4 Gaps: 6
US-09-857-522B-4 (1-509) x AAF62011 (1-1929)
QY 1 MetAspGlySerSer---LysGlySerGlyHisSerGluAla---LeuArgAsnTyrAsn 18
|||||
Db 33 ATGACGGAACAGACAGTCAGGGCACGAGCACTGTGACTCATTTTACGGAATAATA 92
QY 19 LeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeu 38
|||||
Db 93 CTCGGGAAAACACTTGGCATTGGATCGTTCGCAAAAGTTAAATAGCTGAACATAGCTTA 152
QY 39 ThrGlyHisArgValAlaIleLysIleLeuAsnCysArgGlnMetArgAsnMetGluMet 58
|||||
Db 153 ACAGGGCACAAAGTTGCTGTCAAGATTCTTAATCGTCGAAAAATCAGGAATATGACATG 212
QY 59 GluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIle 78
|||||
Db 213 GAGGAGAAAGTCCTAGAGAAATCAAAATATGAGATTGTTCAATGCACTCATATATA 272
QY 79 ArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLys 98
|||||

Db 273 CGGCTTTATGAGTGCATAGACACACCATCAGATATATATGTTGTGATGGAGTATGTGAAA 332
QY 99 TyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArg 118
Db 333 TCTGGCAGATTATTGATTACATGTTGTGAGAAGGCAGATTGCAGAGAGATGAAGCTCGT 392
QY 119 ArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHis 138
Db 393 AACTTTTTCAGCAGATAATTCTGCTGTGAGTACTGCCATAGAAACATGCTGTTCAT 452
QY 139 ArgAspLeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAsp 158
Db 453 AGAGACCTTAAGCCTGAACCTCTCTCTGACTCCAAATGGAATGTGAAGATCGCAGAT 512
QY 159 PheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerPro 178
Db 513 TTTGGTTTGACAAATATCATCGCGCATGTGTCATTTCTGAAGACAAGTTGCGGAAGCCCA 572
QY 179 AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAlaAspVal 198
Db 573 AACTATGCTGCCAGAGGTTATATCAGGTAATGTATGCTGGCCCTGAGGTAGATGTA 632
QY 199 TrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGlu 218
Db 633 TGGAGCTGTGCTGTATTCTTATGCTCTCTCTGTGGCACCCTTCCGTTTGACCATGAA 692
QY 219 AsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeu 238
Db 693 AACATACCCAATCTTTTAAGAAATAAAGGGTGAATATATACTCTGCCACCATTTTA 752
QY 239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIle 258
Db 753 TCAGCTGTGCGAGGATTGATTTCGAGAGATGCTTATAGTCGACCCAATGAAGCGAATG 812
QY 259 ThrIleArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAla 278
Db 813 ACTATTCTGAGATTGCGCTGCACCCCTTGTTCCAAAGTCATTGCCACGCTATTGGCC 872
QY 279 ValProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAsp 298
Db 873 GTGCCTCCACGATACACCAACAAGAAAGATCGATGAAGATCTTCAAGAG 932
QY 299 ValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGln 318
Db 933 GTGCTTAAGATGGGATTGACAGAAACAACCTTACTGAGTCTCTCGCAATAGATTCAA 992
QY 319 AsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGly 338
Db 993 AATGAGGGCACTGTTGCATTAATACTGCTCTCGACAAATCGCCATCGTGTTCACACTGGC 1052
QY 339 TyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
Db 1053 TATCTTGAGCTGAATTTCAGAGAGTCCATGAAATATGTTTACAACCGATCAATTCTAAT 1112
QY 359 GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
Db 1113 GAAACCGCTGCTCCCTGTTGGTCAACGTTTCCAGAAATAATGATATATCAGCAAGCT 1172
QY 379 GlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAla 398
Db 1173 GGTGCAAGA---CAGTTCCTCATGAAAGAAATGGGCTCTTGCCCTCCAGTCTCGAAGCG 1229
QY 399 HisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrp 418
Db 1230 CATCCACGTGAATAATATGACTGAAGTTTGAAGAAGCTCTGCAAGAACTGAATGTATGTTGG 1289
QY 419 LysLysAsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsn 438
Db 1290 AAAAGATT-GGTACAGTAAACATGAATGTGATGGGTTCCTAGCTTACCTGGTCATCAT 1348
QY 439 AspThrLeuAspAlaSer-----AsnSerPheLeuGly---AspSerThrIle 453
Db 1349 GAAGGCATGGGTGTTAATTCATGCATGCGAATCAAGTCTTTGGAGATGATTCATTCATC 1408

QY 454 MetAspAsnAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGlnLeu 473
Db 1409 ATTGAGAAATGATGGGCCACACA---AAGTTAACAAATGTGTCAAAGTTTGAAGTTCAGCTT 1465
QY 474 TyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGlnLeu 493
Db 1466 TACAAACACGAGGAGAGAAAGTACTGCTTGACCTTCAGAGACTTCAGGGTCCACAAATTC 1525
QY 494 LeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
Db 1526 CTCTTCCTGATCTGTGCTGCTTTCTTGCTCAGCTTCGAGTACTT 1573
RESULT 11
AAAS2769
ID AAAS2769 standard; cDNA; 2107 BP.
XX
AC AAAS2769;
XX
DT 03-JAN-2001 (first entry)
XX
DE Corn putative catabolite repression protein SNF1 coding sequence #3.
XX
KW Corn; carbon catabolite repression; sucrose non-fermenting protein 1;
KW SNF1; plant growth; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 2..1739
FT /*tag= a
FT /product= "SNF1"
FT /partial
XX
XX WO200036115-A2.
XX
XX PN 22-JUN-2000.
XX PD 15-DEC-1999; 99WO-US029824.
XX PF 16-DEC-1998; 98US-0112563P.
XX PR
XX
XX PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX PI Allen SM, Heppard BP, Sakai H, Weng Z, Helentjaris TG, Macool DJ;
PI Miao G;
XX
XX DR WPI; 2000-431593/37.
XX DR P-PSDB; AAB03417.
XX
XX PT New nucleic acids encoding sucrose non-fermenting 1 (SNF1) proteins
XX PT involved in carbon catabolite repression in plants and seeds, useful for
XX PT controlling carbon and nitrogen partitioning pathways during plant growth
XX PT and development.
XX
XX PS Claim 2; Page 37; 59pp; English.
XX
XX CC The present sequence is a putative sucrose non-fermenting protein SNF1
XX CC coding sequence from corn. The sequence was isolated by searching a corn
XX CC stem cDNA library for sequences similar to those encoding SNF1 in
XX CC Arabidopsis thaliana, Cucumis sativus, Glycine max and Oryza sativa. The
XX CC protein is involved in carbon catabolite repression, and so the gene and
XX CC protein can be used in plants to control the nitrogen and carbon
XX CC partitioning pathways during plant growth and development. They can also
XX CC be used to alter the accumulation of carbohydrates, lipids and proteins
XX CC during plant growth
XX
SQ Sequence 2107 BP; 578 A; 454 C; 484 G; 591 T; 0 U; 0 Other;
Alignment Scores: 9.81e-187 Length: 2107
Pred. No.: 1931.00 Matches: 372
Score: 83.69% Conservative: 54
Percent Similarity:

Best Local Similarity: 73.08% Mismatches: 77
Query Match: 71.70% Indels: 6
DB: 3 Gaps: 3

US-09-857-522B-4 (1-509) x AA52769 (1-2107)

| | | | |
|----|------|--|------|
| QY | 1 | MetAspGlySerSerLySGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly | 20 |
| DB | 230 | ATGAGGAGGACGGAGA-----GATGCCAACCTTTGAGCGGTTACAGAATTGGC | 280 |
| QY | 21 | ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly | 40 |
| DB | 281 | AAACCCCTGGGAATTGGTCGTTGTAAGTGAAGATCGCGGAACATATATTGACTGGT | 340 |
| QY | 41 | HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGlu | 60 |
| DB | 341 | CATAAGGTGGCATCAAGATTCTCAATCGCAAGAGATCAGAAGCATGGATATGGAAGAG | 400 |
| QY | 61 | LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu | 80 |
| DB | 401 | AAAGTTAAGAGAGAAATCAAGATACTGAGATTATTATGCATCCTCATATCATACGCTT | 460 |
| QY | 81 | TyrGluValIleTyrThrProThrAspIleTyrValIleMetGluTyrCysLysTyrGly | 100 |
| DB | 461 | TATGAGGTAGATAGATACACCTGCTGATATCTGTGTGTATGAGATATGTTAAATCTGGA | 520 |
| QY | 101 | GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnLysAspGluAlaArgArgIle | 120 |
| DB | 521 | GAGTTGTTGATTACATCGTTGAGAAGGAGGCTACACGAAGAGGAGCCGACACTTT | 580 |
| QY | 121 | PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp | 140 |
| DB | 581 | TTTCAGCAGATCATATCTGCTGTGAATATTGCCATAGGAACATGGTTCCTCACCGTGAT | 640 |
| QY | 141 | LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly | 160 |
| DB | 641 | TTAAAGCCAGAGAAATCTTTCTTTGGATTCAAAATGCAATGTTAAGATTGCCGATTTTGGC | 700 |
| QY | 161 | LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr | 180 |
| DB | 701 | TTAAGTAATATTATGCGTGAATGCTCATTCTTAAGACGAGTTGTGTAGCCGAATTAT | 760 |
| QY | 181 | AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSer | 200 |
| DB | 761 | GCAGCACCCTGAGGTCAATCTGTAAACTATATGCTGCTCTGAAGTGCCTGAGC | 820 |
| QY | 201 | CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle | 220 |
| DB | 821 | TGTGAGTATTCTTTATGCTCTTCTTGTGGCACTCTCCCATTTGACGATGAGAATATT | 880 |
| QY | 221 | ProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla | 240 |
| DB | 881 | CCAAACCTTTCAAGAAAAATAAAGGGTGAATATATACCTTCCTAGTCATTGTCACT | 940 |
| QY | 241 | LeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIleThrIle | 260 |
| DB | 941 | TCAGCGAGGACTTGATTCACAGAAATGCTGTTGTGATCCAATGAAAAGATTACAATA | 1000 |
| QY | 261 | ArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAlaValPro | 280 |
| DB | 1001 | CGTGAATCCGTAACATGTGTGTTCAAGATCCGACTTCGCGCTATTGGCTGTGCCG | 1060 |
| QY | 281 | ProProAspThrThrGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal | 300 |
| DB | 1061 | CCTCCAGACACTGCTCAACAAGTTAAAAAGTGCACGAGGAAACTCTTAATGATGTTATT | 1120 |
| QY | 301 | AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu | 320 |
| DB | 1121 | AAGATGGGTTTGACACAGAAATCAAGCTAATTGAATCTCTGCAAAACAGATTGCAGAATGAG | 1180 |
| QY | 321 | AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu | 340 |
| DB | 1181 | GCAACAGTTGCCCTATTATTACTCTTGACAATAGGCTTCGTACCAACAGTGGTTATCTT | 1240 |

| | | | |
|----|------|--|------|
| QY | 341 | GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer | 360 |
| DB | 1241 | GGATCTGAGTTTCAAGATCTATGACTCATCTTGTCTCAAGTAATC---GCTGAACA | 1297 |
| QY | 361 | SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu | 380 |
| DB | 1298 | CCAACCTTACGCAACTGAACCTTCGTCAGCATGGGTTTTCAGAAATCTCCAGGTTCTGCTTG | 1357 |
| QY | 381 | ArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAlaHisPro | 400 |
| DB | 1358 | AGGACGACTTTTGACGCTGAAAGGAAATGGGCCCTTGCTTCACTCTCGACACATCCA | 1417 |
| QY | 401 | ArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrpLysLys | 420 |
| DB | 1418 | CGAGAAATATAAGTGAAGTGTAAAGCTCTGCAGAACTGAATGTTTACTGGAATAAG | 1477 |
| QY | 421 | AsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPheProGluValAsnAspThr | 440 |
| DB | 1478 | ATTGACACTTACAACATGAATGCAATGAGAGTCCGTGCTGCTTGAG-----AGTAG | 1531 |
| QY | 441 | LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn | 460 |
| DB | 1532 | ATGCATTAACAGTATAGCTTCAGTCCGAGTCTGCTATATATGAACGATGTTTCATG | 1591 |
| QY | 461 | GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLysAspAspLys | 480 |
| DB | 1592 | GAGAAATCAACCCGACAGCTGAAGTTGAGATTCAAGCTTTACAAAACGAGGATGAGAAG | 1651 |
| QY | 481 | TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla | 500 |
| DB | 1652 | TACCTTCTTGAACCTGCAAAAGGGTCAAGTGAATCATCATCTTCTTGTGGAAGTTGTTCC | 1711 |
| QY | 501 | AlaPheLeuThrLysLeuArgValLeu | 509 |
| DB | 1712 | GCCTTCTTAATCAAGTGAAGTTCTT | 1738 |

RESULT 12

| | | |
|----------|----|--|
| ACC00744 | ID | ACC00744 standard; cDNA; 2107 BP. |
| XX | AC | ACC00744; |
| XX | DT | 16-MAY-2003 (first entry) |
| XX | DE | Zea mays oil trait related cDNA sequence SEQ ID NO:237. |
| XX | KW | Plant; oil trait; oil phenotype; altered lipid profile; MAP kinase; |
| KW | KW | receptor-like protein kinase; mitogen activated protein kinase; oil; |
| KW | KW | lipid-like transcription factor caleosin; ATP citrate lyase; SNF1; |
| KW | KW | CKC-like transcription factor; antisense inhibition; co-suppression; |
| XX | OS | Zea mays. |
| XX | PN | W02003002751-A2. |
| XX | PD | 09-JAN-2003. |
| XX | PF | 27-JUN-2002; 2002WO-US020152. |
| XX | PR | 29-JUN-2001; 2001US-0301913P. |
| XX | PA | (DUPO) DU PONT DE NEMOURS & CO E I. |
| XX | PI | (PION-) PIONEER HI-BRED INT INC. |
| XX | PI | Allen SM, Allen WB, Cahoon RE, Epelbaum S, Famodu OO, Harvell LT; |
| XX | PI | Jones TJ, Kinney AJ, Klein TM, Li C, Oliveira IC, Sakai H, Shen B; |
| XX | PI | Tarczyński MC; |
| XX | DR | WPI; 2003-201509/19. |
| XX | DR | P-PSDB; ABR40709. |

DT 27-AUG-2003 (revised)
DT 02-MAR-1994 (first entry)
XX
DE SHP gene.
XX
KW Yeast; SNF1; homologous protein; SHP; Nicotinia tabacum; invertase; ss.
XX
OS Saccharomyces cerevisiae.
XX
PN JPO5199884-A.
XX
PD 10-AUG-1993.
XX
PF 13-DEC-1991; 91JP-00330417.
XX
PR 13-DEC-1991; 91JP-00330417.
XX
PA (SUMO) SUMITOMO CHEM CO LTD.
XX
DR WPI; 1993-284682/36.
DR P-PSDB; AAR40842.
XX
XX
PT Yeast SNF1 homologous protein phosphorylase gene of SOLANACEAE plants -
PT useful for controlling expression of invertase for the increase of crop
PT yield.
XX
PS Claim 1; Page 6; 7pp; Japanese.
XX
CC This sequence represents the yeast SNF1 homologous protein gene (SHP).
CC The yeast SHP gene may be obtained from Nicotinia tabacum and may be
CC used to control expression of invertase for the increase of crop yield.
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 1536 BP; 437 A; 291 C; 382 G; 426 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.09e-186 Length: 1536
Score: 1923.00 Matches: 372
Percent Similarity: 83.72% Conservative: 60
Best Local Similarity: 72.09% Mismatches: 72
Query Match: 71.41% Indels: 12
DB: 2 Gaps: 7

US-09-857-522B-4 (1-509) x AAQ47789 (1-1536)

QY 1 MetAspGlySerSer-----LysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsn 18
DB 1 ATGGATGATCAACAGCTCCAAAGGTGGAGCAGCGTGAGTCATTCTACGGAATATTAAG 60
QY 19 LeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeu 38
DB 61 CTGGGAAAACCTCTGGCATTGGATCATTCGAAAAGTTAAATAGCTGAACATTAACCTTA 120
QY 39 ThrGlyHisArgValAlaIleLysIleLeuAsnCysArgGlnMetArgAsnMetGluMet 58
DB 121 ACAGGGCATAAAGTTGCTCTCAAGATTCTCAATCGTGGAAAATCAAGAACATGGAATG 180
QY 59 GluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIle 78
DB 181 GAAGAAAAGTGAGAGGGAATTAATATATGAGATTGTTCATGCATCCCTCATCATTT 240
QY 79 ArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLys 98
DB 241 CGGCTGATGAGGTGTAGACACCATCAGATATATATGTTGTGATGAGATGTGAAA 300
QY 99 TyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArg 118
DB 301 TCTGTGAGCTGTTGATTATCATTTGTGAGAGGCGAGACTACAAAGAGATGAAGCTCGT 360
QY 119 ArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValAlaHis 138
DB 361 AAATCTTCCAGCAGATATCTCTGTGTGAGTACTGCCACAGGAACATGCTGTTCAT 420

QY 139 ArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAlaAsp 158
DB 421 AGAGATCTAAAGCCTGAGAACCTCTTTTGATTCCAAATGGAATGTGAAGATTGCAGAT 480
QY 159 PheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerPro 178
DB 481 TTTGGTGTGAGTAATATCATGCGTGATGCTCACTTCTCAAGACAAAGTTGTGTAGCCCA 540
QY 179 AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspVal 198
DB 541 AATTATGCTGCGCCGAGGTGATATCAGAAAGTTATATGCTGACCTGAGTAGATGTA 600
QY 199 TrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGlu 218
DB 601 TGGAGCTGTGTGTTATTTCTATATGCTCTCTGTGACACCCCTCATTTGATGATGAA 660
QY 219 AsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeu 238
DB 661 AACATTCCCAACCTCTTAAGAAAATTAAGGCTGTATGATATCTCTGCCACCATTTTA 720
QY 239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIle 258
DB 721 TCAGCTGTGCAAGGATCTGATCCCAAGATGCTTATAGTTGACCTATGAAGCGAATG 780
QY 259 ThrIleArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAla 278
DB 781 ACTATTCTGTGAGATTCTGATGCACCCCTTGCTCCAAAGCTCATGTACCAAGCTATTAGCT 840
QY 279 ValProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAsp 298
DB 841 GTACCTCCACAGATACGATGCAACAGGAAAAGATTGATGAGATATTTCTCAAGAG 900
QY 299 ValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGln 318
DB 901 GTGCTCAAAAGGGGATTTGACAGGAACAGCCTTGCTGCTCTGCAATAGAGTTGAG 960
QY 319 AsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGly 338
DB 961 AATGAGGGTACTGTGGCGTACTATTTGCTGTGAGAACCAAGTTCTGCTTCCAGTGGC 1020
QY 339 TyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
DB 1021 TACATGGAGCTGAATTCCAGAGACTATGGAATACGGTTATCATCAATAATTCAAGT 1080
QY 359 GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
DB 1081 GAAGTGTGCTTCCC--TGTGGCAACAATTGCTCGGAATATGAGATTTTCAACAAGTT 1137
QY 379 GlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAla 398
DB 1138 GGTGCGAGG---CAGTTTCCCGTGAAGGAATAGGGCTCTTGACCTCCAGTCTCGAGCG 1194
QY 399 HisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTyr 418
DB 1195 CATCCACGTGAGATATGACAGAGGTTCTGAAGCTCTGCAAGACTGAATGTAAGTTGG 1254
QY 419 LysLysAsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsn 438
DB 1255 AAGAAAGATCGGACCTTACAACATGAATGCCAATGGGTTCTCTGGCGTAACTGGCCATCAT 1314
QY 439 AspThrLeuAspAlaSerAsnSer-----PheLeuGly---AspSerThrIle 453
DB 1315 GAAGGCATG--AGTAATAATTCACATACATCCAAATTTCTTGGAGATGATTAACCCGTC 1371
QY 454 MetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGlnLeu 473
DB 1372 ATTGAAGACGGTGTGCTACT-----ATACCTAATGCAGTGAAGTTGAAGTTCAGCTT 1425
QY 474 TyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGlnLeu 493
DB 1426 TATAAACTCGGAGAGGAATAATACCTGCTTGAACCTTCAAGAGATCAAGGTTCCACAGTTTC 1485
QY 494 LeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509

Db 1486 CTTTCTTGATCTCTGCTGCTTCTTCCTTGCTCAGCTTCGGGTTCTC 1533

RESULT 14
ABZ12357
ID ABZ12357 standard; DNA; 1539 BP.
XX

AC ABZ12357;
XX
DT 21-JAN-2003 (first entry)
XX

DE Arabidopsis thaliana stress regulated gene SEQ ID NO 162.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX

OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX

PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US026685.
XX

PR 24-AUG-2000; 2000US-0227866P.
PR 26-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX

PA (SCRI) SCRIPPS RES INST.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX

PI Harper JF, Kreps J, Wang X, Zhu T;
XX

XX WPI; 2002-304127/34.
DR
XX
XX

PT Identifying a stress condition to which a plant cell has been exposed and
producing plants with increased tolerance to these abiotic stresses.
XX

PS Claim 144; SEQ ID NO 162; 577pp + Sequence Listing; English.
XX

CC The invention relates to identifying a stress condition to which a plant
cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office
XX

XX Sequence 1539 BP; 439 A; 291 C; 369 G; 440 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred. No.: 4.02e-184 Length: 1539
Score: 1903.50 Matches: 362
Percent Similarity: 82.03% Conservative: 58
Best Local Similarity: 70.70% Mismatches: 89
Query Match: 70.68% Indels: 3
DB: 6 Gaps: 1

US-09-857-522B-4 (1-509) x ABZ12357 (1-1539)

QY 1 MetAspGlySerSerLys-----GlySerGlyHisSerGluAlaLeuArgAsnTyr 17
Db 1 ATGATCATTCATCAATAATGATTGGCAATATAGAGTGAATCGATTTCACCGAATTAC 60

QY 18 AsnLeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLys 37
Db 61 AAGCTTGTAACCTCTTGGAATGGGCTTTTGGGAAGGTGAATAATAGACAGCATGTT 120

QY 38 LeuThrGlyHisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGlu 57

Db 121 CTCACAGGGCATTAAGCTTGCTATCAAAATCCTTAATCGTCGTAAGATCAACAATGGAG 180

QY 58 MetGluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIle 77
Db 181 ATGGAAGAGAAAGTGAGGAGGAGATTAGATTCTACGGTTGTTATGATCCTCATATT 240

QY 78 IleArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCys 97
Db 241 ATTGGCAGTATGAGTAATAGAACACCAAGACATTTATGTGTGATGAGTATGTC 300

QY 98 LysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAla 117
Db 301 AAGCTGAGAGACTCTTGATTATATGTTGAGAAAGCAGATTACAGAAGATGAGGCT 360

QY 118 ArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValVal 137
Db 361 CGTAACCTTTTCCAGCAGATAATATCTGGTGAAGTACTGCCATCGTAATATGCTTCTC 420

QY 138 HisArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAla 157
Db 421 CATAGAGACCTGAAGCCTGAGAAATTACTATTGGAFTCGAGGTGTAATATTGAAGATTGCA 480

QY 158 AspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySer 177
Db 481 GACTTTGGGTGAGTAATGTTATGCGGAGTGCATTTTCTAAAGACGAGTGTGGAAGC 540

QY 178 ProAsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAsp 197
Db 541 CCCAAGTACGCTGCTCCCGAGGTTATATCAAGTAATATATGCTGAGCCTGAAGTAGAT 600

QY 198 ValTrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAsp 217
Db 601 GTATGAGTTCGCGAGTTATATTGTCACGCTTATTATGCGGACTCTTCTTTGATGAT 660

QY 218 GluAsnIleProAsnLeuPheLysLysIleLysGlyIleTyrThrLeuProSerHis 237
Db 661 GAAACATTTCCAACTTTTCAAGAAATTGAAGGTGGATTATACACTTCCAAAGTCAT 720

QY 238 LeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArg 257
Db 721 TTATCATCTGAGGCTTAGAGACCTGATCCCAAGATGCTTATAGTTGACCCGGTGAAACGA 780

QY 258 IleThrIleArgGluIleArgLysIleGlnTrpPheGlnIleArgLeuProArgTyrLeu 277
Db 781 ATCACCATTCCCTGAGATCCGTCACACCCGTGGTCCAGACTCATCTCCCTCGTATCTT 840

QY 278 AlaValProProProAspThrThrGlnAlaLysMetIleAspGluAspThrLeuArg 297
Db 841 GCTGCTCTCCACCGGATACAGTAGAGCAGGCTAAAGATCAATGAGAGATAGTTCAA 900

QY 298 AspValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeu 317
Db 901 GAAGTGGTTAACATGGGATTGTGATAGAAACAGGTTTGGAAATCTCTACGCAACAGAAC 960

QY 318 GlnAsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSer 337
Db 961 CAAAACGATGCTACTGTTACATACCTGTTATTGATTAACCGGTTCCGTTCCAAGT 1020

QY 338 GlyTyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSer 357
Db 1021 GGCTATCTGAATCCGAGTTTCAGAGACAACAAGACAGTGGTTCCAAATCCTATGCGCACA 1080

QY 358 SerGluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSer 377
Db 1081 CCTGAAGCGGGCGCTTCAACCTGTAGGCCACTGGATTCTCGCAATGTGGATCACTACGGG 1140

QY 378 SerGlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArg 397
Db 1141 TTGGGAGCAAGATCACAAAGTCCCTGTTGATCGAAATGGGCTCTTGGACTTCAGTCTCAT 1200

QY 398 AlaHisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArg 417

Db 1201 GCGCATCCTCGTGAATCATGATGAAGTTTGAAGCTCTTCAAGAACTCAATGTGTGT 1260
Qy 418 TrPLysLysAsnGlyHisTYrAsnValLysCysargTrpCysProGlyPheProGluVal 437
Db 1261 TGAAGAAGATTGCTCACAACATGAATGTCGATGGTTCCTGGTTTAACTGATGCT 1320
Qy 438 AsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAsp 457
Db 1321 CAGATACTATGCTCAACAATCAGCTGCACCTTCAGAGATGAATCCAGCATCATTTGAGGAT 1380
Qy 458 AspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGlnLeuTYrLysThrLys 477
Db 1381 GACTGTGCCATGACTTCACCCACTGTCATCAAAATTGAACCTTCAGCTATACAAAGCCCGG 1440
Qy 478 AspAspLysTYrLeuLeuAspMetGlnArgValThrGlyProGlnLeuPheLeuAsp 497
Db 1441 GAAGAGAAGTACTTGGTGGATATACAGAGAGTTAACGGTCCGACGTTTCTTCTTGAT 1500
Qy 498 PheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
Db 1501 CTATGCCGCCCTTCTTACAGAGCTTCGTGTGATC 1536

RESULT 15

AAC44825
ID AAC44825 standard; DNA; 1792 BP.

XX AC AAC44825;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44271.

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX XX
PN EP1033405-A2.

XX PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 28-APR-1999; 99US-0130891P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 06-MAY-1999; 99US-0132487P.
PR 07-MAY-1999; 99US-0132863P.
PR 11-MAY-1999; 99US-0134256P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 14-MAY-1999; 99US-0134370P.
PR 18-MAY-1999; 99US-0134768P.
PR 19-MAY-1999; 99US-0134941P.

PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139492P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 26-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
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PR 28-OCT-1999; 99US-0161920P.
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PR 29-OCT-1999; 99US-0162142P.

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Best Local Similarity: 70.70%
Query Match: 70.68%
DB: 3
Length: 1792
Matches: 362
Conservative: 58
Mismatches: 89
Indels: 3
Gaps: 1

US-09-857-522B-4 (1-509) x AAC44825 (1-1792)

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QY 18 AsnLeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLys 37
Db 314 AAGCTTGTAAACTCTTGAATGGGCTTTGGGAAGGTGAATAAGACAGATGTT 373
QY 38 LeuThrGlyHisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGlu 57
Db 374 GTCACAGGGCATTAAGTTGCTATCAAAATCCTTAATCGTGAAGATCAAGAATGAG 433
QY 58 MetGluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIle 77
Db 434 ATGGAAGAGAAAGTGAGGAGGAGATTAGATTCTACGGTGTATTATGCATCTCATATT 493
QY 78 IleArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCys 97
Db 494 ATTCGGCAGTATGAGTAATAGAGACCAGAGTGAACATTATGTTGATGAGTATGTC 553
QY 98 LysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAla 117
Db 554 AAGCTCGAGAGCTCTTGATTATATGTGAGAAAGCAGATTACAGAAAGATGAGGCT 613
QY 118 ArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValVal 137
Db 614 CGTACTTTTTCACAGATAATATCTGGTGTAGAGTACTGCCATCGTAATATGTTGTC 673
QY 138 HisArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAla 157
Db 674 CATAGAGACCTGAAGCCTGAGAATTACTATTGGAATTCGAGGTGTAAATATTAAAGATTGCA 733
QY 158 AspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySer 177
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QY 178 ProAsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAsp 197
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QY 198 ValTrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAsp 217
Db 854 GTATGAGTTCGCGAGTTATATGTACGCTCTATATGCGGTACTCTTCCCTTTGATGAT 913
QY 218 GluAsnIleProAsnLeuPheLysLysIleLysGlyIleTyrThrLeuProSerHis 237
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QY 238 LeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValValGluPrometLysArg 257
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QY 258 IleThrIleArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeu 277
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QY      318 GlnAsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSer 337
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QY      418 TrpLysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPheProGluVal 437
Db      1514 TGGAAAGAAAGATTGGTCACTACAAACATGAATGCGTTCCGTGTTAGCTGATGGT 1573
QY      438 AsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAsp 457
Db      1574 CAGATTAATACTATGTCAACAATCAGCTGCACCTTCAAGATGAATCCAGCATCATTTGAGGAT 1633
QY      458 AspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLys 477
Db      1634 GACTGTGCCATGACTTCACCCCACTGTCAATTTGAACCTTCAAGTATACAAAGCCCGG 1693
QY      478 AspAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAsp 497
Db      1694 GAAGAGAAGTACTTGTGATATATACAGAGAGTTAACGGTCCGAGTTTCTTCTTGAT 1753
QY      498 PheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
Db      1754 CTATGCGCGCCTTTCTTACAGAGCTTCGTGTGATC 1789

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Search completed: July 9, 2004, 15:39:12
 Job time : 662 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 9, 2004, 13:46:15 ; Search time 3777 Seconds
(without alignments)
4024.318 Million cell updates/sec

Title: US-09-857-522B-4
Perfect score: 2693
Sequence: 1 MDGSSKSGSHSEALRNVNLG.....GPQLFLDFCAFLTKRLVL 509

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USPTO_spool/US09857522/runat_07072004_161357_1882/app_query.fasta_1.647
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFC=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09857522@CGN_1_1_3437@runat_07072004_161357_1882 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
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16: em_estom:*
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22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pco:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrt1:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 2693 | 100.0 | 1948 | 11 AY107942 | AY107942 Zea mays |
| 2 | 1356 | 50.4 | 1391 | 11 AY112453 | AY112453 Zea mays |
| 3 | 1331 | 49.4 | 784 | 14 CB620008 | CB620008 OSIEa040 |
| 4 | 1293.5 | 48.0 | 904 | 14 CA272308 | CA272308 SCVPLB208 |
| 5 | 1232 | 45.7 | 782 | 14 CB659701 | CB659701 OSJNEc160 |
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| 8 | 1193 | 44.3 | 829 | 14 CB621531 | CB621531 OSIIEa07H |
| 9 | 1189.5 | 44.2 | 863 | 12 BI950083 | BI950083 HVSME1001 |
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| 14 | 1156 | 42.9 | 704 | 14 CF307150 | CF307150 HDAL--05- |
| 15 | 1122 | 41.7 | 744 | 14 CF069225 | CF069225 EST669946 |
| 16 | 1121 | 41.6 | 725 | 14 CK266614 | CK266614 EST712692 |
| 17 | 1119 | 41.6 | 1707 | 11 AMPKAL | AF100763 Homo sapi |
| 18 | 1111 | 41.3 | 733 | 14 CD938346 | CD938346 OV.109M09 |
| 19 | 1110 | 41.2 | 674 | 13 CA077133 | CA077133 SCQAM104 |
| 20 | 1106.5 | 41.1 | 2698 | 11 AK044030 | AK044030 Mus muscu |
| 21 | 1104 | 41.0 | 706 | 14 CA999071 | CA999071 S234M_G05 |
| 22 | 1095.5 | 40.7 | 848 | 14 CD436812 | CD436812 EL01N0363 |
| 23 | 1079 | 40.1 | 641 | 12 BJ292522 | BJ292522 BJ292522 |
| 24 | 1078 | 40.0 | 650 | 13 CA125391 | CA125391 SCRLR101 |
| 25 | 1077.5 | 40.0 | 778 | 12 BM412960 | BM412960 EST587287 |
| 26 | 1076 | 40.0 | 769 | 13 BQ165510 | BQ165510 EST611379 |
| 27 | 1074 | 39.9 | 676 | 14 CF574471 | CF574471 MCSA115H0 |
| 28 | 1061 | 39.4 | 705 | 14 CD894428 | CD894428 G118_126D |
| 29 | 1054.5 | 39.2 | 727 | 13 BQ245383 | BQ245383 TAB15025C |
| 30 | 1053 | 39.1 | 753 | 14 CB669005 | CB669005 OSJNEe01C |
| 31 | 1046 | 38.8 | 956 | 13 CA149321 | CA149321 SCJLR2102 |
| 32 | 1041 | 38.7 | 679 | 14 CA222838 | CA222838 SCBGF404 |
| 33 | 1040 | 38.6 | 753 | 14 CD836075 | CD836075 BN45_047J |
| 34 | 1037 | 38.5 | 690 | 14 CF441983 | CF441983 EST678328 |
| 35 | 1034 | 38.4 | 699 | 14 CD872331 | CD872331 AZO2_120G |
| 36 | 1026 | 38.1 | 649 | 13 CA009258 | CA009258 HUI13K01x |
| 37 | 1023.5 | 38.0 | 801 | 14 CD826492 | CD826492 BN25_064A |
| 38 | 1023 | 38.0 | 728 | 14 CD938735 | CD938735 OV.110N12 |
| 39 | 1019 | 37.8 | 869 | 13 BQ504943 | BQ504943 EST612358 |
| 40 | 1010.5 | 37.5 | 940 | 13 BX706016 | BX706016 BX706016 |
| 41 | 1010 | 37.5 | 660 | 13 BQ462834 | BQ462834 HI02C11r |
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| 43 | 1003 | 37.2 | 617 | 14 CA997919 | CA997919 S234A1_E0 |
| 44 | 1002 | 37.2 | 620 | 13 BQ579704 | BQ579704 WHE2973_F |
| 45 | 993 | 36.9 | 663 | 12 BJ246813 | BJ246813 BJ246813 |

ALIGNMENTS

| | | | | | |
|------------|-----------------------------------|-------------|------|--------|--|
| RESULT 1 | AY107942 | 1948 bp | mRNA | linear | HTC 16-OCT-2002 |
| LOCUS | AY107942 | | | | |
| DEFINITION | Zea mays PCO079657 mRNA sequence. | | | | |
| ACCESSION | AY107942 | | | | |
| VERSION | AY107942.1 | GI:21211020 | | | |
| KEYWORDS | HTC. | | | | |
| SOURCE | Zea mays | | | | |
| ORGANISM | Zea mays | | | | |
| REFERENCE | 1 (bases 1 to 1948) | | | | |
| | | | | | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. |

AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1948)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schnable, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
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/note="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by DuPont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"

ORIGIN

Alignment Scores:
Pred. No.: 8.43e-298 Length: 1948
Score: 2693.00 Matches: 509
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-857-522B-4 (1-509) x AY107942 (1-1948)

OY 1 MetAspGlySerSerIySgIySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
DB 173 ATGGATGGAAGTAGTAAGGAGGTGGCATTCTGAAGCATTTAAGGAATCAACCTGGGA 232
OY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
DB 233 AGAACTTAGGTATCGGTACATTGGAAAAAGTGAAGATTGCAGAGCATTAAGCTTACTGGA 292
OY 41 HisArgValAlaIleLysIleIleAsnCySAArgGlnMetArgAsnMetGlnMetGluGlu 60
DB 293 CATAGGGTGTCTATAAAGATCATCAACTGCCGCCAATGAGAATATGAAATGGAAGAG 352
OY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
DB 353 AAAGCAAGAGAGAAATTCAGATATTTGAAGTTGTTCATTCACCCCATATCATTCGGCTT 412
OY 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly 100
DB 413 TATGAGGTCAATATACACCTACAGATATATATATGTGTGATGGAATATTGTAGTATGCC 472
OY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
DB 473 GAGTTATTGTATTACATTGTGAGAAAGCGAGATTACAGAAAGATGAAGCTCGTCAATC 532
OY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAsp 140
DB 533 TTCACAGACATCATATCTGGCGTCAATACTGCCATAGAAACATGTTGTCCACCGTGAC 592
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OY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSer 200
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OY 381 ArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAlaHisPro 400
DB 1313 CGGCCATATTATCCTGTTGAAGAAATGGCGCTTGGACTTCAGTCTCGGGCCACCCT 1372
OY 401 ArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrpLysLys 420
DB 1373 CGTGAATATATGTTGAGGCTTTAAAGCACTTCAAGATTAAACGTCAAGATGGAAGAAG 1432
OY 421 AsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPheProGluValAsnAspThr 440
DB 1433 AATGGGCACTACAAAGTGAATGCAGATGGTCCCAAGGTTTCTGTAAGTTAATGACACG 1492
OY 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
DB 1493 TTAGATGCCAGAACAGCTTCTTGTACTCTACCATCATGGAATAATGATGATGCTAAT 1552
OY 461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLysAspAspLys 480
DB 1553 GGGAGGCTACCTACTGTGATCAAGTTGAATTCACAGCTTTACAAAGCAGAAAGCAGCAAG 1612
OY 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
DB 1613 TACCTCTTAGATATGCAGAGAGATTACTGCACTCAGCTGCTCTTCTGACTTCTGTGCG 1672
OY 501 AlaPheLeuThrLysLeuArgValLeu 509
DB 1673 GCCTTCTTACCAGCTTAGGGTTCTA 1699

| RESULT 2 | AY112453 | 1391 bp | mRNA | linear | HTC 17-OCT-2002 |
|--|---|---------------|------|--------|-----------------|
| LOCUS | AY112453 | | | | |
| DEFINITION | Zea mays CL7115_1 mRNA sequence. | | | | |
| ACCESSION | AY112453 | | | | |
| VERSION | AY112453.1 | GI:21217043 | | | |
| KEYWORDS | HTC. | | | | |
| SOURCE | Zea mays | | | | |
| ORGANISM | Zea mays | | | | |
| REFERENCE | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea. | | | | |
| AUTHORS | 1 (bases 1 to 1391) | | | | |
| TITLE | Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V. | | | | |
| JOURNAL | Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes | | | | |
| REFERENCE | Unpublished (2002) | | | | |
| AUTHORS | 2 (bases 1 to 1391) | | | | |
| TITLE | Coe,E.H. | | | | |
| JOURNAL | Direct Submission | | | | |
| COMMENT | Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA | | | | |
| FEATURES | If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org ; ZmDB, www.zmdb.iastate.edu ; TIGR, www.tigr.org ; or NCBI, www.ncbi.nlm.nih.gov . When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu . | | | | |
| source | Location/Qualifiers | | | | |
| | 1..1391 | | | | |
| | /organism="Zea mays" | | | | |
| | /mol_type="mRNA" | | | | |
| | /db_xref="MaizEDB:632803" | | | | |
| | /db_xref="taxon:4577" | | | | |
| | /clone_lib="Maize Mapping Project/DuPont Cornsensus library" | | | | |
| | /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project" | | | | |
| ORIGIN | | | | | |
| Alignment Scores: | | | | | |
| Pred. No.: | 2.8e-144 | Length: | 1391 | | |
| Score: | 1356.00 | Matches: | 265 | | |
| Percent Similarity: | 76.25% | Conservative: | 40 | | |
| Best Local Similarity: | 66.25% | Mismatches: | 91 | | |
| Query Match: | 50.35% | Indels: | 4 | | |
| DB: | 11 | Gaps: | 2 | | |
| US-09-857-522B-4 (1-509) x AY112453 (1-1391) | | | | | |
| QY | 1 MetAaPGLySerSerLySGlySerGlyHisSerGluAlaLeuArgAsnTyArgnLeuGly 20 | | | | |
| DB | 90 ATGAGGAGGAGCGGGAAGA-----GATGCCAACCCCTTTGAGCGGTTACAGAAATTGGC 140 | | | | |
| QY | 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40 | | | | |
| DB | 141 AAAACCTGGGAATTGGGTGCTTCGGTAAAGTGAAGATCGCGGAACATATATGACTGGT 200 | | | | |
| QY | 41 HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGluGlu 60 | | | | |
| DB | 201 CATAAGGTGGCGATCAAGATTCTCAATCGCAAGAGATCAGAAGCATGATANNNNNNNN 260 | | | | |
| QY | 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80 | | | | |
| DB | 261 NNNNNNNNNNNNNNNNNNNNAAGATACCTAGATTAATTATGATCATCTCATATCATACGCCCTT 320 | | | | |

| | | | |
|----|------|---|------|
| QY | 81 | TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly | 100 |
| | | | |
| Db | 321 | TATAGAGTGTAGATACACCTGCTGATATCTGTGTTTATGGAGTATGTTAAATCTGGA | 380 |
| | | | |
| QY | 101 | GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluIleArgArgIle | 120 |
| | | | |
| Db | 381 | GAGTGTGTGATTACATCGTTGGAAGGAGGCTACACGAAGAGGAAGCCGACACMN | 440 |
| | | | |
| QY | 121 | PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp | 140 |
| | | | |
| Db | 441 | NNNCAGCAGATCATATCTGTGTGTTGAATATTGCCATAGAACATGTTGCTCACCGTGAT | 500 |
| | | | |
| QY | 141 | LeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly | 160 |
| | | | |
| Db | 501 | TTAAGCCAGAGAATCTTCTTTGGAATCAAATGCAATGTTAAGATTGCCATTTTGGC | 560 |
| | | | |
| QY | 161 | LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr | 180 |
| | | | |
| Db | 561 | TTAAGTAATATATATGCGTGAATGCTTCTTAAGACGAGTTGTGTAGCCCGAATTAT | 620 |
| | | | |
| QY | 181 | AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSer | 200 |
| | | | |
| Db | 621 | GCAGCACCCTGAGGTCATATCTGTAAACTATATGCTGTCCTGAAGTTGACATCTGGAGC | 680 |
| | | | |
| QY | 201 | CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle | 220 |
| | | | |
| Db | 681 | TGTGAANNNNNNNNNNNNNNNNNNNNNNNTGGCAGCTCTCCATTGACGATGAGAATATT | 740 |
| | | | |
| QY | 221 | ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla | 240 |
| | | | |
| Db | 741 | CCAACCTTTNNNNNNNNNNNNNNNNNNNNNTATACCTTCTAGTCAATTGTACACCT | 800 |
| | | | |
| QY | 241 | LeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIleThrIle | 260 |
| | | | |
| Db | 801 | TCAGCGAGGACTTGATTCCTAGAATGCTGTTGNNNNNNNNNNNNNNNNNNNNNNN | 860 |
| | | | |
| QY | 261 | ArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAlaValPro | 280 |
| | | | |
| Db | 861 | NNNNNNNNNNNNNNNNNTGTGTGTTCAAAATCCGACTTCGGCTATTGCTGTACCG | 920 |
| | | | |
| QY | 281 | ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal | 300 |
| | | | |
| Db | 921 | CCTCCAGACACTGCTCAACAAGTTAAGAAGCTGACGAGGAACCTTAATGATGTTATT | 980 |
| | | | |
| QY | 301 | AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu | 320 |
| | | | |
| Db | 981 | AAGATGGGTTTGGACAGAATCAGCTAATTGAATCTTCACACACAGATTGCCAATGAG | 1040 |
| | | | |
| QY | 321 | AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu | 340 |
| | | | |
| Db | 1041 | GCAACAGTTGCCATTATTACTATCATGACAAATAGCTTCGTACAAACCAAGTGTATCTT | 1100 |
| | | | |
| QY | 341 | GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer | 360 |
| | | | |
| Db | 1101 | GGATCTGAGTTTCAAGAATCTATGAGACTCATCTTCTCTCAAGTAATC--GCTGAACA | 1157 |
| | | | |
| QY | 361 | SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu | 380 |
| | | | |
| Db | 1158 | CCAACCTTCAACAACACTGAACCTTCGCATGAGGTTTTCAGAATCTCCAGGTTCTGGCTTG | 1217 |
| | | | |
| QY | 381 | ArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAlaHisPro | 400 |
| | | | |
| Db | 1218 | AGGACGATTTTGCAGCTGAAGAAATGGCCCTTGTCTTCACTGACGACATCCA | 1277 |
| | | | |

ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 784)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2003)
TITLE Contact: Rod Wing
JOURNAL Arizona Genomics Institute
COMMENT University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
plate: 04 row: 0 column: 23
Seq primer: gta aaa cga cgg cca gtc.
FEATURES
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/mol_type="mRNA"
/cultivar="IR36"
/db_xref="taxon:39946"
/clone="OSIRa04023"
/issue_type="leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSIRa"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Lesion Mimic SPL 11"
ORIGIN
Alignment Scores:
Pred. No.: 7.86e-142 Length: 784
Score: 1331.00 Matches: 249
Percent Similarity: 98.46% Conservative: 7
Best Local Similarity: 95.77% Mismatches: 4
Query Match: 49.42% Indels: 0
DB: 14 Gaps: 0
US-09-857-522B-4 (1-509) x CB620008 (1-784)
QY 54 ArgAsnMetGluMetGluGluValAlaLysArgGluPheLysIleLeuLysLeuPheIle 73
Db 1 AGAAATATGAAATGAGAGAGAAAGCAAAAGAGAGAAATCAAGATACTGAGATTGTTCAAT 60
QY 74 HisProHisIleIleArgLeuTyrGluValIleTyrThrProThrAspIleTyrValVal 93
Db 61 CATCCCATATCATTCGCTTTATGAGGTATATACACTCTACGATATATATGTTGTG 120
QY 94 MetGluTyrCysLysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGln 113
Db 121 ATGAGTACTGCAAGTTTGAGAACTGTTGATTACATTGTTGAGAAAGCGAGTTGCAG 180
QY 114 GluAspGluAlaArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArg 133
Db 181 GAAGATGAGGCTCGCCGATCTTCCAGCAGATATATCTGGGGTAGAATATGCCACAGA 240
QY 134 AsnMetValValHisArgAspLeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsn 153
Db 241 AACATGGTGTTCATCGTATCTGAAGCCAGAAACTTGCTACTGATTCAAAGTATAAT 300
QY 154 ValLysLeuAlaAspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThr 173
Db 301 GTAAAGCTTGCTGACTTTGGTTTGAGTAACGTCATGCATGCGCCATTTTTGAAGACA 360
QY 174 SerCysGlySerProAsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGly 193

Db 361 AGCTGTGGAGTCCAAACTATGCTGCTCCAGAGGTGATCTCTGTAATATATGCTGGA 420
QY 194 ProGluValAspValTyrSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeu 213
Db 421 CCTGAGGTTCATGTATGAGAGCTGTGAGTGCATCCTTATGCTCTCTTGTGACTCTT 480
QY 214 ProPheAspAspGluAsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThr 233
Db 481 CCATTGTATGATGAGAATATCCCAACTATTCAAAAAGATAAAGGTGTATATATACT 540
QY 234 LeuProSerHisLeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValGlu 253
Db 541 CTCCCAAGTCATTTATCTGCTCTGGCCAGAGATTGATCCCAAGATGCTTGTGTGAT 600
QY 254 ProMetLysArgIleThrIleArgGluIleArgGluHisGlnTyrPheGlnIleArgLeu 273
Db 601 CCAATGAAGAGATCACAATTCGTGAATTCGAGAGCATCAGTGGTTTCAGATTGCCCTT 660
QY 274 ProArgTyrLeuAlaValProProProAspThrThrGlnGlnAlaLysMetIleAspGlu 293
Db 661 CCTCGTTACTTAGCAGTGCTCTCCACGACACAGACAGCAAGCCAATGATTGATGAA 720
QY 294 AspThrLeuArgAspValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeu 313
Db 721 GATACCCCTTCAAGATGTCGTANACTTGGGTTATGGAAGAAGCACCATGTGTGATCTCTG 780
RESULT 4
CA272308 904 bp mRNA linear EST 26-SEP-2003
LOCUS SCVPLB2089A09.g LB2 Saccharum officinarum cDNA clone SCVPLB2089A09
DEFINITION 5', mRNA sequence.
ACCESSION CA272308
VERSION CA272308.1 GI:35983605
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
REFERENCE 1 (bases 1 to 904)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCESF
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
CONTACT: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
plate: 089 row: A column: 09
Seq primer: T7 Promoter Primer.
FEATURES
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1..904
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/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCVPLB2089A09"
/lab_host="DH10B"
/clone_lib="LB2"
/note="Organ: lateral buds from plants adult plants
growing in greenhouse; Vector: pSport1; Site_1: SalI;
Site_2: NotI; An unidirectional cDNA library generated
from [lateral buds from plants adult plants growing in
greenhouse]. cDNA was prepared from polyA+ mRNA using
Superscript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details

of each source of RNA and library construction can be
obtained at <http://sucest.lad.ic.unicamp.br/public>"

ORIGIN

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 2.06e-137 | Length: | 904 |
| Score: | 1293.50 | Matches: | 257 |
| Percent Similarity: | 91.28% | Conservative: | 15 |
| Best Local Similarity: | 86.24% | Mismatches: | 25 |
| Query Match: | 48.03% | Indels: | 4 |
| DB: | 14 | Gaps: | 0 |

US-09-857-522B-4 (1-509) x CA272308 (1-904)

| | | | |
|----|-----|--|-----|
| QY | 74 | HisProHisIleIleArgLeuTyrGluValIleTyrThrProThrAspIleTyrValVal | 93 |
| DB | 4 | CACCCCCATATCATCCGCTTTATGAGGTCAATATACACACCAACAGATATATATGTGTG | 63 |
| QY | 94 | MetGluTyrCysLysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGln | 113 |
| DB | 64 | ATGGAATATTGAGGTATGGCGAGTGTGTTGATTACATGTTGTGAGAAAGCGAGTTACTA | 123 |
| QY | 114 | GluAspGluAlaArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArg | 133 |
| DB | 124 | GAAAGATGAGCTCGCCGATCTTCCAGCAGATCATATCTGGTGTGCAATACTGCCATAGA | 183 |
| QY | 134 | AsnMetValHisArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsn | 153 |
| DB | 184 | AACATGGTGTCCACCGCTGACCTAAAGCCAGAAACTTGTACTGTATCAAGATAAT | 243 |
| QY | 154 | ValLysLeuAlaAspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThr | 173 |
| DB | 244 | GTAACACTTGCTGACTTTGTTGAGCAATGTCATGATGGCCATTTTGAAGACC | 303 |
| QY | 174 | SerCysGlySerProAsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGly | 193 |
| DB | 304 | AGCTGTGGAGTCCGAATATGCTGCTCCAGAGTATATCTGTAAACTATATGCTGGA | 363 |
| QY | 194 | ProGluValAspValIrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeu | 213 |
| DB | 364 | CCTGAGGTGATGTAGAGTGTGTGAGTGAATCTTATGCTCTTCTTGTGAACCTCTT | 423 |
| QY | 214 | ProPheAspAspGluAsnIleProAsnLeuPheLysIleLysGlyGlyIleTyrThr | 233 |
| DB | 424 | CCATTGTGATGAGATATATCCCAACCTGTTCAAAAAATTAAAGGAGGATATCTACACA | 483 |
| QY | 234 | LeuProSerHisLeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValGlu | 253 |
| DB | 484 | CTTCCAAGTCATTATCTGCTTTGGCTAGGATTTGATCCACGAATGCTTGTGTGAG | 543 |
| QY | 254 | ProMetLysArgIleThrIleArgGluIleArgGluHisGlnIrpPheGlnIleArgLeu | 273 |
| DB | 544 | CCTATGAAGAGATCACAATTCGGGAATTCGGAGCATCAATGTTCCAGACTCGCCTT | 603 |
| QY | 274 | ProArgTyrLeuAlaValProProProAspThrThrGlnGlnAlaLysMetIleAspGlu | 293 |
| DB | 604 | TCTCGTTACTTGGCAGTGCCTTCACCAAGACGACACACAACAAGCCAAAATGATTGAA | 663 |
| QY | 294 | AspThrLeuArgAspValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeu | 313 |
| DB | 664 | GATACACTTCGAGATGTGGT-AATATGGGATTAACAAG-AAACATGTGTG-GAATCCTG | 720 |
| QY | 314 | CysSerArgLeuGlnAsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPhe | 333 |
| DB | 721 | TGCACCAAACTTAAATAGAGCACTGGTGCATATATTACTATTGGACAATTGGTTA | 780 |
| QY | 334 | ArgAlaThrSerGlyTyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsn | 353 |
| DB | 781 | AAAGCAACTAGTGGCTTTTGGGGCCGAATTCAAAAATCAAGGGGCCAGGATTTTAA | 840 |
| QY | 354 | GlnLeuAlaSerSerGlu-SerSerSerSerGlyThrArgAsnTyrValPro | 370 |
| DB | 841 | TTACTGGCGGGCCAAATAATTAAATTTTGGGCCCAAGAAATTTTTCACA | 892 |

RESULT 5

CB659701

LOCUS

OSJNEC16012.f

clone OSJNEC16012 5', mRNA sequence.

CB659701

CB659701.1

GI:29663426

EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 782)

Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,B.,

Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

large-scale identification of ESTs involved in the interaction

between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: <http://genome.arizona.edu>

PCR Primers

FORWARD: gta aag cga cca gtc

BACKWARD: gga aac agc tat gac cat g

Plate: 16 row: 0 column: 12

Seq primer: gta aag cga cca gtc.

Location/Qualifiers

1..782

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="OSJNEC16012"

/issue_type="Leaf"

/dev_stage="3 week"

/lab_host="DH10B"

/clone_lib="OSJNEC"

/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:

XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN

Alignment Scores:

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|------------------------|----------|---------------|-----|
| Pred. No.: | 1.9e-130 | Length: | 782 |
| Score: | 1232.00 | Matches: | 231 |
| Percent Similarity: | 98.76% | Conservative: | 7 |
| Best Local Similarity: | 95.85% | Mismatches: | 3 |
| Query Match: | 45.75% | Indels: | 0 |
| DB: | 14 | Gaps: | 0 |

US-09-857-522B-4 (1-509) x CB659701 (1-782)

| | | | |
|----|-----|--|-----|
| QY | 1 | MetAspGlySerSerLysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly | 20 |
| DB | 59 | ATGATGGAATGCTAAAGCGCGTGGCATTTCTGAGGCACCTGAAGAACTACATCTTGA | 118 |
| QY | 21 | ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGlnHisLysLeuThrGly | 40 |
| DB | 119 | AGAACTTATGATTTGGCTCATTTTGAAGAAAGTGAAGATTGCAGACGATTAAGCTTACAGGA | 178 |
| QY | 41 | HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGluGlu | 60 |
| DB | 179 | CACAGAGTTCCTATTAAGATCCGGAACCGCCGCAAAATGAGAAATATGAAATGAGAGAG | 238 |
| QY | 61 | LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu | 80 |
| DB | 239 | AAAGCAAGAGAAATCAAGATATGAGATTGTTCAATTCATCCCATATCATTCGCTT | 298 |

| | | | | |
|----|--|-----|--|-----|
| OY | | 81 | TyGluValIleTyrThrProThrasPileTyrValValMetGluTyrCysLysTyrGly | 100 |
| Db | | 299 | TATGAGGTATATAACACTCTCAACGATATATATGTGGTGAGTAGTA | 358 |
| OY | | 101 | GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnIuaspGlualAargArgIle | 120 |
| Db | | 359 | GAACTGTTGATTACATTGTTGAAGAAGGCAGGTTCAGGAAGATGAGGCTCGCCGAATC | 418 |
| OY | | 121 | PheGInglNlleIleSerGlyValGluTyrCysHisArgasnMetValValHisArgasp | 140 |
| Db | | 419 | TTCACAGCATTTATATCTGGGGTTGAATACCTGCCACAGAACATGTGGTTCA | 478 |
| OY | | 141 | LeuLysProGluasnlLeuleuLeuaspserylSTyrAsnValLlysLeuaLaaspPheGly | 160 |
| Db | | 479 | CTGAAGCCAGAAAACCTTGCTACTGATTCAAAGTATATGTAAGCTTGCTGACTTGGT | 538 |
| OY | | 161 | LeuSerAsnValMethIsaspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr | 180 |
| Db | | 539 | TTGAGTAACGTCATGCATGATGGCCATTTTTTGAAGACAAGCTGTGGAGTCCAACATAT | 598 |
| OY | | 181 | AlaAlaProGluValIleSercylLysLeuTyrAlaGlyProGluValAspValTrpSer | 200 |
| Db | | 599 | GCTGCTCCAGAGGTGATCTCTGGTAATAATATATGCTGACCAGCTGAGTTGATGATGAGC | 658 |
| OY | | 201 | CysGlyValIleLeuTyrAlalaLeuLeuCysGlyThrLeuProPheaspGluasnIle | 220 |
| Db | | 659 | TGTGAGGTGATCCTTATGCTCTCCTTGTGTGACTCTTCCATTGATGATGAGAATATC | 718 |
| OY | | 221 | ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla | 240 |
| Db | | 719 | CCCCAACCTATTCAAAAAGATAAAGGGTGATATATATACTCTCCCAAGTCATTATCTGCT | 778 |
| OY | | 241 | Leu 241 | |
| Db | | 779 | CTG 781 | |

```

RESULT 6
LOCUS      CB677208                                779 bp    mRNA    linear    EST 09-APR-2003
DEFINITION OSJNE13013.f OSJNEE Oryza sativa (japonica cultivar-group) cDNA
            clone OSJNE13013 5', mRNA sequence.
ACCESSION  CB677208
VERSION     CB677208.1  GI:29680933
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (bases 1 to 779)
            Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
            Kudrna,D., Dean,R., Sodelund,C., Wing,R. and Wang,G.
            large-scale identification of ESTs involved in the interaction
            between rice and Magnaporthe grisea
            Unpublished (2003)
JOURNAL     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
PCR PRIMERS
FORWARD:   gta aac cga cgg cca gtc
BACKWARD:  gga aac agc tat gac cat g
Plate: 13  row: 0  column: 13
Seq primer: gta aac cga cgg cca gtc.
            Location/Qualifiers
1..779
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"

```

```

/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNE13013"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNE"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (70-15)"

```

ORIGIN

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 8.36e-128 | Length: | 779 |
| Score: | 1209.00 | Matches: | 227 |
| Percent Similarity: | 93.44% | Conservative: | 15 |
| Best Local Similarity: | 87.64% | Mismatches: | 17 |
| Query Match: | 44.89% | Indels: | 0 |
| DB: | 14 | Gaps: | 0 |

US-09-857-522B-4 (1-509) x CB677208 (1-779)

[illegible]

```

RESULT 7
LOCUS      CB632244                      850 bp    mRNA       linear     EST 08-APR-2003
DEFINITION OSIEB10F22.f OSIEB Oryza sativa (indica cultivar-group) cDNA
ACCESSION  CB632244
VERSION     CB632244.1   GI:29627233
KEYWORDS    EST.
SOURCE      Oryza sativa (indica cultivar-group)
ORGANISM    Oryza sativa (indica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartioideae; Oryzaceae; Oryza.
REFERENCE   1 (bases 1 to 850)
AUTHORS     Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
            Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE       Large-scale identification of ESTs involved in the interaction
            between rice and Magnaporthe grisea
JOURNAL     Unpublished (2003)
COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: http://genome.arizona.edu
PCR PRIMERS
FORWARD:    gta aaa cga cgg cca gtg
BACKWARD:    gga aac agc tat gac cat g
Plate: 10 row: F column: 22
Seq primer:  gta aaa cga cgg cca gtg.
FEATURES
    source             location/Qualifiers
                1..850
                     /organism="Oryza sativa (indica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="IR36"
                     /db_xref="taxon:39946"
                     /clone="OSIEB10F22"
                     /tissue_type="Leaf"
                     /dev_stage="3 week"
                     /lab_host="DH10B"
                     /clone_lib="OSIEB"
                     /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after inoculation with Rice Blast (PO6-6-3)"

ORIGIN
Alignment Scores:
Pred. No.:          1.37e-126           length:          850
Score:              1199.00             Matches:           226
Percent Similarity: 97.50%              Conservative:      8
Best Local Similarity: 94.17%            Mismatches:        6
Query Match:        44.52%              Indels:            0
DB:                 14                   Gaps:              0

US-09-857-522B-4 (1-509) x CB632244 (1-850)

QY      1 MetAspGlySerSerLySGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly  20
Db      130 ATGGATGGAATGTCTAAAGGCCGTGGCATTCTGAGGCACCTGAAGAATAACAATCTTGCA  189
QY      21 ArgThrLeuGlyILEGlyThrPheGlyLYsvAllysileaglHisLysLeuthrgly  40
Db      190 AGAACCTTAGGTATTGGCTCATTTGGAAAAAGTGAAGATTGCAGAGCATTAAGCTTACAGGA  249
QY      41 HisArgValAlaIleLysIleleasnCySArgGlnMetArgAsnMetGlnMetGlnGlu  60
Db      250 CACAGAGTTGCTATAAAGATCCTGAACCGCCGCAATGAGAAATATGGAATGAGAGAG  309
QY      61 LySAIalysArGluPhelYslleleuLysleuPheIlleHIsProHISlIleArgLeu  80
Db      310 AAAGCAAAGAGAAATCAAGATACTGAGATTGTTCATTTCATCCCACATATCATTCGCCCTT  369

```

| | | | |
|----|-----|--|-----|
| QY | 81 | TyrgluValIleIyrThrproThraspIleIyrValValmetGluTyrCysIysTyrGly | 100 |
| Db | 370 | TATGAGGTATATACACTCTCCTACGATATATATGTGTGATGGAGTACTGCACAGTTTGGAA | 429 |
| QY | 101 | GluleupheaspTyrIleValGluIysGlyArgleuGlnGluaspGluIaArgArgIle | 120 |
| Db | 430 | GAACGTGTTGATTACATTGTTGAGAAAGGACAGGTTCACGAAAGATGAGGCTCGCCGAAATC | 489 |
| QY | 121 | PheGlnGlnIleIeserGlyValGluTyrCysHisArgAsnMetValIHisArgasp | 140 |
| Db | 490 | TTCACGACAGATTATATCTGGGGTAGAATACTGCCACAGAAACATGGTGTTCATCGTGAT | 549 |
| QY | 141 | LeuIysProGluAsnleuleuleuAspSerIysTyrAsnValIysleuAlaaspPheGly | 160 |
| Db | 550 | CTGAAGCCAGAAACCTGTGCTACTGGATTCAAGATTAATGTAAGCTTGCTGACTTTCGT | 609 |
| QY | 161 | LeuSerAsnValMetHisaspGlyHisPheleuIysThrSerCysGlySerProAsnTyr | 180 |
| Db | 610 | TTGAGTAACGTCATGCATGATGGCCATTTTGTGAAGACAAGCTGTGGAGTCCAAACTAT | 669 |
| QY | 181 | AlaAlaProGluValIleIeserGlyIysleuTyrAlaGlyProGluValAspValTrpSer | 200 |
| Db | 670 | GCTGCTCCAGAGGTGATCTCTGTGATATATATATGCTGCAGCCTGAGGTGATGAGACC | 729 |
| QY | 201 | CysGlyValIleleuTyrAlaIeuleuCysGlyThrleuProPheaspaspGluAsnIle | 220 |
| Db | 730 | TGAGGAGTGATCCCTTATGCTCTCTCTTGTGGCACTCTTCATATGATGATGAGATAATC | 789 |
| QY | 221 | ProAsnleuPheIysIysIleIysGlyGlyIleIyrThrleuProSerHisleuSerAla | 240 |
| Db | 790 | CCCAACCTATTCAAAAAGATAAAGGGTGGTATATATACTCCCGAGTCATTATCTGCT | 849 |

```

RESULT 8
CB621531
LOCUS
DEFINITION CB621531 829 bp mRNA linear EST 08-APR-2003
OSIEa07H13.f OSIEa Oryza sativa (indica cultivar-group) cDNA
clone OSIEa07H13 5', mRNA sequence.
ACCESSION
VERSION CB621531
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: H column: 13
Seq primer: gta aac cga cgg cca gtg.
Location/Qualifiers
1. 829
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/cultivar="IR36"
/db_xref="taxon:39946"
/clone="OSIEa07H13"
/tissue_type="leaf"
/dev_stage="3 week"
FEATURES
Source

```

```

/1ab_host="DH10B"
/clone_lib="OSIRIa"
/note="Vector: pBluescript II KS +, Site_1: EcoRI, Site_2:
XhoI, Lesion Mimic SPL 11"

```

| | |
|------------------------|-----------------|
| Alignment Scores: | |
| Pred. No.: | 6.44e-126 |
| Score: | 1193.00 |
| Percent Similarity: | 98.71% |
| Best Local Similarity: | 95.71% |
| Query Match: | 44.30% |
| DB: | 14 |
| | Gaps: 0 |
| | Length: 829 |
| | Matches: 223 |
| | Conservative: 7 |
| | Mismatches: 3 |
| | Indels: 0 |
| | Gaps: 0 |

US-09-857-522B-4 (1-509) x CB621531 (1-829)

| | | | | |
|----|--|-----|--|-----|
| OY | | 1 | MecaspGlySerSerLySglYserGlyHisSerGlValAlaLeuArgAsnTYrAsnLeuGLy | 20 |
| Db | | 130 | ATGGATGGAATGCTAAAGCGCGTGCCATTCTGAGGCACCTGAAGAATTACAATCTTGA | 189 |
| OY | | 21 | ArgThrleuGLyIleGLyThrpheGLyLysVallysilealGLuHisLysleuthrgLy | 40 |
| Db | | 190 | AGAACTTAGGTATTGGCTCATTTGGAAAAGTGAAGATTGCAGAGCATACTTA CAGGA | 249 |
| OY | | 41 | HisargValAlaIlellysileleasnCySarGLMetArgAsnMetGlumetGluglu | 60 |
| Db | | 250 | CACAGACTTGCTATAAAGATCCTGAACCCGCCCAATGAGAATATGGAATGAGAGAG | 309 |
| OY | | 61 | LysalaLysArgrGLuphelysileleuLysleuPheIleHisProHislelleArgleu | 80 |
| Db | | 310 | AAGCAAGAGAGAAATCAAGATACCTGAGATTGTCATTCAATCCCCATATCATTCGCCCTT | 369 |
| OY | | 81 | TyrGlValIleTyrrThrProthrAspileTyrrValValMetGlutyrcylsTyrgLy | 100 |
| Db | | 370 | TATGAGGTATATACACTCCCTACGATATATATGTGTGATGAGTACTGCAAGTTTGA | 429 |
| OY | | 101 | GluLeupheasPTyrlleValGlulysGLyArgleungluAspGLuaIaArgArgIle | 120 |
| Db | | 430 | GAACGTGTTGATTACATTGTTGAGAAAGCAGGTTGCAGAGATGAGGCTGCCGAATC | 489 |
| OY | | 121 | PheGInglNileIleSerGLyValGlutyrcyshisArgAsnmetValHisArgasp | 140 |
| Db | | 490 | TTCCAGCAGATTATATCTGGGGTAGAATACTGCCACAGAAACATGCTGTTCACTCGTAT | 549 |
| OY | | 141 | LeuLysPrOgluasnlLeuleuleuAspSerLysTYrAsnValLysleulaaspPheGLy | 160 |
| Db | | 550 | CTGAAGCCAGAAAACTTGCTACTCGATTCAAAGTATAATGTAAAGCTTGCTGACTTTGGT | 609 |
| OY | | 161 | LeuSerAsnValmethisAspGLyhisPheleuLysThrSerCysGLyserProAsnTYr | 180 |
| Db | | 610 | TTGAGTACGTCATGCATGATGACCATTTTTGAAGACAAGCTGTGGAGTCCAACCTAT | 669 |
| OY | | 181 | AlaAlaProgluValIleSerGLyLysleuTYraGLyProgluValaSpValTrpSer | 200 |
| Db | | 670 | GCTGCTCCAGAGGTGATCTCTGTAATATATATGCTGGAACCTGAGGTTGATATGAGAC | 729 |
| OY | | 201 | CysGLyValIleleuTYraLaleuleuCysGLyThrleuProPheaspAspGLuasnille | 220 |
| Db | | 730 | TGTGAGTGCATCCTTATGCTCTCCTTTGTGTAACCTTCCATTGTATGATGAGAAATATC | 789 |
| OY | | 221 | ProasnLeuPheLysLysIleLysGLyIleTyrrThr | 233 |
| Db | | 790 | CCCAACTATTCAAAAAGATAAAGGGTGTGATATATATACT | 828 |

RESULT 9
 BI950083
 LOCUS
 DEFINITION
 BI950083 863 bp mRNA linear EST 19-OCT-2001
 HVSME10018H14f Hordeum vulgare spike EST library HVCDNA0012
 (Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
 HVSME10018H14f, mRNA sequence.
 ACCESSION
 BI950083
 VERSION
 BI950083.1 GI:16291889
 KEYWORDS
 EST.

| | |
|----------|--------------------------------|
| SOURCE | Hordeum vulgare subsp. vulgare |
| ORGANISM | Hordeum vulgare subsp. vulgare |

ORGANISM *Hordeum vulgare* subsp. *vulgare*
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticaceae; *Hordeum*.

| REFERENCE AUTHORS | TITLE | JOURNAL |
|---|--|--------------------|
| 1 (bases 1 to 863) Wing, R., Muehlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R., Heinen, S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmonds, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main, D. | Development of a genetically and physically anchored EST resource for barley genomics: Fusarium infected Morex spike cDNA library | Unpublished (2001) |

COMMENT

Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: twing@clemson.edu

Total hg bases = 601
Seq primer: AATTAACTCTCACTAAAGGG
High quality sequence stop: 729.

FEATURES

Source

/organism="Hordeum vulgare subsp. vulgare"

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/mol_type="mRNA"  
/cultivar="Morex"
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/cultivar="Morex"

/sub_species="vulgare"

/db_xref="taxon:112509"

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/clone="HVSME10018H1"
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/usr/local/lib="Hordeum vulgare spike EST library HVCDNA0012
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(Fusarium infected)

/note="Vector: pBluescript SK(-); Site1: EcoRI; Site_2: XhoI; Plants were grown at the University of Minnesota in the GU Muehlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TU Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was

From the material, one plasmid was randomly selected, made, and 1 million pfu were in vivo excised to give phagescript SK(-) cDNA phagemids (Choi, Fenton, Malatras). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Fritsch, Atkins and Wing). Plasmid DNA

preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TV, Wing R, Kleinbols A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

ORIGIN

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 1.74e-125 | length: | 863 |
| Score: | 1189.50 | Matches: | 240 |
| Percent Similarity: | 90.65% | Conservative: | 12 |
| Best Local Similarity: | 86.33% | Mismatches: | 25 |
| Query Match: | 44.17% | Indels: | 4 |
| DB: | 12 | Gaps: | 1 |

US-09-857-522B-4 (1-509) x BI950083 (1-863)

| | | | | |
|------------|--|-----|---|-----|
| OY | | 4 | SerSerIysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGlyArgThrLeu | 23 |
| Db | | 2 | AACACTAGAGAGGGCGGCATTCTGAAGCGTTAAAGAACAATCAATCTGGGCAGAACATTA | 61 |
| OY | | 24 | GlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGlyHisArgVal | 43 |
| Db | | 62 | GGTATAAGCACATTGGAAAAGTGAGATTGCAGAACATAAGCATACAGGGCACAAGTT | 121 |
| OY | | 44 | AlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGluLysAlaLys | 63 |
| Db | | 122 | GCTATAAGATTCTGAACCGTCGTCAAATGAGAATATGAACATGGAAGAAAGCAAAG | 181 |
| OY | | 64 | ArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeuTyrGluVal | 83 |
| Db | | 182 | AGAGAGATCAAGATATTGAGGTGTTCATTCCACCCTCATATCAATCCGGCTTATGAGGTC | 241 |
| OY | | 84 | IleTyrThrProThrAspIleTyrValValMetGluTyrCysIleTyrGlyLuleuphe | 103 |
| Db | | 242 | ATTACACACCTACAGATATATTGTTGTGATGGAATATGCAAGTATGGGAGCTATTTC | 301 |
| OY | | 104 | AspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIlePheGlnGln | 123 |
| Db | | 302 | GACTGCATTGTTGAGAAAGGCGGTTACAGGAAGATGAGGCTCTCGAATCTTCCAGCAG | 361 |
| OY | | 124 | IleIleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAspLeuLysPro | 143 |
| Db | | 362 | ATTATATCTGTTGTAATACCTGCACAGAAACATGTTGTTCACTCGTATCTAAAGCCA | 421 |
| OY | | 144 | GluAsnLeuLeuLeuAspSerIleTyrAsnValLysLeuAlaAspPheGlyLeuSerAsn | 163 |
| Db | | 422 | GAAACCTGTACTTGATTCGAATATAATATGTAAGTGAACCTTGCCGACTTGGATTAGTAAT | 481 |
| OY | | 164 | ValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyrAlaAlaPro | 183 |
| Db | | 482 | GTCATGCATGATGCCCATTTTCTGAAGACTAGCTGCGGAGTCCAACTATGCTGCACCG | 541 |
| OY | | 184 | GluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSerCysGlyVal | 203 |
| Db | | 542 | GAGTTATCTCAGGTAATGTGACCTGGAACCTGAGTTGATGTTTGAGCTGTGGGTG | 601 |
| OY | | 204 | IleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIleProAsnLeu | 223 |
| Db | | 602 | ATACTTATGCTCTTCTTTGGGCACTCTTCCATNTGATGATGACATAATTCCAACCTG | 661 |
| OY | | 224 | PheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAlaLeuAlaArg | 243 |
| Db | | 662 | TTCAAAAAGATAAGGAGGCATCTATATCTTCCAAATCATTTATCTGCTTGCAAGG | 721 |
| OY | | 244 | AspLeuIleProArgMetLeuValGluProMetLysArgIleThrIleArgGluIle | 263 |
| Db | | 722 | GATTTGATCCCAAG-ATGCTGTGTTGTGATTTCTATGAAGAGATA-CCAATTCGTGAATT | 779 |
| OY | | 264 | ArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAlaValProPro | 281 |
| Db | | 780 | CGAAA-CACCCTGGGTTAGATCGCCTCCCG--TACCTGACGGGCTCCCCA | 829 |
| RESULT 10 | | | | |
| BM084571 | | | | |
| LOCUS | | | | |
| DEFINITION | | | | |
| ACCESSION | | | | |
| VERSION | | | | |
| KEYWORDS | | | | |
| SOURCE | | | | |
| ORGANISM | | | | |
| REFERENCE | | | | |
| AUTHORS | | | | |
| TITLE | | | | |

JOURNAL
COMMENT

library of Pennisetum ciliare
Unpublished (2001)
Contact: Schulze SR
Plant Genome Mapping Lab
University of Georgia, Center for Applied Genetic Technologies
Riverbend Research Building, Room 162, 110 Riverbend Rd., Athens,
GA 30602, USA
Tel: 706 583 0166
Fax: 706 583 0160
Email: sschulze@arches.uga.edu.
location/Qualifiers

FEATURES
source
1..951
/organism="Pennisetum ciliare"
/mol_type="mRNA"
/cultivar="PI409164"
/db_xref="taxon:35520"
/clone_lib="Apomictic pistil cDNA library"

ORIGIN

Alignment Scores:

| Pred. No.: | 1.09e-123 | Length: | 951 |
|------------------------|-----------|---------------|-----|
| Score: | 1174.50 | Matches: | 237 |
| Percent Similarity: | 86.05% | Conservative: | 16 |
| Best Local Similarity: | 80.61% | Mismatches: | 36 |
| Query Match: | 43.61% | Indels: | 5 |
| DB: | 12 | Gaps: | 1 |

US-09-857-522B-4 (1-509) x BM084571 (1-951)

QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleLeuArgLeu 80
|||||LysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleLeuArgLeu
1 AAGTGAAGAGAGAATCAAGATCTCAGATTATTATGACCCCTCATATCAACGCCCTT 60

QY 81 TyrGluValIleIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly 100
61 TATGAGGTGATAGATACACCGTGTGATATTATGTTGTTATGAGTATGTTAAATCTGGA 120

QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
121 GAACCTTTTGATTACATGTTGAGAGGAAGACTACATGAAGAAGAAGCTCGCCGTTT 180

QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp 140
181 TTCCAGCAGATCATATCTGCTGTTGAATATTGCCATGAACAATGGTGTTCACCGTGAT 240

QY 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
241 CTAAAGCCAGAGAACCTTCTTTGGATTCAAAATGTAATGTTAAGATTGCTGATTTGGC 300

QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
301 TTAAGTAATGTTATGCGTGAATGCTCACTTCTAAAGACGAGCTGTGTAGCCCAATTTAT 360

QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
361 GCAGCACTGAGTCAATATCTGTGAACATAATATGCTGTCTCTGAAGTTGACGCTGGAGC 420

QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
421 TGTGCTGTTATCTTTATGCTCTCTTTGTTGCTGATCCCTTCCATTGATGATGAATATT 480

QY 221 ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
481 CCAAACCTTTTAAAGAAATAAAGGGGTGGAATATATACCCCTTCTAGTCATTGTTCACCT 540

QY 241 LeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle 260
541 TCAGCAAGGATTTAAATGCCAGAAATGCTGTTGTTGATCCAAATGAAGAATTACCATC 600

QY 261 ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
601 CGTGAATCCGTGAACATGTGTGGTTCAAGATTGACTTNCACGCTATTTGGCTGTGCCG 660

Qy 281 ProProAspThrThrGlnGlnAla-LysMetIleAspGluAsp-ThrLeuArgAspValV 300
Db 661 NCTTCAGACACTGCACAACAAGTTAAAAAGCTTGACGAGAAAACTCTTAATGATGTA 720
Qy 300 aLAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnG 320
Db 721 TTAAGATGGTTTTCACAAGAATCTGTAATGTGAATCTGTGCAACAGAGNTGACAGATG 780
Qy 320 lu-AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArg-PheArgAlaThrSerGlyTy 339
Db 781 AGGCAACAGTTCCTTAATTAATTAATCTGTGACATAGAGNCTCGTACACCAAGTGGTT 840
Qy 339 rLeuGly--AlaAspTyrGlnGluSerMetAsp 349
Db 841 TATCTCCGAACCAAGTTCGAANGATCTATGAC 874
RESULT 11
BQ805778 794 bp mRNA linear EST 31-JUL-2002
LOCUS aestivum cdna clone WHE3570_H07_P14, mRNA sequence.
DEFINITION WHE3570_H07_P14ZS wheat developing grains cdna library Triticum
BQ805778
BQ805778.1 GI:22029987
EST.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 794)
Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J.,
Cronin, K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J.,
Rausch, C.J., Wilson, C. and Woo, J.
The structure and function of the expressed portion of the wheat
genomes - Developing grains cdna library
Unpublished (2002)
JOURNAL
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequences have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: SK primer.
FEATURES
Source
1. .794
/organism="Triticum aestivum"
/mol_type="mRNA"
/culturivar="Butte 86"
/db_xref="taxon:4565"
/clone="WHE3570_H07_P14"
/tissue_type="whole grains"
/dev_stage="3-44 days post anthesis seed"
/lab_host="E. coli SOLr"
/note="Vector: lambda ZAP II, excised phagemid; Site 1:
EcoRI; Plants were grown under six following different
environmental regimes in greenhouse, Environment 1)
24OC/17OC day/night, well-watered, with post-anthesis
fertilizer, Environment 2) 24OC/17OC day/night,
well-watered, without post-anthesis fertilizer,
Environment 3) 37OC/17OC day/night, well-watered, with
post-anthesis fertilizer, Environment 4) 37OC/17OC
day/night, well-watered, without post-anthesis fertilizer,
Environment 5) 37OC/17OC day/night plus drought, with
post-anthesis fertilizer, Environment 6) 37OC/17OC
day/night plus drought, without post-anthesis fertilizer,
developing wheat grains from the following were excised
and frozen in liquid nitrogen, Environment 1 at 3, 5, 7,
8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment
2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44

Alignment Scores: 2.86e-122 Length: 794
Pred. No.: 1161.00 Matches: 216
Score: 92.58% Conservative: 21
Percent Similarity: 84.38% Mismatches: 19
Best Local Similarity: 43.11% Indels: 0
Query Match: 13 Gaps: 0
US-09-857-522B-4 (1-509) x BQ805778 (1-794)
Qy 73 lLeHisProHisIleIleArgLeuTyrGluValIleTyrThrProThrAspIleTyrVal 92
Db 25 ATTCACCCCTGCATATCATCCGGGTTATGAGTTCATTGAGACACACCTAAGATATATTGTT 84
Qy 93 ValMetGluTyrCysLysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeu 112
Db 85 GTGATGAATATTGCCAGAATGAGTATGATTGATTACATGTTGAGAAAGCGGTTA 144
Qy 113 GlnGluAspGluAlaArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHis 132
Db 145 CAGGAAGATGAAGCTCGTGAATCTTCCAGAGATATATCTGTGTGATGATACTGCCAC 204
Qy 133 ArgAsnMetValValHisArgAspLeuLysProGluAsnLeuLeuAspSerLysTyr 152
Db 205 AGAACAATGTTGTTTCATCGTATCTTAAGCCAGAAAACCTGTACTTGAATTAATAT 264
Qy 153 AsnValLysLeuAlaAspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLys 172
Db 265 AATGTGAACCTGTTGACTTGGGTTAATGATGATGATGATGATGATGATGATGATGATG 324
Qy 173 ThrSerCysGlySerProAsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAla 192
Db 325 ACTAGCTGCGGAGTCTAAACTATGCTGCACAGACTTATCTCAGGTAACTGTACGCT 384
Qy 193 GlyProGluValAspValTyrSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThr 212
Db 385 GGACCTGAGGTGATGCTGTGAGCTGTGAGATGATACTTATGCTCTTGTGGCAGA 444
Qy 213 LeuProPheAspAspGluAsnIleProAsnLeuPheLysLysIleLysGlyLysIleTyr 232
Db 445 GTTCATTGAGCATGACAATATTTCCCACTGATCAAAAAGATTAAGGAGGTTCTAT 504
Qy 233 ThrLeuProSerHisLeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValVal 252
Db 505 ATCCTTCCAAAGTTATTATCTGATCTTGCAATGGAATTGATCCCAAGATACTTATGTT 564
Qy 253 GluProMetLysArgIleThrIleArgGluIleArgGluHisGlnTyrPheGlnIleArg 272
Db 565 GATCCCATGAAGAATCACAAATTCTGGAATTCTGGGACCACCCATGTTTCAGAAATCGC 624
Qy 273 LeuProArgTyrLeuAlaValProProProAspThrThrGlnGlnAlaLysMetIleAsp 292
Db 625 CTTCTCTGCTACTGCGCAGTGCCTCCGCCAACAACGACACAGCAAGCCAAATGATTGAT 684
Qy 293 GluAspThrLeuArgAspValValAsnMetGlyPheAsnLysAsnHisValCysGluSer 312
Db 685 AAAGATACACTTCAAGACATTTGCAATCTGGGATATGATAAAGATCATGTGGTGATCA 744
Qy 313 LeuCysSerArgLeuGlnAsnGluAlaThrValAlaTyrTyrLeuLeu 328

DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28,
32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20,
24, 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12,
16, 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10,
12, 16, 20, 24, 28, 30 DPA and total RNA was prepared by
S. Altenbach and K. Cronin at USDA-ARS, Albany, CA. A
cdna library was made using poly (A) RNA, and the cdna
clones were in vivo excised to give pBluescript SK(-)
phagemids in the TJ Close lab (Chin, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (others). "

|||||:::|||||
Db 745 CTGTGCAATAGGCTGCAAAATGAGGCAACTGTTCATATTACTTGCTC 792
RESULT 12
CK195998
LOCUS
DEFINITION FGAS004444 Triticum aestivum FGAS: Library 3 Gate 6 Triticum
aestivum cDNA, mRNA sequence.
ACCESSION CK195998
VERSION CK195998.1 GI:39558388
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 862)
AUTHORS Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,
Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,
Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilson,D.,
Penniket,C., Roach,J.L. and Sarhan,F.
FUNCTIONAL Genomics of Abiotic Stress In Wheat and Canola Crops
UNPUBLISHED (2003)
CONTACT: Wm L Crosby
COMMENT
TITLE
JOURNAL
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_est@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [102,683].
Plate: L3C105 row: H column: 15.
FEATURES
source
Location/Qualifiers
1..862
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone_lib="Triticum aestivum FGAS: Library 3 Gate 6"
/note="Organ: Root; Vector: pCMV.SPORT6; Root tissue from
control, cold-acclimated and salt stressed wheat cultivar
Norstar. 7 mRNA populations were combined before
constructing the library; 7 day non-acclimated roots, 1,
23, and 53 days cold-acclimated at 4C, and 30 minutes, 3
hours and 6 hours treated roots with 200mM NaCl.
Non-acclimated and cold-acclimated plants were grown in
vermiculite while salt stressed plant were grown
hydropotonically. First strand synthesis in this library was
done in the presence of methylated dCTP thereby protecting
from internal cleavage with NotI."
ORIGIN
Alignment Scores:
Pred. No.: 4.3e-122 Length: 862
Score: 1160.00 Matches: 226
Percent Similarity: 93.28% Conservative: 10
Best Local Similarity: 89.33% Mismatches: 16
Query Match: 43.07% Indels: 2
DB: 14 Gaps: 0
US-09-857-522B-4 (1-509) x CK195998 (1-862)
Qy 51 ArgGlnMetArgAsnMetGlnMetGluGluLysAlaLysArgGluPheLysIleLeuLys 70
Db 107 CGTCCGATGAGAACTATGAAATGGAAGAAAGCGAAGAGAGATCAAGATATTGAGG 166
Qy 71 LeuPheIleHisProHisIleIleArgLeuTyrgluValIleTyrThrProThrAspIle 90
Db 167 TTGTC-ATTGACCCCTCATATCATCCGGCTTATGAGGTGATTACACCTACAGATATA 225

Qy 91 TyrValValMetGluTyrCysLysTyrGlyGluLeuPheAspTyrIleValGluLysGly 110
Db 226 TTGTGTGTGATGGAATATTGCAAGATATGTGAGCTATTTCGACTGCTATTGTGAGAAAGGG 285
Qy 111 ArgLeuGlnGluAspGluAlaArgArgIlePheGlnGlnIleIleSerGlyValGluTyr 130
Db 286 CGGTTACAGGAAGATGAGGCTCGTCAATCTTCACAGCAGATTATATCTGGTGTGAATAC 345
Qy 131 CysHisArgAsnMetValValHisArgAspLeuLysProGluAsnLeuLeuAspSer 150
Db 346 TGCCACAGAAACATGTTGCTCATCGTCACTTAAAGCCAGAAACCTGTTACTTGATTCC 405
Qy 151 LysTyrAsnValLysLeuAlaAspPheGlyLeuSerAsnValMetHisAspGlyHisPhe 170
Db 406 AATATATATGTGAAGAACTTGCCGACTTGGGTTAAGTATGTGATGATGCCATTCTT 465
Qy 171 LeuLysThrSerCysGlySerProAsnTyrAlaAlaProGluValIleSerGlyLysLeu 190
Db 466 CTGAAGACTAGCTCGCGGAGTCCAAACTATGCTGCACACAGAGGTTATCTCAGGTAATT 525
Qy 191 TyrAlaGlyProGluValAspValTyrSerCysGlyValIleLeuTyrAlaLeuLysCys 210
Db 526 TACGCTGGAAGCTGAGTTGATGTGTGAGCTGTGGGTGATACTTATGTCTTCTTGT 585
Qy 211 GlyThrLeuProPheAspAspGluAsnIleProAsnLeuPheLysIleLysGlyGly 230
Db 586 GTGACTCTTCCATTGATGATGACAAATATTCCTCAACTGTTCAAAAGATAAAGGAGGC 645
Qy 231 IleTyrThrLeuProSerHisLeuSerAlaLeuAlaArgAspLeuIlePro-ArgMetIle 250
Db 646 ATCTATATCTTCCAAAGTCATTTATCTGCTCTTGCAAGGAGCTGATCCGAGAATGCT 705
Qy 250 uValValGluProMetLysArgIleThrIleArgGluIleArgGluHisGlnTyrPheGly 270
Db 706 TGTGTGTGATCTTATGAGGAGAAATCAGATTCTGTGACATTCCGGGAACACCATGTTTCA 765
Qy 270 nIleArgLeuProArgTyrLeuAlaValProProProAspThrThrGlnGlnAlaLysMe 290
Db 766 GAATGCTTCTCTCGCTTACTGTGGCAGTGGCTCCACAGACACAGCGCAGTCAACCAAT 825
Qy 290 tIleAspGluAspThrLeuArgAspValValAsnMet 302
Db 826 GATTGCTGAGATACACTTAAAGAGATTGTCAACCTG 862
RESULT 13
CA076858 690 bp mRNA linear EST 23-SEP-2003
LOCUS SCMCAM1105D11.g AM1 Saccharum officinarum cDNA clone SCMCAM1105D11
DEFINITION 5', mRNA sequence.
ACCESSION CA076858
VERSION CA076858.1 GI:34929119
KEYWORDS EST.
SOURCE Saccharum officinarum
ORGANISM Saccharum officinarum
REFERENCE Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum.
1 (bases 1 to 690)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
CONTACT: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 105 row: D column: 11

Seq primer: T7 Promoter Primer.
Location/Qualifiers
1. .690
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCMCAM1105D11"
/lab_host="DH10B"
/clone_lib="AM1"
/note="Organ: Apical meristem and tissues surrounding of mature plants; Vector: pSport1; Site_1: SalI; Site_2: NotI; An unidirectional cDNA library generated from [Apical meristem and tissues surrounding of mature plants]. cDNA was prepared from polyA+ mRNA using Superscript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"

Alignment Scores:
Pred. No.: 4.98e-122 Length: 690
Score: 1158.00 Matches: 218
Percent Similarity: 97.35% Conservative: 2
Best Local Similarity: 96.46% Mismatches: 6
Query Match: 43.00% Indels: 0
DB: 13 Gaps: 0

US-09-857-522B-4 (1-509) x CA076858 (1-690)

Oy 1 MetAspGlySerSerlySGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 11 ATGATGGAAGTACTAGAGGGGGTGGACATTGTGAAGCAATTGAAGAACTTAACAACCTGGGA 70
Oy 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
Db 71 AGAAGCTTAGGTATGGCACAATTGGAAAAAGTGAAGATTGCCGAGCATTAAGCTTAACGGGA 130
Oy 41 HisArgValAlaIleLysIleIleAsnCySArgGlnMetArgAsnMetGluMetGluGlu 60
Db 131 CATAGGGTGTCTAAAGATCATCAATGTGCGCAATGAGAATATATGGAATGGAAGAG 190
Oy 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
Db 191 AAAGCAAGAGAGAAATCAAGATATTGAAGTGTTCATTCACCCCATATCATCCGGCTT 250
Oy 81 TyrGluValIleIleTyrThrProThrAspIleIleValValMetGluTyrCysLysTyrGly 100
Db 251 TATGAGGTCAATATACACCAACAGATATATATGTGTGATGGAATATGTAAAGTATGGC 310
Oy 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
Db 311 GAGTTGTTGATTACATTGTTGAGAAAGGACAGATTACTAGAAGATGAGGCTCGCCGATC 370
Oy 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAsp 140
Db 371 TTCCAGCAGATCATATCTGGGTGTGCAATACTGCCATAGAAACATGTTGCCACCGTGAC 430
Oy 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
Db 431 CTAAGCCAGAAACTGTACTTGATTCAAGTATATATGTAATAAAGCTTGCACTTGGT 490
Oy 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
Db 491 TTGACCAATGTGATGATGCGCATTTTGTGAAGACCAAGCTGTGGAGTCCGAATAT 550
Oy 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
Db 551 GCTGCTCCAGAGTAATATCTGTAAACTATATGCTGGAAGCTGAGGTGATGTAGAGT 610
Oy 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220

Db 611 TGTGAGTGAACCTTATGCTCTTTTGTGGGACTCTTTCATTGATGATGAGATATT 670
Oy 221 ProAsnLeuPheLysLys 226
Db 671 CCCAACTGTTCAAAAA 688

RESULT 14
CF307150 704 bp mRNA linear EST 15-AUG-2003
LOCUS HDAl--05-006.g1 OSHDAC1-overexpressing transgenic rice lambda phage
DEFINITION cDNA library 1 (HDAl) Oryza sativa cDNA clone HDAl--05-006, mRNA
sequence.
ACCESSION CF307150
VERSION CF307150.1 GI:33678911
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa

REFERENCE
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
TITLE Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
JOURNAL Large-scale Sequencing Analysis of Rice ESTs
COMMENT Unpublished (2003)
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1. .704
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="HDAl--05-006"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OSHDAc1-overexpressing transgenic rice lambda
phage cDNA library 1 (HDAl)"
/note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA
was inserted into lambda Uni-ZAP XR vector at 5' end with
EcoRI and 3' end with XhoI site. mRNA was derived from
rice Histone Deacetylase overexpression line."

Alignment Scores:
Pred. No.: 8.75e-122 Length: 704
Score: 1156.00 Matches: 216
Percent Similarity: 98.67% Conservative: 7
Best Local Similarity: 95.58% Mismatches: 3
Query Match: 42.93% Indels: 0
DB: 14 Gaps: 0

US-09-857-522B-4 (1-509) x CF307150 (1-704)

Oy 1 MetAspGlySerSerlySGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 25 ATGATGGAATGCTAAAGCGGTGGGCACTTGAGGCACTGAAGAACTAACAATCTTGA 84
Oy 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
Db 85 AGAAGCTTAGGTATTTGGCTCATTTGGAAAAAGTGAAGATTGCAGAGCATTAAGCTTACAGGA 144
Oy 41 HisArgValAlaIleLysIleIleAsnCySArgGlnMetArgAsnMetGluMetGluGlu 60
Db 145 CACAGAGTGTCTATAAAGATCCTGAACCGCCGCAATGAGAAATATGGAATGAGAGAG 204

| | | | |
|----|-----|---|-----|
| QY | 61 | LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu | 80 |
| Db | 205 | AAAGCAAGAGAGAAATCAAGATACTGAGATTGTCATTCAATCCCATATCATTCGCCCTT | 264 |
| QY | 81 | TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly | 100 |
| Db | 265 | TATGAGGTTATATACACTCCCTACGGATATATATGTTGTGATGAGTACTGCAAGTTTGA | 324 |
| QY | 101 | GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle | 120 |
| Db | 325 | GAAGCTTTGATTACATTGTTGAGAAAGCAGGTTGCAGGAAGATGAGGCTCCCGGAATC | 384 |
| QY | 121 | PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAsp | 140 |
| Db | 385 | TTCCAGCAGATTATATCTGGGGTTGATACTGCCACAGAAACATGGTGGTTCATCGTGA | 444 |
| QY | 141 | LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly | 160 |
| Db | 445 | CTGAAGCCAGAAACTTGCTACTGCAATCAAGTATAATGTAAGAAGCTTGCTGACTTGGT | 504 |
| QY | 161 | LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr | 180 |
| Db | 505 | TTGAGTAACGTCATGCATGATGGCCATTTTGTGAAGACAAAGCTGTGGAGTCCAAACTAT | 564 |
| QY | 181 | AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSer | 200 |
| Db | 565 | GCTGCTCCAGAGTGATCTCTGTTAAATTATATGCTGACACCTGAGTTGATGTATGAGC | 624 |
| QY | 201 | CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrIleuProPheAspAspGluAsnIle | 220 |
| Db | 625 | TGCGAGTGATCCCTTATGCTCTCTTGTGTGTAATCTTCCATTGATGATGAGAATATC | 684 |
| QY | 221 | ProAsnLeuPheLysLys | 226 |
| Db | 685 | CCCAACTTATTCAAAAG | 702 |

| | |
|-----------------|--|
| RESULT | 15 |
| LOCUS | CF069225 |
| DEFINITION | 744 bp mRNA linear EST 21-JUL-2003 EST669946 MTUS Medicago truncatula cDNA clone MTUS-17H5, mRNA sequence. |
| ACCESSION | CF069225 |
| VERSION | GI:33105884 |
| KEYWORDS | EST. |
| SOURCE | Medicago truncatula (barrel medic) |
| ORGANISM | Medicago truncatula Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago. 1 (bases 1 to 744) VandenBosch,K., Endre,G., Silverstein,K., Town,C.D., Van Aken,S., Utterback,T., Cheung,F. and Fraser,C.M. The Medicago truncatula 6K unigene set: cDNA clones selected and re-arrayed from various libraries Unpublished (2002) Contact: VandenBosch K Department of Plant Biology University of Minnesota 220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA Tel.: 612 624 2755 Fax: 612 625 1738 Email: kvandenb@cbs.umn.edu TIGR sequence name: MTUSO89TK Alias Clone name:PGVN-51G6 More information is available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gtg gat CC). |
| JOURNAL COMMENT | |

```

FEATURES
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    Location/Qualifiers
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        /mol_type="mRNA"
        /cul_tivar="A17"
        /db_xref="taxon:3880"

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/clone="MTUS-17H5"
/tissue_type="mixed tissues"
/dev_stage="various stages"
/lab_host="XtOLR"
/clone_lib="MTUS"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XtOLR cells."

```

[illegible]

US-09-857-522B-4 (1-509) x CF069225 (1-744)

[illegible]

Dy 34 AlaGluHisLysLeuThrGlyHisArgValAlaIleLysIleIleAsnCysArgGlnMet 53
| | | | | : : : : :
Db 69 GCGGCATGTACTGACTGGGCACAAAGTTGCCATTGAATTCGCGCGAAGATA 128

```
Dy      54 ArgAsnMetGluMetGluGlulysAlalysArgGluPheLysileLeuLysLeuPheIle   73  
       :::|::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
Db     129 AAAAATATCGAAATGGAGACAGAAGCTGCACAAGAAAATTAGATTTTAAgATTGTTCATG  188
```

QY 74 HisProHisIleIeIeaRgLeuTYrGUValIleTYrThrProthrAspIleTYrValVal 93
 ||| |||||||||::: |||||||||
Db 189 CACATCACA TCATAGCGCTTATGAGGTGTGGAAACCCCTACAGACATTATGTGTG 248

| | | | |
|----|-----|--|-----|
| Qy | 94 | MeGIuTyrcyslsyTyrGlglgIuepheaSPtyrIlevalGIuLysGIaArgleuGln | 113 |
| | | | |
| Db | 249 | ATGAGTATGTGAATCCGGAGAGCTTTGATTACATTGTAGAAAAGGTAGCCTACAA | 308 |

QY 114 GIuaspGLuAlaArgArgIlePheGInGInIleIleSerGlyValGluIrrCysHisArg 133
 309 GAAGATGAAGCCCGCAGTTTCTTCACAGACATATATCTGGTGTGAATACTGTCATAGC 368
 Db

QY 134 AsnMetValValHisArgAspLeuYsProGluAsnLeuLeuLeuAspSerLysTyrAsn 153
|||
Db 369 AATATGCTAGTTCATAGAGACTTGAAGCTGAGAATTACTTTTGACCTCAAAATGGAGT 428

QY 154 VALLYSLEUALAASPHEGLYLEUSERRASVALMETHIASPGLYHISPHENULYSTHR 173
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 429 GTCAAGATTGCTGATTTTGGCCGTACACAATCATCGGTGATGGCACCATTTCCTTAAGACA 488

QY 174 SercysglySerProAsnTyraIaIaProgluValIleSerGlyLysLeuTyraIaGly 193
 Db 489 AGTTGTGGAAGCCCTAACTATGCAAGTCCCGAGGTTATCTCTGGGAATTATGCTGGA 548

QY 194 ProGluValAspValTTrpSerCysGlyValIleLeuTyrrAlaLeuLeuCysGlyThrLeu 213
|||
Db 549 CCTGAGGTAGATGTTTGAGACCTGTGGGTAAATTATATGCACCTTCCTGTGGCACTCA 608

QY 214 ProPheAspAspGluAsnIleProAsnLeuPheLysIleLysGlyGlyIleTyrThr 233
|||
Db 609 CCTTTGATGATGAAATATTTCCCACTCTTCAAAAAATAAAGGTGGGATATATACT 668

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Qy      234  LeuProSerHisLeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValValGlu 253
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Db      669  CTTCCTAGCATCTATCTCCTGTGCGCAGAGAATTGATACCGAGGTGCTTGTGGTGAT 728

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QY 254 Prometly8 256

|||||||
Db 729 CCCATGAA 737

Search completed: July 9, 2004, 18:19:36
Job time : 3789 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 9, 2004, 15:12:45 ; Search time 694 Seconds
(without alignments)
3574.649 Million cell updates/sec

Title: US-09-857-522B-4
Perfect score: 2693
Sequence: 1 MDGSSKSGSHSEALRNYNLG.....GPQLFLDCAFLTKRLVL 509

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3183909 segs, 2436941669 residues

Total number of hits satisfying chosen parameters: 6367818

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US09857522/runat_07072004_161357_1904/app_query.fasta_1.647
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09857522@CGN_1_1_511@runat_07072004_161357_1904
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOB=6 -DELEXT=7

Database : Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
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| | | | | | | |
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| 1 | 2693 | 100.0 | 1926 | 13 | US-10-425-114-5805 | Sequence 5805, Ap |
| 2 | 2693 | 100.0 | 1948 | 13 | US-10-183-687-235 | Sequence 235, App |
| 3 | 2411.5 | 89.5 | 2119 | 13 | US-10-425-114-22369 | Sequence 22369, A |
| 4 | 2411.5 | 89.5 | 2607 | 17 | US-10-437-963-49666 | Sequence 49666, A |
| 5 | 2378 | 88.3 | 1899 | 13 | US-10-183-687-255 | Sequence 255, App |
| 6 | 2338 | 86.8 | 2484 | 17 | US-10-437-963-49667 | Sequence 49667, A |
| 7 | 1977 | 73.4 | 2224 | 17 | US-10-437-963-80980 | Sequence 80980, A |
| 8 | 1974.5 | 73.3 | 2123 | 13 | US-10-183-687-247 | Sequence 247, App |
| 9 | 1969.5 | 73.1 | 1539 | 9 | US-09-938-842A-2657 | Sequence 2657, Ap |
| 10 | 1969.5 | 73.1 | 1539 | 11 | US-09-938-842A-2657 | Sequence 2657, Ap |
| 11 | 1945 | 72.2 | 1991 | 13 | US-10-425-114-35131 | Sequence 35131, A |
| 12 | 1942 | 72.1 | 2052 | 13 | US-10-183-687-239 | Sequence 239, App |
| 13 | 1939 | 72.0 | 2543 | 13 | US-10-183-687-251 | Sequence 251, App |
| 14 | 1937 | 71.9 | 1778 | 13 | US-10-425-114-2148 | Sequence 2148, Ap |
| 15 | 1931 | 71.7 | 2107 | 13 | US-10-183-687-237 | Sequence 237, App |
| 16 | 1922.5 | 71.4 | 1742 | 13 | US-10-425-114-4365 | Sequence 4365, Ap |
| 17 | 1903.5 | 70.7 | 1539 | 9 | US-09-938-842A-162 | Sequence 162, App |
| 18 | 1903.5 | 70.7 | 1539 | 11 | US-09-938-842A-162 | Sequence 162, App |
| 19 | 1890.5 | 70.2 | 2006 | 13 | US-10-183-687-257 | Sequence 257, App |
| 20 | 1794 | 66.6 | 1626 | 16 | US-10-260-238-491 | Sequence 491, App |
| 21 | 1748 | 64.9 | 1300 | 13 | US-10-425-114-5415 | Sequence 5415, Ap |
| 22 | 1680.5 | 62.4 | 2291 | 13 | US-10-424-599-37563 | Sequence 37563, A |
| 23 | 1448.5 | 53.8 | 1277 | 13 | US-10-424-599-38233 | Sequence 38233, A |
| 24 | 1139 | 42.3 | 3079 | 9 | US-09-834-975-974 | Sequence 974, App |
| 25 | 1013.5 | 37.6 | 1902 | 9 | US-09-801-368-337 | Sequence 337, App |
| 26 | 1013.5 | 37.6 | 1902 | 16 | US-10-369-493-25383 | Sequence 25383, A |
| 27 | 863.5 | 32.1 | 1264 | 16 | US-10-369-493-27551 | Sequence 27551, A |
| 28 | 862.5 | 32.0 | 2047 | 16 | US-10-369-493-46451 | Sequence 46451, A |
| 29 | 817.5 | 30.4 | 986 | 9 | US-09-770-445-263 | Sequence 263, App |
| 30 | 802 | 29.8 | 1317 | 17 | US-10-437-963-94109 | Sequence 94109, A |
| 31 | 749 | 27.8 | 2352 | 9 | US-09-815-915-3 | Sequence 3, Appli |
| 32 | 749 | 27.8 | 2352 | 15 | US-10-393-316-3 | Sequence 3, Appli |
| 33 | 749 | 27.8 | 2968 | 9 | US-09-815-915-1 | Sequence 1, Appli |
| 34 | 749 | 27.8 | 2968 | 15 | US-10-393-316-1 | Sequence 1, Appli |
| 35 | 749 | 27.8 | 4700 | 13 | US-10-425-114-26032 | Sequence 26032, A |
| 36 | 746 | 27.7 | 2193 | 15 | US-10-161-565-17 | Sequence 17, Appl |
| 37 | 746 | 27.7 | 2271 | 9 | US-09-919-585-1 | Sequence 1, Appli |
| 38 | 745 | 27.7 | 2698 | 15 | US-10-161-565-13 | Sequence 13, Appl |
| 39 | 745 | 27.7 | 2698 | 16 | US-10-174-319-4 | Sequence 4, Appli |
| 40 | 742 | 27.6 | 3373 | 15 | US-10-161-565-18 | Sequence 18, Appl |
| 41 | 737.5 | 27.4 | 2085 | 15 | US-10-161-565-20 | Sequence 20, Appl |
| 42 | 737.5 | 27.4 | 2278 | 15 | US-10-161-565-21 | Sequence 21, Appl |
| 43 | 737.5 | 27.4 | 2462 | 13 | US-10-363-616-158 | Sequence 158, App |
| 44 | 737.5 | 27.4 | 3226 | 15 | US-10-161-565-23 | Sequence 23, Appl |
| 45 | 737.5 | 27.4 | 3269 | 16 | US-10-258-106-34 | Sequence 34, Appl |

ALIGNMENTS

RESULT 1
US-10-425-114-5805
; Sequence 5805, Application US/10425114
; General Information:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack B
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 5805
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700473306_FLI

US-10-425-114-5805

Alignment Scores:

| | | | |
|------------------------|-----------|---------------|------|
| Pred. No.: | 1.53e-315 | Length: | 1926 |
| Score: | 2693.00 | Matches: | 509 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 13 | Gaps: | 0 |

US-09-857-522B-4 (1-509) x US-10-425-114-5805 (1-1926)

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OY      1 MetAspGlySerSerIySeGlySerGlyHisSerGluAlaLeuArgAsnTYrAsnLeuGly 20
DB      156 ATGATGGAAGTAGTAAGCGAGTGGGCATTCTGAAGCATTAAAGGAAGCACTGCGGA 215
OY      21 ArgThrLeuGlyIleGlyThrPheGlyLysValIySileAlaGluHisLysLeuThrGly 40
DB      216 AGAAGCTTAGGTATCGGTACATTGTGAAAAGTGAAGATTGCAGAGCAATAAGCTTAAGCTGA 275
OY      41 HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGluGlu 60
DB      276 CATAGGGTGTCTATAAGATCATCAACTGCCCAATGAGAAATATGAAATGAAAGAG 335
OY      61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
DB      336 AAAGCAAGAGAGATTCAGATATTTGAAGTGTTCATTCACCCCATATCATTCGGCTT 395
OY      81 TyrGluValIleTyrThrProThrAspIleTyrValIleMetGluTyrCysLysTyrGly 100
DB      396 TATGAGGTCAATATACACCTACAGATATATATGTTGTGATGGAATATGTAACTATGGC 455
OY      101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
DB      456 GAGTTATTGATTACATTGTTGAGAAAAGCGAGATTACAGGAAGATGAAGCTCTCGAATC 515
OY      121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValIleHisArgAsp 140
DB      516 TTCCAGACAGATCATATCTGGCGTCGAATACCTGCCATAGAAAACATGGTGTCCACCGTGAC 575
OY      141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValIySLeuAlaAspPheGly 160
DB      576 CTAAAGCCGAAACTGTCTACTGATTCAAGGTATATGTAATAACTTGGCGATTTTGGT 635
OY      161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
DB      636 CTGAGCAATGTGCATGCATGATGCCCATTTTCTGAAGACTAGCTGTGGAGTCGGAATAT 695
OY      181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
DB      696 GCTGCTCCAGAGGTATATCTGTGTAACACTATATGCTCGAACCTGAGGTGATATGAGT 755
OY      201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyTyrIleuProPheAspAspGluAsnIle 220
DB      756 TGTGGGTGATTCTTTATGCTCTTCTTTGTGGAAGCTCTTCCATTGTGATGATGAGATATT 815
OY      221 ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
DB      816 CCCAATCTGTTCAAAAAATTAAAGGAGGTATCTACACACTTCCAAAGTCATTGTGCTGCT 875
OY      241 LeuAlaArgAspLeuIleProArgMetLeuValAlaGluProMetLysArgIleThrIle 260
DB      876 TTGGCCAGGATTTGATCCCAAGATGCTTGTGTGAGCCTATGAAGAGAAATCACAATT 935
OY      261 ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrIleuAlaValPro 280
DB      936 AGGGAATTCGGAGCATCATGTGTTCCAGATTGGCTTCCACGTTACTTGGCAGTGCCCT 995
OY      281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal 300
DB      996 CCACCAGATACGACACACAAAGCCCAAAATGATTGATGAAGATACACTTCGAGATGTTGTT 1055
OY      301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
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DB      1056 AATATGGGATTTAAACAAGACCATGTGTGTAATCACTGTGACAGCACTTCAAAATGAG 1115
OY      321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
DB      1116 GCACTGTGTGCATATATTATTACTATGGAACAATCGGTTTAGAGCACTAGTGCTATCTT 1175
OY      341 GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer 360
DB      1176 GGGCAGATTATCAAGAATCAATGACAGCAAAATTTAAATCAGCTGCGCTCATCTGAATCA 1235
OY      361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
DB      1236 TCTAGTTCGTGTAAGAGAAATTATGTTCCAGGAAGCAGTGAATCTCATAGCAGTGTGTTG 1295
OY      381 ArgProTyrTyrProValGluArgLysTyrPalaleuGlyLeuGlnSerArgAlaHisPro 400
DB      1296 CGGCATATTAATCCTGTTGAAAGAAATGGCGCTTGACCTTCAGTCTCGGGCCACCCCT 1355
OY      401 ArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTyrLysLys 420
DB      1356 CGTGAATATATGTTGAGGTCTTAAGACACTTCAAGAAATTAACGTCAGATGGAAGAAG 1415
OY      421 AsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsnAspThr 440
DB      1416 AATGGGCACCTACAAACGTGAATGACAGATGTCGCCAGGGTTCCTGAAGTTAATGACACG 1475
OY      441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
DB      1476 TTAGATGCCAGCAACAGCTTCTTGTGTGACTCTACCATCATGATGATATGATGCTAAT 1535
OY      461 GlyArgLeuProThrValIleLysPheGlnPheGlnLeuTyrLysThrLysAspAspLys 480
DB      1536 GGGAGGCTACTTACTGTGATCAAGTTTGAATTCAGCTTTTCAAGACGAAGACGACAAG 1595
OY      481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
DB      1596 TACCTCTTAGATATGACAGAGATTACTGACCTCAGCTGCTCTTCTTGAACCTTGTGCG 1655
OY      501 AlaPheLeuThrLysLeuArgValLeu 509
DB      1656 GCCTTCCTTACCAAGCTTAGGGTTCTA 1682

RESULT 2
US-10-183-687-235
; Sequence 235, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B01458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 235
; LENGTH: 1948
; TYPE: DNA
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ORGANISM: Zea mays
US-10-183-687-235

Alignment Scores:

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| Score: | 2693.00 | Matches: | 509 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 100.00% | Indels: | 0 |
| DB: | 13 | Gaps: | 0 |

US-09-857-522B-4 (1-509) x US-10-183-687-235 (1-1948)

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| Db | 173 | ATGATGGAAGTAGTAAGGAGGTGGGCATTCTGAAGCATTAAGGAATCAACCTGGGA | 232 |
| QY | 21 | ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly | 40 |
| Db | 233 | AGAACTTAGGTATCGGTACATTGGAAAAAGTGAAGATTGCAGACATTAAGCTTACTGGA | 292 |
| QY | 41 | HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGlu | 60 |
| Db | 293 | CATAGGGTTGCTATAAAGATCATCAACTGCCCAATGAGAAATATGGAATGGAAGAG | 352 |
| QY | 61 | LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu | 80 |
| Db | 353 | AAAGCAAGAGAGAAATTCAGATATGGAAGTTGTTCAATCCACCCCATATCATTCGGCTT | 412 |
| QY | 81 | TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly | 100 |
| Db | 413 | TATGAGGTCAATATACACACCTACAGATATATATGTGTGATGGAATATTGTAAGTATGGC | 472 |
| QY | 101 | GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle | 120 |
| Db | 473 | GAGTTATTGATTACATTGTGAGAAAGGCAGATTACAGAGATGAAGCTCGTGAATC | 532 |
| QY | 121 | PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValAlaHisArgAsp | 140 |
| Db | 533 | TTCCAGCAGATCATATCTGGCGTCGAATACTGCCATAGAAACATGTTGTCCACCGTGAC | 592 |
| QY | 141 | LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly | 160 |
| Db | 593 | CTAAAGCCGGAACCTGTACTTGATTCAAGTATATGTAACAATTCGCGATTTTGGT | 652 |
| QY | 161 | LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr | 180 |
| Db | 653 | CTGAGCAATGTCAATGATGATGCGCAATTTTCTGAAGACTAGCTGTGGAGTCCGAACCTAT | 712 |
| QY | 181 | AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer | 200 |
| Db | 713 | GCTGCTCCAGAGTAATATCTGGTAAACTATATATGCTGGACCTGAGGTCGATGTATGAGT | 772 |
| QY | 201 | CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle | 220 |
| Db | 773 | TGTGGGTGATTCCTTATGCTCTCTTCTTGTGGAACCTCTCAATTGATGATGAGAATATT | 832 |
| QY | 221 | ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla | 240 |
| Db | 833 | CCCAATCTGTTCAAAAAAATTAAAGGAGGTATCTACACACTTCCAAGTCATTGTCTGCT | 892 |
| QY | 241 | LeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle | 260 |
| Db | 893 | TTGGCCAGGGATTTGATCCCAAGATGCTGTGTGTGAGCCATGAAGAGATCAACAATT | 952 |
| QY | 261 | ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro | 280 |
| Db | 953 | AGGGAATTCGGGAGCATCAATGTTCCAGATTGCGCTTCCACGTTACTTGGCAGTGCCT | 1012 |
| QY | 281 | ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal | 300 |
| Db | 1013 | CCACCAGATACGACACACAAGCCAAAATGATTGATGAAGATACACTTCGAGATGTTGTT | 1072 |

| | | | |
|----|------|--|------|
| QY | 301 | AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgGluGlnAsnGlu | 320 |
| Db | 1073 | AATATGGGATTTAAACAAGAACCATGTGTGTGAATCACTGTGCAGCAGACTTCAAAATGAG | 1132 |
| QY | 321 | AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu | 340 |
| Db | 1133 | GCAACTGTGCATATTATTAACTATTGGACAATCGGTTTAGAGCAACTGTGGCTATCTT | 1192 |
| QY | 341 | GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer | 360 |
| Db | 1193 | GGGGCAGATTATCAAGAATCAATGCACAGAAATTAATCAAGCTGGCCGTCACTGAATCA | 1252 |
| QY | 361 | SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu | 380 |
| Db | 1253 | TCTAGTTCTGTGACGAGGAATTATGTTCCAGGAAGCAGTGAATCCTCATACAGTGGTTTG | 1312 |
| QY | 381 | ArgProTyrTyrProValGluArgLysTrpAlaLeuGlnLeuGlnSerArgAlaHisPro | 400 |
| Db | 1313 | CGGCCATATTATCCTGTTGAAGAAATGGCGCTTGGACTTCAGTCTCGGCCCAACCT | 1372 |
| QY | 401 | ArgGluLeuMetValGluValLeuLysAlaLeuGlnGlnLeuAsnValArgTrpLysLys | 420 |
| Db | 1373 | CGTGAATAATGTTGAGGCTCTTAAAGCAGCTTCAAGAAATTAACGTCAGATGAAGAAG | 1432 |
| QY | 421 | AsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPheProGluValAsnAspThr | 440 |
| Db | 1433 | AATGGGCACTACAACGTAATGCAGATGGTGCCAGGGTTTCTGAAGTTAATGCACAGC | 1492 |
| QY | 441 | LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn | 460 |
| Db | 1493 | TTAGATGCAGCAACAGCTTTCTTGGTGAAGCTTACCATCATGATTAATGATGCTAAT | 1552 |
| QY | 461 | GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLysAspAspLys | 480 |
| Db | 1553 | GGGAGGCTAAGCTACTGTGATCAAGTTTGAATTCAGCTTTACAAGACGAAGACGAAGAAG | 1612 |
| QY | 481 | TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla | 500 |
| Db | 1613 | TACCTCTTAGATATATGCAGAGAGTTACTGGAAGCTCAGCTGCTCTTCTTGAAGCTCTGTCG | 1672 |
| QY | 501 | AlaPheLeuThrLysLeuArgValLeu 509 | |
| Db | 1673 | GCCTTCTTAACCAAGCTTAGGGTTCTA 1699 | |

RESULT 3
US-10-42

; Sequence 22369, Application US/10425114
; Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K

APPLICANT: Tabaska, Jack F

APPLICANT: Cao, Yonqwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 32369

```

; SEQ ID NO 24363
; LENGTH: 2119

```

```

      /
      | ZENONIAN: 2117
      | TYPE: DNA
      | ;

```

ORGANISM:

FEATURE:

OTHER INFORMATION:

Alignment Scores:

| | | | |
|------------|-----------|----------|------|
| Pred. No.: | 2.45e-281 | Length: | 2119 |
| Score: | 2411.50 | Matches: | 453 |

Best Local Similarity: 89.00%
Query Match: 89.55%
DB: 13 Gaps: 1

Mismatches: 26

Indels: 1

US-09-857-522B-4 (1-509) x US-10-425-114-22369 (1-2119)

QY 1 MetAspGlySerSerLySGLySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
DB 130 ATGGATGGAAATGCTAAAGCGGCGGCGCATTTCTGAGGCACCTGAAGAACTACAATCTTGA 189
QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
DB 190 AGAAGCTTTAGGTATGTGGCTCATTTGAAAAGTGAAGATTGCAGAGCATTAAGCTTACAGGA 249
QY 41 HisArgValAlaIleLysIleLeuAsnCySAArgGlnMetArgAsnMetGluMetGluGlu 60
DB 250 CACAGAGTGTCTATAAAGATCCTGAACCGCCGCCAAATGAGAAATATGGAATGAGAGAG 309
QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
DB 310 AAAGCAAGAGAGAAATCAAGATACGTGATGTTTCATTCATCCCAATATCATTCGCTT 369
QY 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly 100
DB 370 TATGAGGTTATATACACTCTCCTACGATATATATGTGTGATGAGTACTGCAAGTTTGA 429
QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnLysAspGluAlaArgArgIle 120
DB 430 GAACTGTTGATTACATGTGTGAGAAAGCAGGTTGCAGAGAAAGATGAGGCTCGCCGAATC 489
QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValAlaHisArgAsp 140
DB 490 TTCCAGCAGATTATATCTGGGGTGAATACCTGCCACAGAAACATGGTGTTCATCGTGAT 549
QY 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
DB 550 CTGAAGCCAGAAACTTGCTACTGATTCGAATCAAGTATATAGTAAAGCTTGCTGACTTGGT 609
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
DB 610 TTGAGTAACTGATGATGATGCCATTTTGTGAAGACAAGCTGTGGAGTCCAACTAT 669
QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSer 200
DB 670 GCTGCTCCAGAGGTGATCTCTGTAATATATATGCTGACCTGAGGTTGATGTATGAGC 729
QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
DB 730 TGTGAGTGATCCTTATATGCTCTCTTGTGTGACTCTTCCATTGATGATGAGAATATC 789
QY 221 ProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
DB 790 CCCAACCTATTCAAAAGATAAAGGGTGATATATATCTCCCAAGTCATTATCTGCT 849
QY 241 LeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle 260
DB 850 CTGGCCAGAGATTGATCCCAAGAGATGCTTGTGTGATCCCAATGAAGAGAAATCACAATT 909
QY 261 ArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
DB 910 CGTGAATTCGAGAGCATCAGTGTTCAGATTCGCTTCTCCTGTTACTTGACAGTGCCCT 969
QY 281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal 300
DB 970 CCACCAGACACAGCACAGCAAGCCAAATGATTGATGAAGATACCCCTTCAAGATGTCGTA 1029
QY 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
DB 1030 AACTTGGGTTATGAAAGACCATGTGTGTGAATCTCTGCCAATAGACTGCAATGAG 1089
QY 321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
DB 1090 GCAACTGTGCATATATTAATTAATCTTGGACAATGATTCGAGCTACCAAGTGGCTATTGTG 1149

QY 341 GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer 360
DB 1150 GGAGCAGACTATCAAGAACTCTTGGAGAGGAATTTTAATCGCTTGTGCTCATCGGAATCA 1209
QY 361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
DB 1210 GCAAGTCAATATCAAGGACATTAATCTTCCAGGAAGCAGTATCTCATGCGAGTGTTC 1269
QY 381 ArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAlaHisPro 400
DB 1270 CGCCACATTAATCCTGTTGAAGAAATGGGCTCTTGACTTCAGTCACGAGCTCAACCT 1329
QY 401 ArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrpLysLys 420
DB 1330 CGCGAGATAATGATTGAGGTCTTAAGGCACTTCAAGACTTAATGTCTCTGGAAGAG 1389
QY 421 AsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPheProGluValAsnAspThr 440
DB 1390 AATGACAGTACACACATGAATGACATGAGCGTGGG---ACTCAGGCCACTGATATG 1446
QY 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
DB 1447 TTAGATGTTAAACAACAGCTTGTGTGATGACTCAATCATATATGATAACGGTATTAAT 1506
QY 461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLysAspAspLys 480
DB 1507 GCGAGGCTAAGCTGCTGTGATCAAGTTTGAATCCAGCTTTTACAAGACCAGAGCAGAG 1566
QY 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
DB 1567 TATCTGTGATATGACAGAGATTACGGGGCTCAGCTCCTTTCTGGACTTCTGTGCA 1626
QY 501 AlaPheLeuThrLysLeuArgValLeu 509
DB 1627 GACTTCCTTAACAAGCTGAGGGTTCCTA 1653

RESULT 4

US-10-437-963-49666/C

; Sequence 49666, Application US/10437963

; Publication No. US2004012343A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; APPLICANT: Wu, Wei

; APPLICANT: Boukharov, Andrey A.

; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 49666

; LENGTH: 2607

; TYPE: DNA

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_52228C.1

US-10-437-963-49666

Alignment Scores:

pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

Length: 2607

Matches: 453

Conservative: 29

Mismatches: 26

Indels: 1

Gaps: 1

US-09-857-522B-4 (1-509) x US-10-437-963-49666 (1-2607)

QY 1 MetAspGlySerSerlySGlySerglyHisSergluAlaLeuArgAsnTYrAsnLeuGly 20
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 2033 ATGGATGGAATGCTAAAGCGGCGTGCCATTCTGAGGCCACTGAAGAACTACAAATCTTGGA 1974
QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1973 AGAAGTTAGGTATGCTGCTCATTTGGAAAAAGTGAAGATTGCAGAGCATTAAGCTTACAGGA 1914
QY 41 HisArgValAlaIleLysIleIleAsnCYsArgGlnMetArgAsnMetGluMetGluGlu 60
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1913 CACAGAGTTGCTATAAGATCCTGAACCGCCGCCAAATGAGAATATGGAATGAGAGAG 1854
QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1853 AAAGCAAGAGAGAAATCAAGATACAGATTGTTCAATTCATCCCATATCATTCGCCTT 1794
QY 81 TyrGluValIleTYrThrProThrAspIleTYrValValMetGluTYrCYsLysTYrGly 100
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1793 TATGAGGTATATACACTCTTACCGATATATATGTTGTGATGAGTACTGCATGTTTGA 1734
QY 101 GluLeuPheAspTYrIleValGluLysGlyArgLeuGlnLysAspGluAlaArgArgIle 120
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1733 GAACTGTTGATTACATTGTTGAAGAGGAGGTTGCAGAGATGAGGCTCGCCGAATC 1674
QY 121 PheGlnGlnIleIleSerglyValGluTYrCYsHisArgAsnMetValValHisArgAsp 140
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1673 TTCCAGCAGATTATATCTGGGGTTGAATACTGCCACAGAAACATGTTGTTTCATCTGTGAT 1614
QY 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTYrAsnValLysLeuAlaAspPheGly 160
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1613 CTGAAGCCAGAAACTTGCTACTGATTCAAAGTATATGTAAGCTTGCTGACTTGTGT 1554
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCYsGlySerProAsnTYr 180
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1553 TTGAGTAAACGTCAATGCATGATGCCCATTTTGAAGACAAAGCTGTGGAGTCCAAACTAT 1494
QY 181 AlaAlaProGluValIleSerglyLysLeuTYrAlaGlyProGluValAspValTyrSer 200
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1493 GCTGCTCCAGAGTGATCTCTGTGAATTATATGCTGACCTGAGGTTGATGTATGAGC 1434
QY 201 CysGlyValIleLeuTYrAlaLeuLeuCYsGlyThrLeuProPheAspAspGluAsnIle 220
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1433 TGTGAGTGATCCTTATGCTCTCTCTTGTGTACTCTTCCATTGATGATGAGAATATC 1374
QY 221 ProAsnLeuPheLysLysIleLysGlyGlyIleTYrThrLeuProSerHisLeuSerAla 240
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1373 CCCAACCTATCAAAAAGATAAAGGGTGATATATACTCTCCCAAGTCATTTATCTGCT 1314
QY 241 LeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle 260
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1313 CTGGCCAGAGATTGATCCCAAGATGCTGTGTTGATCCCAATGAAGAGATCAACAT 1254
QY 261 ArgGluIleArgGluHisGlnTYrPheGlnIleArgLeuProArgTYrLeuAlaValPro 280
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1253 CGTGAATTCGAGAGCATCAGTGGTTTCAGATTGCCCTTCTCGTTACTTACAGAGTGCCT 1194
QY 281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal 300
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1193 CCACCAGACACAGCACAGCAAGCAAAATGATGAAAGATACCCCTTCAAGATGTCGTA 1134
QY 301 AsnMetGlyPheAsnLysAsnHisValCYsGluSerLeuCYsSerArgLeuGlnAsnGlu 320
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1133 AACTTGGGTATGGAAGAACCATGTGTGTGAATCTCTGCGCAATAGACTGCAGAAATGAG 1074
QY 321 AlaThrValAlaTYrTYrLeuLeuLeuAspAsnArgPheArgAlaThrSerglyTYrLeu 340
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1073 GCAACTGTTCATATTAATTAATCTTGGACAATCGAATTCGAGCTACAGGCTATTTTG 1014
QY 341 GlyAlaAspTYrGlnGlnSerMetAspArgAsnLeuAsnGlnLeuAlaSerSergLysSer 360
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 1013 GGAGCAGACTATCAGAATCTTGGAGAGAGAAATTTTAATCGCTTGTTCATCGGAATCA 954

QY 361 SerSerSerglyThrArgAsnTYrValProGlySerSerAspProHisSerglyLeu 380
: : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 953 GCAAGTTCAATATACAGAGCATTAATCTTCCAGGAAGCAGTGAATCCTCATGCGAGTTTG 894
QY 381 ArgProTYrTYrProValGluArgLysTYrAlaLeuGlyLeuGlnSerArgAlaHisPro 400
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 893 CGCCACATTAATCCTGTTGAAGAAGAAATGGGCTCTTGACTTCAGTCACGAGCTCAACCT 834
QY 401 ArgGluIleMetValGluValLeuLysAlaLeuGlnGlnLeuAsnValArgTYrLysLys 420
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 833 CGCAGATTAATGATTGAGGTCCTTAAGGCACCTTCAAGACTTAATGTCTCTGGAAGAG 774
QY 421 AsnGlyHisTYrAsnValLysCYsArgTYrCYsProGlyPheProGluValAsnAspThr 440
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 773 AATGACAGTACAAACATGAATGACAGATGAGCGTTGG--ACTCAGGCCACTGATATG 717
QY 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 716 TTAGATGTTAACAAACAGCTTGTGATGACTCAATCATATGATGAATACGGTGATGTAAT 657
QY 461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTYrLysThrLysAspAspLys 480
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 656 GGGAGGCTACTGCTGTGATCAAGTTGAATCCAGCTTTACAGACCAAGACGAGAAG 597
QY 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 596 TATCTGCTGATATGACAGAGATTACGGGCTCAGCTCCTTTCTGGAATCTGTGCA 537
QY 501 AlaPheLeuThrLysLeuArgValLeu 509
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
Db 536 GACTTCCTTACCAAGCTGAGGGTTCTTA 510

RESULT 5

US-10-183-687-255
; Sequence 255, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: B81458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; PRIORITY FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 255
; LENGTH: 1899
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-183-687-255

Alignment Scores:
Pred. No.: 2.37e-277 Length: 1899
Score: 2378.00 Matches: 442
Percent Similarity: 93.52% Conservative: 34
Best Local Similarity: 86.84% Mismatches: 33
Query Match: 88.30% Indels: 0
DB: 13 Gaps: 0

US-09-857-522B-4 (1-509) x US-10-183-687-255 (1-1899)

QY 1 MetAspGlySerSerlySGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 67 ATGGAAGGAAACACTAGAGAGAGGTGGCATTCGACGCAATTAAAGAACTACAATGTGGGC 126
QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
Db 127 AGAACATTAGGTATAGGACCATTTGGAAAAGTGAGATTGCAGAGCATAGCATACAGAGG 186
QY 41 HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGluGlu 60
Db 187 CATAAAGTTGCTATAAGATTCTGAACCGTCGTCAAATGAGAACTATGGAATGAGAGAG 246
QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
Db 247 AAAGCAAGAGAGAGATCAAGATATTGAGGTTGTTCAATCCACCTCATATCATCCGGCTT 306
QY 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly 100
Db 307 TATGAGGTCATTACACACCTACAGATATATTGTTGTGATGGAATATTGCAAGTATGGT 366
QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnLysAspGluAlaArgArgIle 120
Db 367 GAGCTATTGCACTGCATGTTGTGAGAAAGGCGGTTACAGGAAGATGAGGCTCGTGAATC 426
QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAsp 140
Db 427 TTCCAGCAGATTATATCTGCTGTGATACTGCCACAGAAACATGTTGCTCATCGTGAT 486
QY 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
Db 487 CTAAAGCCAGAGAACCTGTGTTACTTGATTCCAAATACAAATGTGAACCTTGCCGACTTGGG 546
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
Db 547 TTAAGTAATGTCAATGATGATGCGCATTTTCTGAAGACTAGCTGCGGAGTCCAAACTAT 606
QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
Db 607 GCTGCACCAAGAGTTATCTCAGGTAATATATACGCTGACCTGAGGTTGATGTTTGAGC 666
QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
Db 667 TGCGGGGTGATACTTATGCTCTTCTTGTGGCACTCTTCATTGTGATGATGACAATATT 726
QY 221 ProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
Db 727 CCCAACTGTTCAAAAAGATAAAGGAGGACATCTATATCTTCCAAGTCAATTATCTGCT 786
QY 241 LeuAlaArgAspLeuIleProArgMetLeuValValGluPrometLysArgIleThrIle 260
Db 787 CTTGCAAGGATTGATCCCAAGATGCTGTTGTTGATCCTATGAAGAGATCACAATT 846
QY 261 ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
Db 847 CGTGAATTCGAGAACACCCATGCTTCAGAATCGCCTTCCTACCTGCGCAGTGCCCT 906
QY 281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal 300
Db 907 CCACCAGACACGCGCGCAGCAAGCCAAAATGATGATGAAGATACACTTAAGAGATTGTC 966
QY 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
Db 967 AACCTGGATATGATAAGACCATGTGTGTAATCATTTGTGCATATAGGCTGCAAAATGAG 1026
QY 321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
Db 1027 GCAACTGTTGCATATTACTTACTCTTGGAACAATCGGTTCCGGGCCACTAGTGCTATTG 1086
QY 341 GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer 360
Db 1087 GGGGCTGACTATCTACAATCAATGGGCTAGGAGTTTAAATCAGTTTACTTCAATTGGAAATCA 1146

QY 361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
Db 1147 GCAAGCCCAAGTACCAGGCGAGTATCTTCCAGCAAGCAATGATTTCAAGGAGTGCTTG 1206
QY 381 ArgProTyrTyrProValGluArgLysThrAlaLeuGlyLeuGlnSerArgAlaHisPro 400
Db 1207 CGGCCATATTAACCCCGTTGAAGAAGAAATGGGCTCTTGGGCTCCAGTCTCGAGCTCA 1266
QY 401 ArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrrLysLys 420
Db 1267 CGTGAGATTAATGATCGAGGTTCTTAAAGGCACCTCAAGAAATTAAATGTCTGCTGGA 1326
QY 421 AsnGlyHisTyrAsnValLysCysArgTrrCysProGlyPheProGluValAsnAspThr 440
Db 1327 AATGACACTACAACATGAATGCAAGGTGCTGCCCTGGGTTTCTCAGGTCAAGTATATG 1386
QY 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
Db 1387 TTAGATGCCCAACCAAGCTTTGTTGATGACTCTACCATCATGATGAACGGCATGTAAT 1446
QY 461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLysAspAspLys 480
Db 1447 GGGAGGCTACCTGCCGTGATCAAGTTGAATCCAGCTTTACAGAACCAAGATGACAAAG 1506
QY 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
Db 1507 TACCTGCTAGATATGACAGAGAGTTACTGCACTCAGCTCCTCTTGATTTTGCGCG 1566
QY 501 AlaPheLeuThrLysLeuArgValLeu 509
Db 1567 GCCCTTCTTACCACCTTAGGGTTCTTA 1593

RESULT 6

US-10-437-963-49667
; Sequence 49667, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 49667
; LENGTH: 2484
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_52229C.1
US-10-437-963-49667

Alignment Scores:
Pred. No.: 2,6e-272 Length: 2484
Score: 2338.00 Matches: 451
Percent Similarity: 78.14% Conservative: 35
Best Local Similarity: 72.51% Mismatches: 23
Query Match: 86.82% Indels: 113
DB: 17 Gaps: 1

US-09-857-522B-4 (1-509) x US-10-437-963-49667 (1-2484)

QY 1 MetAspGlySerSerlySGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 162 ATGGAAGGAATGCTAGAGGCGGTGGCATTTCTGAGGCACTGAAGAACTACAATCTAGGA 221

QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
DB 222 AGAAGCTTAGGTATGGTTCATTTGGAAAAGTGAAGATTCAGAGCATTAAGCTTACAGGG 281
QY 41 HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGlu 60
DB 282 CACAGAGTTGCTATAAAGATTCCTGAACCGTCGCCAAATGAGAAATATGGAATGAGAGAG 341
QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
DB 342 AAAGCAAGAGAGAAATCAAGATTTGAGGTTGTTCAATCCCATATCATTCGCTT 401
QY 81 TyrGluValIleTyrThrProThrAspIleTyrValIleMetGluTyrCysLysTyrGly 100
DB 402 TATGAGTCATATACACTCCCTACGAGTATATATGTTGATGAGTACTGCAAGTTTGA 461
QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnLysAspGluAlaArgArgIle 120
DB 462 GAAGCTTTGATTACATTTGTTGAGAAAGGCAAGGTTGCAAGAGATGAGGCTCGCCGAATC 521
QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValIleHisArgAsp 140
DB 522 TTCACAGAGATTATATCTGGGGTTGAATACTGCCACAGAAACATGGTGTTCATTCGTGAT 581
QY 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
DB 582 CTGAAGCCAGAAAACCTTGCTAAGTTCGATTCGAAAGTAAAGCTTGTGCTGCTTGGT 641
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
DB 642 TTGAGTAATGTCATGATGATGAGCCATTTTAAAGACAAGCTGCCGAGTCCGAATTAT 701
QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSer 200
DB 702 GCTGCTCCAGAGGTGATCTCTGTAATATATATGCTGACCCGAGGTGATGATGAGC 761
QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
DB 762 TGTGAGTGATCCTTATGCTCTCCTTGTGCTACTCTTCCATTGTGATGACGAGAAATATC 821
QY 221 ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
DB 822 CCCAACCTATTCAAAAAGATAAAGGGTGTATATATCTCCCAAGTCATTATCTGCT 881
QY 241 LeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIleThrIle 260
DB 882 CTGGCCAGGATTTGATCCCAAGAGTCTGTTGTGATCCAATGAAGAGAAATCACAATT 941
QY 261 ArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
DB 942 CGTGAATTCGAGAGCATCAATGCTTTCAGATTCGCTTCTGTTACTTACGAGTGCTT 1001
QY 281 ProProAspThrThrGlnGlnAlaLysMet----- 290
DB 1002 CCACCAGACACAGACAGCAAGCCAAATGTACTTGTGTCCACATTCTTAAAGAGTTGT 1061
QY 290 ----- 290
DB 1062 TCATTATGTATCAAACTTATATACTAATATAATTCTTGAGATATACTTATAGAGTA 1121
QY 290 ----- 290
DB 1122 TGATAAATATATGTTTTCACAACATAAAACCGTATAAAGCAGTGTGAAGGCAATTGAA 1181
QY 290 ----- 290
DB 1182 TAACATTTATGATATGAGGCTTGTGAGTATTTCTGTAGTAGATTATCTTAGC 1241
QY 290 ----- 290
DB 1242 AGAATCCTTCATGATGATGATAAAGAGAGAGATAAGTTTCACTTGCATATATCACTTATT 1301

QY 290 ----- 290
DB 1302 ACATGTTGATTTTATATATATCTTGGCACTTGTCTAATATCTTGATATATGACCTTC 1361
QY 291 -----1LeAspGluAspThrLeuArgAspValAsnMetGlyPheAsnLysAsnHis 308
DB 1362 TTTGAAGATGTGATGAAGATACCTTCAAGACGTGTGAACCTTGGTTATGAAAAGACCA 1421
QY 308 sValCysGluSerLeuCysSerArgLeuGlnAsnGluAlaThrValAlaTyrTyrLeuLe 328
DB 1422 TGTGTGAATCTCTGCCAATAGACTGCAAAATGAGGCACTGTTGATATTTGCT 1481
QY 328 uLeuAspAsnArgPheArgAlaThrSerGlyTyrLeuGlyAlaAspTyrGlnGluSerMe 348
DB 1482 ATTGACAATCGATTCGAGCTACAGTGCATATCTGGAGCAGACTATCAAGAATCAT 1541
QY 348 tAspArgAsnLeuAsnGlnLeuAlaSerSerGluSerSerSerSerGlyThrArgAsnTyr 368
DB 1542 GGAGAGCAATCTTAATCGCTTGTGCTTCATCAAGATCAGCAAGTTCAATACAAGCATTA 1601
QY 368 rValProGlySerSerAspProHisSerSerGlyLeuArgProTyrTyrProValGluArg 388
DB 1602 TCTCCAGAGAGAGATGATCCTCATGCGCAGGTGTGCGCCACATATCTGTTGAAG 1661
QY 388 gLysTrpAlaLeuGlyLeuGlnSerArgAlaHisProArgGluIleMetValGluValLe 408
DB 1662 AAAATGGGCTCTTGGAATCTTCAAGTCTCGAGCTCAGCCTCGCAGATATGATTGAGTCT 1721
QY 408 uLysAlaLeuGlnGluLeuAsnValArgTrpLysLysAsnGlyHisTyrAsnValLysCy 428
DB 1722 AAAGGCACTTGAAGACTTAATGTCTGCTGGAAGAAGATGACAGTACATGAAGTG 1781
QY 428 sArgTrpCysProGlyPheProGluValAsnAspThrLeuAspAlaSerAsnSerPheLe 448
DB 1782 CAGATGAGCGTTGGGTATCTCAGGCCACTGATATGTTAGATGTCAACACAGCTTTGT 1841
QY 448 uGlyAspSerThrIleMetAspAsnAspAlaAsnGlyArgLeuProThrValIleLys 468
DB 1842 TGATGACTCAATTAATGATATGCGCATGTAAACGGAGGTTACTGCTGTGATCAA 1901
QY 468 sPheGluPheGlnLeuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgVa 488
DB 1902 GTTGAATCCAGCTTTCACAGAGCAGACAGAGAATATCTGCTGATATGACAGAGAT 1961
QY 488 lThrGlyProGlnLeuLeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgVa 508
DB 1962 TACGGGGCTCAGCTCTTCTTCTGACTTCTGTGACGCTTCTTAACCAACTGAGGCT 2021
QY 508 lLeu 509
DB 2022 TCTA 2025
RESULT 7
US-10-437-963-80980
; Sequence 80980, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 80980
; LENGTH: 2224

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; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_80552C.1
US-10-437-963-80980

Alignment Scores:
Pred. No.:      1.3e-228      Length:      2224
Score:          1977.00      Matches:      377
Percent Similarity: 84.28%      Conservative: 52
Best Local Similarity: 74.07%      Mismatches:  76
Query Match:    73.41%      Indels:      4
DB:             17          Gaps:             2

US-09-857-522B-4 (1-509) x US-10-437-963-80980 (1-2224)

QY      1 MetAspGlySerSerLysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
      199 ATGAGGAGGAGCTGGCAGA-----GATGGAAACCTCTTGCGGTTACCGGATTGGC 249
DB
QY      21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
      250 AAAACCCCTAGGATGGGTGATTTGGCAAGTGAAGATCGCGAGCATATATTGACTGGT 309
DB
QY      41 HisArgValAlaIleLysIleLeuAsnGlySerGlnMetArgAsnMetGluGlu 60
      310 CACAAGGTGGCAATCAAGATCCTCAATCGCCGTAAAGATCAAGAGCATGAGATGAAGAG 369
DB
QY      61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleLeuArg 80
      370 AAAGTTAAAGAGAAATCAAGATACTTAGATTATTATGCACCCACATATCATTCGCTT 429
DB
QY      81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly 100
      430 TATGAGGTGATAGACACCCCAAGCTGATATTATTATTGTTATGAGATATGCAAACTGGA 489
DB
QY      101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
      490 GAGTTGTTGATTACATCGCTTGAGAGAGGAAGACTGCAAGAGGAAGACTGACGCTTT 549
DB
QY      121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAsp 140
      550 TTCCAGCAGATCATATCTGGTGTGATATATGCCATAGAAACATGATGTTTCATCGTGAT 609
DB
QY      141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
      610 CTTAAGCCAGAGAACCTTCTTTGGACTCCAAATGCAATGTTAAGATTGACACTTTGGC 669
DB
QY      161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
      670 TTGAGTAATGTTATGCTGATGCTGATCACTTCTTGAGACAAAGTTGTGAGCCCAATTAT 729
DB
QY      181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer 200
      730 GCAGCACCTGAGGTGATATCTGTAAACTATATGCTGGCCCTGAAGTTGATGTGTGAGT 789
DB
QY      201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
      790 TGTGTTGTTATCTTTATGCTCTTCTTGTGTGACCTTCCATTGATGACGAATAATT 849
DB
QY      221 ProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240
      850 CCCAACCTTTTAAAGAAATAAAGGGTGCATATATACCTTCCAGTCAATTGTCACT 909
DB
QY      241 LeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIleThrIle 260
      910 TTGGCAAGGATTTGATTCACGAATGCTTGTGTTGATCCCATGAAGAGATCAACATA 969
DB
QY      261 ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
      970 CGTGAATCCGTGAACATCACTGCTTACAGTTGCTTCCGCGTTATTAGCTGTGCCA 1029
DB
QY      281 ProProAspThrThrGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal 300
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DB      1030 CCTCTGCACACTGCACACAGGTTAAAGAGCTGCAGCATGAAGTCTGATGATGTTATC 1089
QY      301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLysCysSerArgLeuGlnAsnGlu 320
      1090 AATATGGGGTTTGACACAGATCAAGTCAATGCAATCACTTCAACAGAGACTGCAAAACGAG 1149
DB
QY      321 AlaThrValAlaIleTyrThrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
      1150 GCGACAGTTGCTTACTATTATTACTATTGGAACAATAGGCTGCGCACAAACAGTGGCTACT 1209
DB
QY      341 GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer 360
      1210 GGAGCTGAGTTCCATGATCAATCTATGGAATCTTCTCGCTCAAGTAACTCCAGCTGAGACA 1269
DB
QY      361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
      1270 CCAAACTGACGCCACTGATCATCGGACGACATGGGCATATGGAATCTCTGGGTTGGCTTG 1329
DB
QY      381 ArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAlaHisPro 400
      1330 AGGCATCATTTTCGACGCTGACAGGAATGGGCCCTTGCTTCAGTCTCGAGACATCCCA 1389
DB
QY      401 ArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrpLysLys 420
      1390 CGAGAAATATATTAATCTGAAGTTCTTAAAGCTCTGCAAGAGCTAAATGTTTGTGGAAGAAG 1449
DB
QY      421 AsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPheProGluValAsnAspThr 440
      1450 ATTGACATTAATTAACATGAATGCAATGCAATGCAATGCTTAGTTTCCAGTCATGAGAGTATG 1509
DB
QY      441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
      1510 ATGCAATACCAACCATGCTGCTTGTGCAAGATCTGTATATATGAAACTGATGACAGTGAG 1569
DB
QY      461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLysAspAspLys 480
      1570 AAATCAACCCACACTGTG--AAATTTGAATTCAGCTTTACAAACAAAGGATGAAAAA 1626
DB
QY      481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
      1627 TACCTTCTTGACTTGCAAAAGGTCAGTGAACACACAGCTTCTCTTGGAACCTGTGCTCT 1686
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QY      501 AlaPheLeuThrLysLeuArgValLeu 509
      1687 GCCTTTCACTCACTGAGAGTCTCTT 1713
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RESULT 8
US-10-183-687-247
; Sequence 247, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: BBI458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; PRIOR FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
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SOFTWARE: Microsoft Office 97
; SEQ ID NO 247
; LENGTH: 2123
; TYPE: DNA
; ORGANISM: Glycine max
US-10-183-687-247

Alignment Scores:
Pred. No.: 2.42e-228 Length: 2123
Score: 1974.50 Matches: 382
Percent Similarity: 83.53% Conservative: 49
Best Local Similarity: 74.03% Mismatches: 76
Query Match: 73.32% Indels: 9
DB: 13 Gaps: 3

US-09-857-522b-4 (1-509) x US-10-183-687-247 (1-2123)

QY 1 MetAspGlySerSer-----LysGlySerGlyHisSerGluAlaLeuArgAsnThrAsn 18
DB 123 ATGGATGACCAAGCTGGCCGAGGTGGTGTGCTGGCCCTGGACATGTTCTTACCAATTTATAA 182
QY 19 LeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeu 38
DB 183 TTGGGAAAAACACTCGGATTGGATCTTTTGGCAAGGTGAAAATTGCAGAACATGTGTG 242
QY 39 ThrGlyHisArgValAlaIleLysIleIleAsnCySarGlnMetArgAsnMetGlnMet 58
DB 243 ACTGGCCATAGGTTGGATTCAGATCCTTAACCGACGCAAGATTAAGAACAATGGAATG 302
QY 59 GluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIle 78
DB 303 GAAGAAAAAGTGAGAAGAAATCAAAATTTAAGATTGTTCATGCATCCTCACAATTATT 362
QY 79 ArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLys 98
DB 363 CGACTTTATGAGTCAATGAACTCCAACGTACATATATGTTGTCAATGAGTATGGAAG 422
QY 99 TyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArg 118
DB 423 TCTGAGAGCTTTTCGATTATCATAGTAGAAGGGTAGGTTGCAGGAAGATGAAGCTCGT 482
QY 119 ArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHis 138
DB 483 AATTTTTCAGACAGATATCTCTGGGGTGAGTACTGTCAAGAAATATGTGCTCAT 542
QY 139 ArgAspLeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAsp 158
DB 543 AGAGATTGGAAGCTGGAATTTACTTTTGACCTCAAAATGTAATGTCAAGATTGCTGAT 602
QY 159 PheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerPro 178
DB 603 TTTGGCTTGAGCAACATCATGCGTGATGTCACTTTCTTAAACAAGTTGTGGAAGCCCT 662
QY 179 AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspVal 198
DB 663 AACTATGAGCTCCTGAGGTTATCTCTGGAAATTTATGTCTGAGCCTGAAGTGATGTC 722
QY 199 TyrSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGlu 218
DB 723 TGGAGCTGTGGTGAATTTTATATGCCCCCTTCTTGTGGCAACCCTTCTTTGATGATGAA 782
QY 219 AsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeu 238
DB 783 AATATTCCAAATCTTCAAGAAATAAAGGGTGAGTTTACACTCTTCCCATCATCTA 842
QY 239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIle 258
DB 843 TCACCCGGTGTAGATTGATACCAAGGATGCTTGTGTTGACCCCTATGAGAGAATG 902
QY 259 ThrIleArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAla 278
DB 903 ACCATACCTGAGATCCGTCACAACCCATGTGTTCCAAGCTCGACTTCCACGTTATTAGCT 962

QY 279 ValProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAsp 298
DB 963 GTGCACCACCACGATACAATGCAACAGGCCCAAAAGATTGATGAGAGATCCTTCAGGAA 1022
QY 299 ValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGln 318
DB 1023 GTGGTGAATAATGGGATTTGACAGGAATCAATTGGTGAATCTCTTGGGAACAGATACAA 1082
QY 319 AsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGly 338
DB 1083 AATGAGGTTACTGTGGCATACTATTGTATTGGAACAACGATTTGTTTCCAGTGCC 1142
QY 339 TyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
DB 1143 TATCTTGAGCTGAGTTTCAAGAGACCATGATTCGGGTTTAAATCAATGCATTCAGT 1202
QY 359 GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
DB 1203 GAACCTGCTTCTCAGTTGTGTGGAACCGCTTTCAGGCTACATGGAATATCCAGAGTA 1262
QY 379 GlyLeuArgProTyrTyrProValGluArgLysThrAlaLeuGlyLeuGlnSerArgAla 398
DB 1263 GGATCGAGGCCAACACTCCCTGTTGAAGAAGAAATGGGCCCTTGGGCTTCAGTCTCGAGCC 1322
QY 399 HisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTyr 418
DB 1323 CATCTCTGTAATAATGACTGAGGTTCTTAAAGCTTTGCAAGAATTAATGTTTGTGG 1382
QY 419 LysLysAsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPhePro----- 435
DB 1383 AAGAAGATTGGTCACTACAACATGAAGTGAAGTGGTGTGCTGGCATTCCTGGTCACCAC 1442
QY 436 -----GluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThrIle 453
DB 1443 GAAGAAATGTTAACAATATGTCATAGTAATCATTTACTTTGAGATGATTCACAACATT 1502
QY 454 MetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGlnLeu 473
DB 1503 ATTGAGAATGATGCTGTTCT-----ACTTCAATGTGTCAAGTTGAAGTGACAGCTT 1556
QY 474 TyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGlnLeu 493
DB 1557 TACAATAACCCGGGAAGAAAGATATCTGCTTGAATCTTCAAAAGGGTGACGGTCCACAAGTTT 1616
QY 494 LeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
DB 1617 CTTTCTTGATCTATGTGTGCTTTCCTTGACACAGCTTCGTGTCCTC 1664

RESULT 9
US-09-938-842A-2657
; Sequence 2657, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938, 842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227, 866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264, 647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300, 111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2657
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana

US-09-938-842A-2657

Alignment Scores:

Pred. No.: 5.81e-228 Length: 1539
Score: 1969.50 Matches: 377
Percent Similarity: 82.82% Conservative: 52
Best Local Similarity: 72.78% Mismatches: 74
Query Match: 73.13% Indels: 15
DB: 9 Gaps: 4

US-09-857-522B-4 (1-509) x US-09-938-842A-2657 (1-1539)

QY 1 MetAspGlySerSerIysGly-----SerGlyHisSerGluAlaLeuArgAsnTyrAsn 18
DB 1 ATGGATGGATCAGGCACAGCGCAGTAGAAGTGGGGTAGAATCGATTCTACCAATTTACAAG 60
QY 19 LeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeu 38
DB 61 CTTGGAGAACTCTTGATTTGGTTCTTGGTAGGGTGAAGATAGCTGAGCATGCATTG 120
QY 39 ThrGlyHisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMet 58
DB 121 ACAGACATTAAGGTTGCTATCAAGATCCTCAATCGTCGCAAAATCAAGAACATGGAGATG 180
QY 59 GluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIle 78
DB 181 GAGGAGAAAGTGAGGAGAGAGATCAAAATCTTGAGCTATTATGATCATCTCAGCATCATC 240
QY 79 ArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLys 98
DB 241 CGTCTCTATGAGGTTATAGAGACTCCACAGATATTATCTTGTCATGAGTATGTGAAC 300
QY 99 TyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArg 118
DB 301 TCTGTGAGCTATTGACTATATATTGTTGAGAGGGTAGATTGCAGAGAGATGAGCGAGG 360
QY 119 ArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHis 138
DB 361 AACTTTTTCAGCAGATAATATCAGAGAGTGAATACTGCCATCGAAACATGTGTGTAC 420
QY 139 ArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAlaAsp 158
DB 421 AGAGACCTCAAGCCTGAACCTTGCTTTGGACTCTAAATGCAATGTAAGATGTGCTGAT 480
QY 159 PheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerPro 178
DB 481 TTTGGCCTGAGCAACATATAATGCGAGATGTCATTTTGAAGACAAAGTTGTGAAGTCCA 540
QY 179 AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspVal 198
DB 541 AATTATGCCGCTCCAGAGTAATTTCCGGCAAGTATATGCTGGCCCTGAAGTAGATGTC 600
QY 199 TrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGlu 218
DB 601 TGGAGCTGTGTGTGATCTTACGCTCTTCTGTGGGACGCTTCCATTGATGATGAA 660
QY 219 AsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeu 238
DB 661 AACATTCCCAACCTTTTAAGAAGATAAAGGAGGAGATATACACATTACCTAGCCATTTA 720
QY 239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIle 258
DB 721 TCTCCTGTGCTAGAGATTGATCCCCCGGATGCTTGTAGTTGACCCCATGAACGAGTA 780
QY 259 ThrIleArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAla 278
DB 781 ACCATCCCTGAGATCCGGCAACACCTTGTTCCAAGCTCATCTTCCGAGGTAATTTAGCT 840
QY 279 ValProProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAsp 298
DB 841 GTTCCTCTCCAGATACTGTGCAACAGGCAAAAAAGATTGACGAGGAGATTCTCCAAGAA 900
QY 299 ValValAsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGln 318

DB 901 GTTATCATATAGGATTGTGACAGAAACCACTCATCGAATCGCTCCGCAACCGAACCCAG 960
QY 319 AsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGly 338
DB 961 AATGATGGCACTGTGACGCTACTATCTGATACTGGAACAATCGTTCCGCTCTAGTGTG 1020
QY 339 TyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
DB 1021 TATCTCGGGGCTGAGTTTCAAGAGACCATGGAA--GGTACTCCCGGTATGCATCCAGCA 1077
QY 359 GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
DB 1078 GAAAGCGTTGCTTCACCTGTTAGCCATCGGCTTCCAGAGCTGATGGAATATCAAGAGATT 1137
QY 379 GlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAla 398
DB 1138 GGCTTGAGATCTCAATACCCCTGTTGAGAGAAATGGGCTCTTGACCTTCAAGTCTCGGCT 1197
QY 399 HisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrp 418
DB 1198 CATCCCCGTGAATATATGACGGAAGTCTGAAAGCCCTGCAAGATTGATGATGTTGG 1257
QY 419 LysLysAsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsn 438
DB 1258 AAGAAGATAGGGCACTACACATGAAAGTGCAGATGGGTTCTT-----AAC 1302
QY 439 AspThrLeuAspAla-----SerAsnSerPheLeuGlyAspSer 451
DB 1303 AGCAGCGCAGATGCTATGCTCAGTAACCTGCATGCACGATAACACTTCTTGAGAGACGAG 1362
QY 452 ThrIleMetAspAsnAspAlaAsnGlyArgLeuProThrValIleLysPheGluPhe 471
DB 1363 TCCAGCATATAGAGAAGCAAGCAGCTGTAAATCGCCCAATGTTGTCAAGTTGAAATT 1422
QY 472 GlnLeuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyPro 491
DB 1423 CAGTTGTATAAACTCGGAGCAGCAAGTATCTACTGATTTGCAGAGAGTACAAGTCTCT 1482
QY 492 GlnLeuLeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
DB 1483 CAGTCTGTGTTCTTGATCTGTGTGCTTTCTTGTCTCAGCTCGAGTCTCCTC 1536

RESULT 10

US-09-938-842A-2657
; Sequence 2657, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2657
; LENGTH: 1539
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2657

Alignment Scores:

Pred. No.: 5.81e-228 Length: 1539
Score: 1969.50 Matches: 377

Percent Similarity: 82.82% Conservative: 52
Best Local Similarity: 72.78% Mismatches: 74
Query Match: 73.13% Indels: 15
DB: 11 Gaps: 4

US-09-857-522B-4 (1-509) x US-09-938-842A-2657 (1-1539)

QY 1 MetAspGlySerSerlySgLy-----SerGlyHisSerGluAlaLeuArgAsnTyrAsn 18
DB 1 ATGATGATGATCAGGACAGACAGACAGTAGAAGTGGGTGAATCGATTCTACCAATTACAAAG 60
QY 19 LeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValIleAlaGluHisLysLeu 38
DB 61 CTGGAGAGAACTCTGGTATTGGTTGCTTCTGTAGGTGAAGATAGCTGAGCATGCATTG 120
QY 39 ThrGlyHisArgValAlaIleLysIleLeuAsnCybArgGlnMetArgAsnMetGluMet 58
DB 121 ACAGGACATAAGGTTGCTATCAAGATCCTCAATCGTCGCAAAATCAAGAACATGGAGATG 180
QY 59 GluGlyLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIle 78
DB 181 GAGGAGAAAGTGAGGAGAGAGATCAAAATCTTGAGACTATTATGTCATCTCCATCATC 240
QY 79 ArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCybLys 98
DB 241 CGTCTCTATGAGGTATAGAGACTCCACAGATATTATCTGTGATGAGTATGTGAAC 300
QY 99 TyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnIuAspGluAlaArg 118
DB 301 TCTGATGAGCTATTGACTATATTGTTGAGAAAGGTAGATTGCAGAGAGATGAGCGAGG 360
QY 119 ArgIlePheGlnGlnIleIleSerGlyValGluTyrCybHisArgAsnMetValHis 138
DB 361 AACTTTTTCAGACAGATATATACAGAGTGAATACTGCCATCGAAACATGGTGTAC 420
QY 139 ArgAspLeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAsp 158
DB 421 AGAGACCTCAAGCCTGAAAACCTTCTTTGGACTTAATAATGCAATGTAAGATTGCTGAT 480
QY 159 PheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCybGlySerPro 178
DB 481 TTTGGCCTGAGCAACATATATGCGAGATGGTCAITTTTGAAGACAAGTTGTGAAGTCCA 540
QY 179 AsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspVal 198
DB 541 AATTATGCCGCTCCAGAGTAATTTCCGGCAAGTTATATGCTGGCCCTGAAGTAGATGTC 600
QY 199 TrpSerCybGlyValIleLeuTyrAlaLeuLeuCybGlyThrLeuProPheAspGlu 218
DB 601 TGGAGCTGTGTGTACTACTACGCTCTTCTGTGGGACGCTTCCATTGTATGATGA 660
QY 219 AsnIleProAsnLeuPheLysLysIleLysGlyLysIleTyrThrLeuProSerHisLeu 238
DB 661 AACATTCCCAACCTTTTAAGAAGATAAGGAGGAGATATACACATTACTTACCATTTTA 720
QY 239 SerAlaLeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIle 258
DB 721 TCTCCTGTGCTAGAGATTGATCCCCCGGATGCTTGTAGTTGACCCCATGAACGAGTA 780
QY 259 ThrIleArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAla 278
DB 781 ACCATCCCTGAGATCGGCAACACCCTTGTTCCAACTCATCTCCGAGTATTTAAGCT 840
QY 279 ValProProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAsp 298
DB 841 GTTCCTCTCCAGATACTGTGCAACAGGCAAAAAGATTGACGAGAGATTCTCCAAAGAA 900
QY 299 ValValAsnMetGlyPheAsnLysAsnHisValCybGluSerLeuCybSerArgLeuGln 318
DB 901 GTTATCAATATGGAATTGACAGAACAACCACTCATCGAATCGCTCCGCAACGAAACCCAG 960
QY 319 AsnGluAlaThrValAlaIleTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGly 338

DB 961 AATGATGGCACTGTGACGTACTATCTGATCTGACCAATCGTTTCCGTGCTTAGTGT 1020
QY 339 TyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSer 358
DB 1021 TATCTCGGGCTGAGTTTCAAGAGACCATTGAA---GGTACTCCCCGTTATGCATCCAGCA 1077
QY 359 GluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer 378
DB 1078 GAAAGCGTTGCTTCACTGTTAGCCATCGGCTTCCAGGACTGATGAATATCAAGAATT 1137
QY 379 GlyLeuArgProTyrTyrProValGluArgLysTyrAlaLeuGlyLeuGlnSerArgAla 398
DB 1138 GGCTTGAGATCTCAATACCCTGTTGAGAGAAAATGGGCTCTTGACTTCACTCTCGGGCT 1197
QY 399 HisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTyr 418
DB 1198 CATCCCCGTGAATATAGACGGAAGTCCCTGAAAGCCCTGCAGATTTGATGTGTGG 1257
QY 419 LysLysAsnGlyHisTyrAsnValLysCybArgTyrCybProGlyPheProGluValAsn 438
DB 1258 AAGAAGATAGGGCACTACAACATGAAGTGCAGATGGCTTCT-----AAC 1302
QY 439 AspThrLeuAspAla-----SerAsnSerPheLeuGlyAspSer 451
DB 1303 AGCAGCGCAGATGATATGCTCAGTAACTCGATGCATGACAGATAACAACACTTGTGAGACGAG 1362
QY 452 ThrIleMetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPhe 471
DB 1363 TCCAGCATATATAGAGAACGAAGCAGCTGTTAAGTCGCCCAATGTTGTCAAGTTGAATT 1422
QY 472 GlnLeuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyPro 491
DB 1423 CAGTTGTATAAACTCGGAGCAGACAAGTATCTGATTTGCAGAGAGTACAAGGTCT 1482
QY 492 GlnLeuLeuPheLeuAspPheCybAlaAlaPheLeuThrLysLeuArgValLeu 509
DB 1483 CAGTTCTGTGTTCTTGATCTGTGTGCTGCTTTCTTCTGCTCAGCTCCGAGTCTC 1536

RESULT 11

US-10-425-114-35131
; Sequence 35131, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yinhua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 35131
; LENGTH: 1991
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE089A07_FLI
US-10-425-114-35131

Alignment Scores:

Pred. No.: 8.25e-225 Length: 1991
Score: 1945.00 Matches: 373
Percent Similarity: 83.89% Conservative: 54
Best Local Similarity: 73.28% Mismatches: 76
Query Match: 72.22% Indels: 6
DB: 13 Gaps: 3

US-09-857-522B-4 (1-509) x US-10-425-114-35131 (1-1991)

| | | | |
|----|------|---|------|
| QY | 1 | MetAspGlySerSerLysGlySerGlyHisSerGluValLeuArgAsnTyrAsnLeuGly | 20 |
| Db | 216 | ATGAGGGGGCAGCGCAG-----GATGCAACCCGTTGAGGAATTATCGGATTGGC | 266 |
| QY | 21 | ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly | 40 |
| Db | 267 | AAGACTCTCGGAATTGGCTCATTCGGGAAGAGTGAAATTCGGGACATATCAGCACTGGA | 326 |
| QY | 41 | HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGluGlu | 60 |
| Db | 327 | CACAAGGTGGCAATCAAGATTCTCAACCGCCGTAATAATCAGAGGCAATGAGATGGAAGAG | 386 |
| QY | 61 | LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu | 80 |
| Db | 387 | AAAGTTAAAGAGAGATTAGATTATGAGGTTATTATTCATCCACATATTATCCGCCCTC | 446 |
| QY | 81 | TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly | 100 |
| Db | 447 | TATGAGGTTATAGACACACCGGCTGATATTATGTTGTTATGAGTATGTTAAGTGTGGG | 506 |
| QY | 101 | GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle | 120 |
| Db | 507 | GAATTATTGATTACATTGTTGCAAGAGTAGGCTGCAGAAGAGAAGACTCGCCGTTTC | 566 |
| QY | 121 | PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp | 140 |
| Db | 567 | TTCCAACAGATTATATCCGGTGTGAATATTGCCATAGAACAATGGTGTGCATCGTAT | 626 |
| QY | 141 | LeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly | 160 |
| Db | 627 | CTAAAGCCAGAAAACCTCCTATTGGATTCAAAATGCAATGTTAAGATTGCAGATTTGGC | 686 |
| QY | 161 | LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr | 180 |
| Db | 687 | TTAAGTAATGTTATGCGGAGTGTTCATTTCTGAAGACAAAGTGTGTAAGCCCAATTAT | 746 |
| QY | 181 | AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer | 200 |
| Db | 747 | GCTGCTCCTGAGGTGATATCTGTAAACTATATATGCTGCAGCCTGAAGTTGATGTGGAGC | 806 |
| QY | 201 | CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle | 220 |
| Db | 807 | TGTGGGTTATTCTTATGCTCTTTTATGTGTACTCTGCCATTGTATGACGAGAACATA | 866 |
| QY | 221 | ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla | 240 |
| Db | 867 | CCAACCTTTTAAGAAATAAGGTTGAATATATACCCTTCCAGCCATTGTCTGGT | 926 |
| QY | 241 | LeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle | 260 |
| Db | 927 | GCAAGCAAGGATTTGATTCAGAATGCTAGTTGTGCATCTTATGAAGCGGATCACCAATT | 986 |
| QY | 261 | ArgGluIleArgGluHisGlnThrPheGlnIleArgLeuProArgTyrLeuAlaValPro | 280 |
| Db | 987 | CGTGAATAATTCGGAACATGATTGGTTCAAAATCTTCTCCGCGCTATTGTGACTGTGCTT | 1046 |
| QY | 281 | ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal | 300 |
| Db | 1047 | CCTCCAGATAGTGCAGCAACAGTCAAAAAAGTTGATGAGGAACCTCCGTGAGGTTTTA | 1106 |
| QY | 301 | AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu | 320 |
| Db | 1107 | GGTATGGGATATGACAAGAACTGTTGGTGAATCAATCCAAAAAAGGCTGCAAAATGAG | 1166 |
| QY | 321 | AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu | 340 |
| Db | 1167 | GCAACTGTGCATATTACTTACTCTTGGAACAATAGGCTCCGTACAACCAAGTGCTATCTT | 1226 |
| QY | 341 | GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGlu--- | 359 |
| Db | 1227 | GGAGCTGAATGTCAAGAGCTATGGACTCTCATTTCTCAACATCGCATCATATGAACA | 1286 |

| | | | | |
|----|-------|--|---|------|
| QY | 360 | --- | SerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSer | 378 |
| | | ::: ::: | | |
| Db | *1287 | CCAAGTT | CAGCAGCAGCGTGGGAATAGACAGCAAAATATTATTGAGTCT-----CCAGTT | 1337 |
| | | ::: ::: | | |
| QY | 379 | GlyLeuArgProTyrTyrProValGluArgGlySTrPalaleuGlyLeuGlnSerArgAla | 398 | |
| | | ::: ::: | | |
| Db | 1338 | GCGTTGAGACCACATCTTCCAGCTGAGAGGAATGGGCTCTTGCTTCAGTCTCGAGCA | 1397 | |
| | | ::: ::: | | |
| QY | 399 | HisProArgGluIleMetValGluValLeuLysAlaleuGlnGluLeuAsnValArgTrp | 418 | |
| | | ::: ::: | | |
| Db | 1398 | CATCCAAAAGAAATAAATGCTCTGAAGTGCTGAAAGCTCTGCAAGAATTAATGTTTAACTGG | 1457 | |
| | | ::: ::: | | |
| QY | 419 | LysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPheProGluValAsn | 438 | |
| | | ::: ::: | | |
| Db | 1458 | AAAAAGATAGGTCACTATAACATGAAGTCAGATGAGATCTGGCTTCTCTGCT----- | 1511 | |
| | | ::: ::: | | |
| QY | 439 | AspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAsp | 458 | |
| | | ::: ::: | | |
| Db | 1512 | ---CAAATTCATAACATCATACTTCAGTCAGAGGTC-----ATTGAACCTGATAGC | 1562 | |
| | | ::: ::: | | |
| QY | 459 | AlaAsnGlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLysAsp | 478 | |
| | | ::: ::: | | |
| Db | 1563 | CTGAGTGAGAGGTTA--AGTTTAATTAGTTGAATTACAGCTGTACAAACAAGAGAC | 1619 | |
| | | ::: ::: | | |
| QY | 479 | AspLysTyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPhe | 498 | |
| | | ::: ::: | | |
| Db | 1620 | GAGAAATACCTCCTCGATTTCGAAAGAGTCAGTGGGCCACAGCTCCTCTTCTGACTTG | 1679 | |
| | | ::: ::: | | |
| QY | 499 | CysAlaAlaPheLeuThrLysLeuArgValLeu | 509 | |
| | | ::: ::: | | |
| Db | 1680 | TGCGCGGCTTCTTACTCAACTGAGAGTTCTT | 1712 | |
| | | ::: ::: | | |

```

RESULT 13
US-10-183-687-251
; Sequence 251, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczyński, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: BBI458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 251
; LENGTH: 2543
; TYPE: DNA
; ORGANISM: Glycine max
US-10-183-687-251

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| | | | |
|------------------------|-----------|---------------|------|
| Alignment Scores: | 6.55e-224 | Length: | 2543 |
| Pred. No.: | 1939.00 | Matches: | 373 |
| Score: | 83.37% | Conservative: | 58 |
| Percent Similarity: | 72.15% | Mismatches: | 76 |
| Best Local Similarity: | 72.00% | Indels: | 10 |
| Query Match: | 13 | Gaps: | 4 |
| DB: | | | |

US-09-857-522B-4 (1-509) x US-10-183-687-251 (1-2543)

QY 1 MetAspGlySerSer---LysGlySerGlyHisSer-----GluAlaLeuArgAsnTyr 17
| | | | | : : : : : | | | | |
Db 73 ATGGACAGATCAATGGCCGTGGTGGTGAAGTGTGACATGTTTCTCCGAAATTAT 132
QY 18 AsnLeuGlyArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLys 37
| | | | | : : : : : | | | | |
Db 133 AAGTTGGGAAACAACTCGGCATTGGGCTCTTGGCAAGGTGAATAATGCTGAGCATGTA 192
QY 38 LeuThrGlyHisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGlu 57
| | | | | : : : : : | | | | |
Db 193 CGGACTGGTCATTAAGTGTCTATTAAGATCTTTAACCGCCACAAGATTAAACATGGAA 252
QY 58 MetGluGluLysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIle 77
| | | | | : : : : : | | | | |
Db 253 ATGGAAGAAAAGTTAGAAGAGAATACTAAATTGAAGATTGTTATGCATCATCACATT 312
QY 78 IleArgLeuTyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCys 97
| | | | | : : : : : | | | | |
Db 313 ATAAGACTATATGAGGTTGTAGAAACCCCAAGACATATATGTTGTAAGAGTATGTG 372
QY 98 LysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAla 117
| | | | | : : : : : | | | | |
Db 373 AAATCTGAGAGAGCTCTTGATATACATAGTAGAAGGGTCGGCTGCAAGAGATGAAGCC 432
QY 118 ArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValVal 137
| | | | | : : : : : | | | | |
Db 433 CGTCATTTTTCACAGACATAATTCTGTGTGTGAGTACTGTCAAGAGATATGTGTGTT 492
QY 138 HisArgAspLeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAla 157
| | | | | : : : : : | | | | |
Db 493 CATAGAGACCTGAAGCTGAAGAAATTACTCTTGACCTCAAAATTTAACATCAAGATTGCT 552
QY 158 AspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySer 177
| | | | | : : : : : | | | | |
Db 553 GATTTTGGTGGAGCAACATCATGCGTAGAGGTCACTTCTTAAGACAAGTTGTGAAGC 612
QY 178 ProAsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAsp 197
| | | | | : : : : : | | | | |
Db 613 CCTAATTATGCGGCTCCAGAGGTATCTCTGGAATAATTGTATGCTGAGCCGAAGTAGAT 672
QY 198 ValTyrSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAsp 217
| | | | | : : : : : | | | | |
Db 673 GTCTGAGCTGTGTGAATTTTATATGCTCTTCTGTGACACTCTTCTTTTGATGAT 732
QY 218 GluAsnIleProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHis 237
| | | | | : : : : : | | | | |
Db 733 GAAAAACATTCCCAATCTCTTCAAAAAATAAGGTTGGATATACACTCTTCTTAGTCAT 792
QY 238 LeuSerAlaLeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArg 257
| | | | | : : : : : | | | | |
Db 793 CTATCACCTGTGTGAGAGATTGTATACCAAGAGTCTTGTGTGATCCCATGAAGAGG 852
QY 258 IleThrIleArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeu 277
| | | | | : : : : : | | | | |
Db 853 ATGACCATACCTGAGATACGCCAACACCCATGGTTCCAAGTTTCATCACCCTTATTTTA 912
QY 278 AlaValProProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArg 297
| | | | | : : : : : | | | | |
Db 913 GCAGTGCCACCAACAGATACACTGCAACAAGCCAAAAGATTGATGAGAGATTCTTCAG 972
QY 298 AspValValAsnMetCysPheAsnLysAsnHisValCysGluSerLysCysSerArgLeu 317
| | | | | : : : : : | | | | |
Db 973 GAAGTGGTTAATATGGGATTGACAGGAATCAATGGTTGAATCTCTTAGCAACAGATA 1032
QY 318 GlnAsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSer 337
| | | | | : : : : : | | | | |
Db 1033 CAAATGAGGGTACTGTACATACTATTGTTATTGACAACCGGTTTCGTGTTTCTAGT 1092
QY 338 GlyTyrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSer 357
| | | | | : : : : : | | | | |
Db 1093 GGTATCTTGAGCTGAATTTCAGAAGACAATGATTTCTGTTTAAACCGTATGCATTCC 1152

QY 358 SerGluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSer 377
| | | | | : : : : : | | | | |
Db 1153 GGCGAAGTTCCTTCTCCAGTTGTGGACACACACAGACAGGGTATATGATTATCAAGGG 1212
QY 378 SerGlyLeuArgProTyrTyrProValGluArgLysTyrAlaLeuGlyLeuGlnSerArg 397
| | | | | : : : : : | | | | |
Db 1213 GTAGGAATGCGGCAACAGTTCCCTGTTGAGAGAAAATGGGCCCTTGAGTCTCGA 1272
QY 398 AlaHisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArg 417
| | | | | : : : : : | | | | |
Db 1273 GCCCAACCAAGTGAATAATGACTGAGGTCTTAAAGCTCTACAGAAATTAAATGTTGT 1332
QY 418 TyrLysLysAsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPhePro----- 435
| | | | | : : : : : | | | | |
Db 1333 TGAAGAAGATTGGACACTATTAACATGAAGTGCAGATGGTTGCTGCACTGTGCAT 1392
QY 436 -----GluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThr 452
| | | | | : : : : : | | | | |
Db 1393 CATGAAGAAATGATTAACAATTCTGTGCATAGTAATCATTAATTGGAATGATCCGGC 1452
QY 453 IleMetAspAsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGln 472
| | | | | : : : : : | | | | |
Db 1453 ATTATTGAAATGAAGCTGTTCT-----AAGTCAATGTGTGTAAGTTCAG 1506
QY 473 LeuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGln 492
| | | | | : : : : : | | | | |
Db 1507 CTTTACAAAACCTCGTGAGGAGAAATATCTGCTTGATCTTCAAAAGGCTCCAGGCCACAG 1566
QY 493 LeuLeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
| | | | | : : : : : | | | | |
Db 1567 TTTCTTTTCTTGATCTGTGCGCTGCTTCTTTCACAGCTACGTGTTCTC 1617

RESULT 14

US-10-425-114-2148
; Sequence 2148, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2148
; LENGTH: 1778
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700204782_FLI
US-10-425-114-2148

Alignment Scores:
Pred. No.: 6.41e-224 Length: 1778
Score: 1937.00 Matches: 374
Percent Similarity: 83.66% Conserves: 56
Best Local Similarity: 72.76% Mismatches: 68
Query Match: 71.93% Indels: 16
DB: 13 Gaps: 5

US-09-857-522B-4 (1-509) x US-10-425-114-2148 (1-1778)

QY 1 MetAspGlySerSerLysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
| | | | | : : : : : | | | | |
Db 128 ATGAGAGGAGCTGGAAGA-----GATGCCAACCCCTTGGCGGCTTACCGAATTGGC 178
QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40

Db 179 AAAACCTAGCAATGGGTCGTCGTAAGTGAAGATCGCGGAACATATATATGACTGGC 238
QY 41 HisArgValAlaIleIysIleIleAsnCybArgGlnMetArgAsnMetGluMetGluGlu 60
Db 239 CATAAAGTGGCAATCAAGATCCTCAATCGCCGTAAGATCAAGAAGCATGGAATGGAAGAG 298
QY 61 LysAlaLysArgGluPheIysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
Db 299 AAAGTGAAGAGAAATCAAGATACTGAGATTATTATGATCCTCATATCATACGCCCTT 358
QY 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysIleTyrGly 100
Db 359 TATGAGGTGATAGATACCTGCTGATATTATTGTTATGAGTATGTTAAATCTGGA 418
QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
Db 419 GAGTTGTTGATTACATGTTGAGAAGGAGAAGACTGACGAAGAAGAGCCCGGCTTT 478
QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAsp 140
Db 479 TTTCAGCAGATCATATCTGGTGTGAATATTGCCATAGGAACATGTTGCTCACCGTGAT 538
QY 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
Db 539 TTAAAGCCAGAAATCTTTTGGATTGCAATGCAATTAAGATTGCTGATTTTGGC 598
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
Db 599 TTAAGTAATGTTATGCGTGATGCTCACTTCTTAAGACAGATGTGTAGCCGCAATTAT 658
QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSer 200
Db 659 GCAGCACCCTGAGGTCAATCTGTAACACTATATGCTGCTCGAAGTTGATGTCGAGC 718
QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
Db 719 TGCGGCGTTATCTTATGCTCTTCTTGTGGCACCTTCCATTGACGATGAGAATATT 778
QY 221 ProAsnLeuPheLysIleLysGlyGlyIleTyrThrLeuProSerHisIleSerAla 240
Db 779 CTAAACCTTTTAAGAAATAAAGGGTGAATATATACCTTCTAGTCATTGTTCACCT 838
QY 241 LeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle 260
Db 839 TCAGCGAGGACTTGATTCCTAGAATGCTGTTGATCCGATGAAAAAGATTAACAATA 898
QY 261 ArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAlaValPro 280
Db 899 CGTGAATCCGTGAACATGTGTGTTCAAAATTCACCTCCGCGCTATTAGCTGTACCG 958
QY 281 ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal 300
Db 959 CCTCCGGACACTGCACACAAGTTAAGAAGCTGGACGAGAAACCCTTAATGATGTTATT 1018
QY 301 AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu 320
Db 1019 AAGATGGGTTTGACAGAATCAAGCTAATTGAATCTCTGCAACAACAGATGCAAGATGAG 1078
QY 321 AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu 340
Db 1079 GCAACAGTTGCTATTATTACTCATGACACAATAGGCTTCGTACAACACAGTGTATCTT 1138
QY 341 GlyAlaAspTyrGlnGlnSerMetAspArgAsnLeuAsnGlnLeu--AlaSerSerGlu 359
Db 1139 GGATCTGAGTTTCAAGATCTATGAGCCCATCTTCTCAAGTACATGCTGAACAACCA 1198
QY 360 SerSerSerSerGlyThrArgAsnTyrVal-----ProGlySerSerAspPro 375
Db 1199 ACTTCAGCAACTGAACATCGACAGCATGTGTTACAGAATCTCCGGG----- 1246
QY 376 HisSerSerGlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGln 395

Db 1247 -----TCTGTTTGAGGCGACGATTTTGATCTGAAAAGAAATGGCCCTTGCTTCAG 1300
QY 396 SerArgAlaHisProArgGluIleMetValGluValIleLysAlaLeuGlnGluLeuAsn 415
Db 1301 TCTCGAGCACATCCACGAGAATAATAGTGAAGTCTTAAAGCACCTGCAAGAACTGAAT 1360
QY 416 ValArgTrpLysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPhePro 435
Db 1361 GTTACTGGAATAAGATTGGACACTACACATGAATAAGATGAGTCCCTGGCTGCCCTT 1420
QY 436 GluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAsp 455
Db 1421 GAG-----AGTATGATGCATTAAGTGTGATGGCTTTAGTGACAGAGTCTGCTATAATTGAA 1474
QY 456 AsnAspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLys 475
Db 1475 ACTGATGATCTCATAGCGAAATCAACCCGTATAGTGAAGTTGAGATTGAGCTTTACAAA 1534
QY 476 ThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPhe 495
Db 1535 ACGAGGATGAGAGTACCTTCTTGACCTGCAAGGGTCAGTGACGACGAACTCCTCTTT 1594
QY 496 LeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
Db 1595 CTGGACTGTGTGTCGCCCTTTCTTAACGACGCTGAGATTCTT 1636

RESULT 15

US-10-183-687-237
; Sequence 237, Application US/10183687
; Publication No. US20030204870A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Allen, William B.
; APPLICANT: Cahoon, Rebecca
; APPLICANT: Epelbaum, Sabine
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Harvell, Leslie T.
; APPLICANT: Jones, Todd
; APPLICANT: Kinney, Tony
; APPLICANT: Klein, Ted
; APPLICANT: Li, Changjiang
; APPLICANT: Oliveira, Igor Cunha
; APPLICANT: Sakai, Hajime
; APPLICANT: Shen, Bo
; APPLICANT: Tarczynski, Mitchell C.
; TITLE OF INVENTION: Alteration Of Oil Traits In Plants
; FILE REFERENCE: BBI458 US NA
; CURRENT APPLICATION NUMBER: US/10/183,687
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/301,913
; PRIOR FILING DATE: 2001-06-29
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 237
; LENGTH: 2107
; TYPE: DNA
; ORGANISM: Zea mays
US-10-183-687-237

Alignment Scores:
Pred. No.: 4.51e-223 Length: 2107
Score: 1931.00 Matches: 372
Percent Similarity: 83.69% Conservative: 54
Best Local Similarity: 73.08% Mismatches: 77
Query Match: 71.70% Indels: 6
DB: 13 Gaps: 3

US-09-857-522B-4 (1-509) x US-10-183-687-237 (1-2107)

QY 1 MetAspGlySerSerLysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db 230 ATGAGGAGGAGCGGGAAGA-----CATGCCAACCTTTGAGCGGTTACAGAATTGGC 280

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: July 9, 2004, 11:38:20 ; Search time 5849 Seconds
(without alignments)
3771.859 Million cell updates/sec

Title: US-09-857-522B-4
Perfect score: 2693
Sequence: 1 MDGSSKSGHSEALRNYNLG.....GPQLLFLDFCAFLTKLRVL 509

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO_spool/US09857522/runat_07072004_161357_1874/app_query.fasta_1.647
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09857522@CGN_1_1_3731@runat_07072004_161357_1874 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*

29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|--------------|----------------------|
| 1 | 2422 | 89.9 | 1838 | 8 D82035 | D82035 Oryza sativ |
| 2 | 2422 | 89.9 | 2213 | 8 AK100591 | AK100591 Oryza sat |
| 3 | 2422 | 89.9 | 2245 | 8 AK072723 | AK072723 Oryza sat |
| 4 | 2411.5 | 89.5 | 1872 | 8 D82038 | D82038 Oryza sativ |
| 5 | 2411.5 | 89.5 | 2161 | 8 D82036 | D82036 Oryza sativ |
| 6 | 2384 | 88.5 | 2927 | 8 AK069206 | AK069206 Oryza sat |
| 7 | 2378 | 88.3 | 1899 | 8 BT009004 | BT009004 Triticum |
| 8 | 2356.5 | 87.5 | 1770 | 8 OSU55768 | OSU55768 Oryza sativ |
| 9 | 2100 | 78.0 | 1542 | 8 HVTU7990 | HVTU7990 Hordeum v |
| 10 | 2072 | 76.9 | 1539 | 8 HVBKIN12M | X65604 H.vulgare B |
| 11 | 2062.5 | 76.6 | 1809 | 8 RYERKIN1 | M74113 Secale cere |
| 12 | 2056 | 76.3 | 2138 | 8 D82037 | D82037 Oryza sativ |
| 13 | 1977 | 73.4 | 2073 | 8 AK067158 | AK067158 Oryza sat |
| 14 | 1977 | 73.4 | 2209 | 8 D82039 | D82039 Oryza sativ |
| 15 | 1969.5 | 73.1 | 1539 | 6 AX507962 | AX507962 Sequence |
| 16 | 1969.5 | 73.1 | 1608 | 8 BT010386 | BT010386 Arabidops |
| 17 | 1969.5 | 73.1 | 1869 | 8 ATSKIN2 | X94757 A.thaliana |
| 18 | 1969.5 | 73.1 | 2209 | 8 AY093170 | AY093170 Arabidops |
| 19 | 1968 | 73.1 | 1778 | 8 CSSNFRPK | Y10036 C.sativus m |
| 20 | 1960.5 | 72.8 | 1948 | 8 AF143743 | AF143743 Lycopersi |
| 21 | 1945 | 72.2 | 1453 | 8 HVBKIN2 | X82548 H.vulgare m |
| 22 | 1942 | 72.1 | 8146 | 8 AB101656 | AB101656 Oryza sat |
| 23 | 1942 | 72.1 | 94710 | 8 AP005918 | AP005918 Oryza sat |
| 24 | 1942 | 72.1 | 124835 | 2 AP004164 | AP004164 Oryza sat |
| 25 | 1937.5 | 71.9 | 1929 | 6 AR184289 | AR184289 Sequence |
| 26 | 1923 | 71.4 | 1536 | 6 E05288 | E05288 DNA encodin |
| 27 | 1923 | 71.4 | 2028 | 8 TOBNPK5 | D26602 Tobacco mRN |
| 28 | 1909 | 70.9 | 2100 | 8 AF062479 | AF062479 Oryza sat |
| 29 | 1903.5 | 70.7 | 1539 | 6 AX505467 | AX505467 Sequence |
| 30 | 1903.5 | 70.7 | 1539 | 8 AY149927 | AY149927 Arabidops |
| 31 | 1903.5 | 70.7 | 1809 | 8 AY070468 | AY070468 Arabidops |
| 32 | 1903.5 | 70.7 | 1834 | 8 ATNPK | X99279 A.thaliana |
| 33 | 1903.5 | 70.7 | 1966 | 8 STU83797 | U83797 Solanum tub |
| 34 | 1899.5 | 70.5 | 1825 | 6 AX497023 | AX497023 Sequence |
| 35 | 1899.5 | 70.5 | 1852 | 8 ATSKIN1 | X94755 A.thaliana |
| 36 | 1896.5 | 70.4 | 127426 | 8 AC137075 | AC137075 Genomic s |
| 37 | 1895.5 | 70.4 | 7074 | 8 AB101657 | AB101657 Oryza sat |
| 38 | 1893.5 | 70.3 | 1941 | 8 AF128443 | AF128443 Glycine m |
| 39 | 1891.5 | 70.2 | 1825 | 6 AX497027 | AX497027 Sequence |
| 40 | 1890.5 | 70.2 | 2006 | 8 BT009349 | BT009349 Triticum |
| 41 | 1626.5 | 60.4 | 3416 | 8 ATHAKIN10A | M93023 Arabidops |
| 42 | 1616 | 60.0 | 93735 | 8 ATAC008261 | AC008261 Arabidops |
| 43 | 1616 | 60.0 | 258024 | 2 AC084046 | AC084046 Trypanoso |
| 44 | 1543.5 | 57.3 | 6112 | 8 AB101655 | AB101655 Oryza sat |
| 45 | 1537 | 57.1 | 3550 | 6 AX497024 | AX497024 Sequence |

RESULT 1

ALIGNMENTS

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D82035      1838 bp      mRNA      linear      PLN 06-FEB-1999
LOCUS       D82035
DEFINITION  Oryza sativa mRNA for OSK4, complete cds.
ACCESSION   D82035
VERSION     D82035.1  GI:4107000
KEYWORDS    OSK4.
SOURCE      Oryza sativa
ORGANISM    Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1 (sites)
AUTHORS     Takano,M., Kajiya-Kanegae,H., Funatsuki,H. and Kikuchi,S.
TITLE       Rice has two distinct classes of protein kinase genes related to
            SNF1 of Saccharomyces cerevisiae, which are differently regulated
            in early seed development
JOURNAL     Mol. Gen. Genet. 260 (4), 388-394 (1998)
MEDLINE     99086251
PUBMED      9870704
REFERENCE   2 (bases 1 to 1838)
AUTHORS     Takano,M.
TITLE       Direct Submission
JOURNAL     Submitted (15-DEC-1995) Makoto Takano, National Institute of
            Agrobiological Resources, Department of Molecular Genetics; 2-1-2
            Kannondai, Tsukuba, Ibaraki 305-8602, Japan
            (E-mail:mtakano@abr.affrc.go.jp, Tel:81-298-38-7446,
            Fax:81-298-38-7408)
FEATURES
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        /codon_start=1
        /product="OSK4"
        /protein_id="BAA36299.1"
        /db_xref="GI:4107001"
        /translation="MEGNARGGGSHSEALKNYNLGRLLIGSGFKVKIAEHKLTGHRVA
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            ATSGYLGDADYQESLELNLRNRPASSESSASNTRYLPGSSDPHAGTMRPHYVERKWA
            GLQSRAPQREIMIEVLKALDELNVCKMNGYNNKCRWSVGYPQATMDLDVNSFVDD
            SIIMDNGDVNGRLPAVVIKFEIQLYKSRDEKYLDMQRTVGQLLFDPCAFLTKLRV
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     1838
        /gene="osk4"

polYA_site
1838
/gene="osk4"

ORIGIN
Alignment Scores:
Pred. No.:      1.17e-211      Length:      1838
Score:          2422.00        Matches:      451
Percent Similarity: 95.48%      Conservative: 35
Best Local Similarity: 88.61%      Mismatches: 23
Query Match:      89.94%        Indels:      0
DB:              8            Gaps:        0

US-09-857-522B-4 (1-509) x D82035 (1-1838)

QY      1 MetAspGlySerSerIysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20
Db      92 ATGGAAGCAATGCTAGAGCGCGGTGGGCATTCTGAGCGCACTGAAGAATACTACATCTAGGA 151

QY      21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
Db      152 AGAAGCTTTAGGTAATGGTTCATTGGAAAAAGTGAAAGATTGCAGAGCATTAAGCTTACAGGG 211

```

| | | | |
|----|------|---|------|
| QY | 41 | HisArgValAlaIleLeuSilelleAsnCysArgGlnMetArgAsnMetGluMetGlu | 60 |
| Db | 212 | CACAGAGTTGCTATAAGATCCTGACCCTGCCAAATGAGAATATGAAATGAGAG | 271 |
| QY | 61 | LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu | 80 |
| Db | 272 | AAAGCAAGAGAGAAATCAAGATATTGAGGTTGTTCAATTCAATCCCATATCATTCGCCCTT | 331 |
| QY | 81 | TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly | 100 |
| Db | 332 | TATGAGGTCAATACACTCCTACGATATATATGTTGTGATGAGTACTGCAGATTGGA | 391 |
| QY | 101 | GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle | 120 |
| Db | 392 | GAACTGTTGATTAACATTTGTGAGAAAGCAGGTTCAGAAAGATGAGGCTCGCCGATC | 451 |
| QY | 121 | PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp | 140 |
| Db | 452 | TTCCAGCAGATTATCTGGGGTTGATACTGCCACAGAAACATGGTGTTCATCGTGAT | 511 |
| QY | 141 | LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly | 160 |
| Db | 512 | CTGAAGCCAGAAACTTGCTACTGATTCAAGTATTAACGTAAGCTTGCTGACTTGGT | 571 |
| QY | 161 | LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr | 180 |
| Db | 572 | TTGAGTAATGTCATTCATGATGCGCATTTTAAAGACAAGCTGCGGAGTCCGAATTAT | 631 |
| QY | 181 | AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSer | 200 |
| Db | 632 | GCTGCTCCAGAGTGATCTCTGTAATTATATGCTGGAACCGAGTTGATGATGAGC | 691 |
| QY | 201 | CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle | 220 |
| Db | 692 | TGTGAGTGATCCTTATGCTCTCTTGTGTGTACTCTTCCATTGATGACGAGAAATATC | 751 |
| QY | 221 | ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla | 240 |
| Db | 752 | CCCAACCTATTCAAAAAGATTAAGGGTGGTATATATACTCTCCCAAGTCATTATCTGCT | 811 |
| QY | 241 | LeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle | 260 |
| Db | 812 | CTGGCAGGAGATTGATCCCAAGGATGCTTGTTGATCCCAATGAAGAATCACAAATT | 871 |
| QY | 261 | ArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAlaValPro | 280 |
| Db | 872 | CGTGAATTGAGAGCATCAATGTTTCAGATTGCGCTTCTCGTTACTTAGCAGTGCT | 931 |
| QY | 281 | ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal | 300 |
| Db | 932 | CCACCAGACACAGCACAGCAAGCCAAATGATTGATGAAGATACCTTCAAGACGTTGTA | 991 |
| QY | 301 | AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu | 320 |
| Db | 992 | AACTTGGGTATGAAGAACCATGTGTGTAATCTCTGCCAATAGACTGCAAAATGAG | 1051 |
| QY | 321 | AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu | 340 |
| Db | 1052 | GCAACTGTTGCATATTATTGCTATTGGACAATCGATTCCGAGCTACCAAGTGGCTATCTG | 1111 |
| QY | 341 | GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer | 360 |
| Db | 1112 | GGAGCAGACTATCAGAATCATTTGAGAGGAATCTTAATCGCTTGTCTTCAACAGATCA | 1171 |
| QY | 361 | SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu | 380 |
| Db | 1172 | GCAAGTTCAAATACAGGCATTTATCTCCACAGAGCAGTGATCCTCATGCCAGTGTGTTG | 1231 |
| QY | 381 | ArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAlaHisPro | 400 |
| Db | 1232 | CGCCACACATTATCTCTGTGAAGAAATGGGCTTTGCACTTCAGTCTCGAGCTCAGCCT | 1291 |
| QY | 401 | ArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrpLysLys | 420 |

|||||
Db 1292 CGCGAGATATGATGAGTTCCTAAAGGCACCTTGAAGACTTAATGTCTGCTGAAGAAG 1351
Qy 421 AaNgLyHISTYraaNVallysCySaRGTTPCySProGLyPheProGLuValaAsnaSPThr 440
Db 1352 AATGGACAGTACACATGAAAGTGCAAGATGAGCGCTGGGTATCTCAGGCCACTGATATG 1411
Qy 441 LeuAspAlaSerAsnSerPheLeuGLyAspSerThrIleMetAspAsnaSPalaAsn 460
Db 1412 TTAGATGTCAACCAACGCTTTGTTGATGACTCAATTATATGATATAGCGCATGTAAAC 1471
Qy 461 GLYArgLeuProThrValIleIleLySPheGLuPheGLnLeuTYrLySThrLySaSPaSPlys 480
Db 1472 GGGAGGTACTGCTGCTGATCAAGTTGAATCCAGCTTTACAAGAGACAGACGAGAAG 1531
Qy 481 TyrLeuLeuAspMetGLnArgValThrGLyProGLnLeuLeuPheLeuAspPheCysAla 500
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Qy 501 AlaPheLeuThrLyLeuAArgValLeu 509
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RESULT 2
AK100591 2213 bp mRNA linear PLN 24-JUL-2003
LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:J023106J08, full
DEFINITION insert sequence.
ACCESSION AK100591
VERSION AK100591.1 GI:32985800
KEYWORDS FLI_CDNA; CAP trapper.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 The Rice Full-Length cDNA Consortium, National Institute of
Agricultural Sciences Rice Full-Length cDNA Project Team;
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Ootomo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
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Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
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Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
JOURNAL Science 301 (5631), 376-379 (2003)
MEDLINE 22752273
PUBMED 12869764
REFERENCE 2 (bases 1 to 2213)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
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Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2002) Shoeni Kikuchi, National Institute of
Agricultural Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
COMMENT This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL : http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Ootomo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
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Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.
FEATURES
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/db_xref="taxon:39947"
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Percent Similarity: 95.48% Conservative: 35
Best Local Similarity: 88.61% Mismatches: 23
Query Match: 89.94% Indels: 0
Gaps: 0
US-09-857-522B-4 (1-509) x AK100591 (1-2213)
Qy 1 MetAspGLySerSerLySGLySerGLyHisSerGLuAlaLeuArgAsnTYrAsnLeuGLy 20
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Qy 21 ArgThrLeuGLYIleGLyThrPhcGLyLySVallySIlealagluHisLySLeuThrGLy 40
Db 288 AGAAGCTTAGGTATTTGTTTCATTTGGAAAAAGTGAAGATTGCAAGCATTAAGCTTACAGG 347
Qy 41 HisArgValAlaIleIleLySIleleAsnCySaRGLnMetArgAsnMetGLumetGLuGLu 60
Db 348 CACAGAGTTGCTATTAAGATCCTGAACCGTCGCCAAATGAGAAATATGAAATGAGAGAG 407

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| QY | 61 | LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu | 80 |
| Db | 408 | AAAGCAAAGAGAGAAATCAAGATATGAGGTGTTCATTCATCCCATATCATTCGCCTT | 467 |
| QY | 81 | TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly | 100 |
| Db | 468 | TATGAGGTCAATATACACTCCCTACGATATATATGTGTGATGAGTACTGCAAGTTTGA | 527 |
| QY | 101 | GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle | 120 |
| Db | 528 | GAAGTGTTCATTACATTGTTGAGAAAGCCAGGTTGCAGGAAGATGAGGCTCGCCGAAATC | 587 |
| QY | 121 | PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAsp | 140 |
| Db | 588 | TTCCAGCAGATTATATCTGGGGTTGAATACTGCCACAGAAACATGGTGTTCATCGTAT | 647 |
| QY | 141 | IleuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly | 160 |
| Db | 648 | CTGAAGCCAGAAACTGTCTACTGGATTCAAGTATAACGTAAAGCTTGCTGACTTGTGT | 707 |
| QY | 161 | LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr | 180 |
| Db | 708 | TTGAGTAAATGTCATGCATGATGCGCAATTTTAAAGACACAGCTCGGGAGTCCGAATTAT | 767 |
| QY | 181 | AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSer | 200 |
| Db | 768 | GCTGCTCCAGAGGTGATCTCTGTAAATTATATGCTGACCCGAGGTGATGATGGAGC | 827 |
| QY | 201 | CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle | 220 |
| Db | 828 | TGTGAGTGCATCCTTATGCTCTCTTGTGTGACTCTTCATTTGATGACGAGAATATC | 887 |
| QY | 221 | ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla | 240 |
| Db | 888 | CCCACTTATTCAAAAAGATAAGGCGTATATATATCTCTCCCAAGTCATTATCTGCT | 947 |
| QY | 241 | IleuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle | 260 |
| Db | 948 | CTGGCAGGAGATTGATCCCAAGAGTCTTGTGTGATCCATGAAAGAAATCACAAATT | 1007 |
| QY | 261 | ArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAlaValPro | 280 |
| Db | 1008 | CGTGAATTCGAGAGCATCAATGGTTCAGATTGCGCTTCCTCGTTACTTAGCAGTGCTT | 1067 |
| QY | 281 | ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal | 300 |
| Db | 1068 | CCACCACACACACACAGCAAGCCAAATGATTGATGAAGATACCTTCAAGACGTTGTA | 1127 |
| QY | 301 | AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu | 320 |
| Db | 1128 | AACTTGGGTTATGAAAAAGCACCATGTGTGTGAATCTCTGCGCAATAGACTGCCAAATGAG | 1187 |
| QY | 321 | AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu | 340 |
| Db | 1188 | GCAACTGTTCATATTATTGCTATTGCAACAATCGATTCCGAGCTAACAGTGCTATCTG | 1247 |
| QY | 341 | GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer | 360 |
| Db | 1248 | GGAGCAGACTATCAAGATCATTTGAGAGGAATCTTAATCGCTTTCATCAGAATCA | 1307 |
| QY | 361 | SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu | 380 |
| Db | 1308 | GCAAGTTCAAATACAAAGCATTAATCTCCACAGGAAGCATGATCTCATGCCAGTGGTTTG | 1367 |
| QY | 381 | ArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAlaHisPro | 400 |
| Db | 1368 | CGCCACATTAATCTCTGTGAAGAAATGGGCTCTTGACATTCAGTCTCGAGCTCAGCCT | 1427 |
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| Db | 1428 | CGCGAGATAATGATGAGGTCCTAAAGGCACTGAAGACTTAATGTCTGGAAGAG | 1487 |
| QY | 421 | AsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPheProGluValAsnAspThr | 440 |

D_b 1489 AATGACAGTACACATGAAGTCAGATGGAGCGTTGGGTATCCTCAGGCCACTGATATG 1547
QY 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnaSpAspAlaasn 460
D_b 1548 TTAGATGTCAACCACAGCTTTGTGTGATGACTCATATTATAATGATTAATGGCGATGTAAC 1607
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| RESULT 3 | AK072723 | LOCUS | DEFINITION | ACCESSION | VERSION | KEYWORDS | SOURCE | ORGANISM |
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| | AK072723 | 2245 bp | mRNA | | | | | |
| | Oryza sativa (japonica cultivar-group) | linear | cdna clone:J023135H07, full | | | | | |
| | insert sequence. | | | | | | | |
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| | AK072723.1 | GI:32982746 | | | | | | |
| | FLI_CDNA; CAP trapper. | | | | | | | |
| | Oryza sativa (japonica cultivar-group) | | | | | | | |
| | Oryza sativa (japonica cultivar-group) | | | | | | | |

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Euhartoideae; Oryzaeae; Oryza.

| REFERENCE AUTHORS | TITLE |
|---|---|
| The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team; Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Ninkura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN; Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y. japonica rice Science 301 (5631), 376-379 (2003) | |
| JOURNAL MEDLINE PUBMED | 22752273 12869764 |
| REFERENCE AUTHORS | 2 (bases 1 to 2245) Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., |

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Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S.,
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| Db | 1604 | GGAGGTTACTGCTGCTGATCAAGTTGAAATCCAGCTTTACAAGACGACAGAGAAG | 1663 |
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| DEFINITION | Oryza sativa mRNA for OSK3, complete cds. | linear | PLN 06-FEB-1999 |
| ACCESSION | D82038 | | |
| VERSION | D82038.1 | GI:4107006 | |
| KEYWORDS | OSK3. | | |
| SOURCE | Oryza sativa | | |
| ORGANISM | Oryza sativa | | |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza. | | |
| REFERENCE | 1 (sites) | | |
| AUTHORS | Takano, M., Kajiya-Kanegae, H., Funatsuki, H. and Kikuchi, S. | | |
| TITLE | Rice has two distinct classes of protein kinase genes related to SNF1 of Saccharomyces cerevisiae, which are differently regulated in early seed development | | |
| JOURNAL | Mol. Gen. Genet. 260 (4), 388-394 (1998) | | |
| MEDLINE | 99086251 | | |
| PUBMED | 9870704 | | |
| REFERENCE | 2 (bases 1 to 1872) | | |
| AUTHORS | Takano, M. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (15-DEC-1995) Makoto Takano, National Institute of Agricultural Resources, Department of Molecular Genetics; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan | | |
| | (E-mail:mtakano@abr.affrc.go.jp, Tel:81-298-38-7446, Fax:81-298-38-7408) | | |
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| ORIGIN | | | |
| Alignment Scores: | 1.09e-210 | Length: 1872 | |
| Pred. No.: | 2411.50 | Matches: 453 | |
| Score: | 94.70% | Conservative: 29 | |
| Percent Similarity: | | | |

| | | | |
|--|--------|--|------|
| Best Local Similarity: | 89.00% | Mismatches: | 26 |
| Query Match: | 89.55% | Indels: | 1 |
| DB: | 8 | Gaps: | 1 |
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| Qy | 21 | ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly | 40 |
| Db | 187 | AGAACTTAGGTATTGGCTCAATTGAAAAAGTGAAGATTGCAGACATTAAGCTTACAGA | 246 |
| Qy | 41 | HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGluGlu | 60 |
| Db | 247 | CACAGAGTTGCTATAAGATCCTGAACCGCCCAATGAGAATATGAAATGAGAGAG | 306 |
| Qy | 61 | LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu | 80 |
| Db | 307 | AAAGCAAGAGAGAAATCAAGATACTGAGATTGTTCAITTCATCCCATATTCATTCGCC | 366 |
| Qy | 81 | TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly | 100 |
| Db | 367 | TATGAGTTATATACACTCCACGATATATATGTTGATGAGTACTGCAAGTTTGA | 426 |
| Qy | 101 | GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle | 120 |
| Db | 427 | GAACGTGTTGATTACATTCATGTTGAGAAAGCAGGTGCAGAGAGATGAGGCTCGCCAA | 486 |
| Qy | 121 | PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValValHisArgAsp | 140 |
| Db | 487 | TTCACGACGATTATATCTGGGGTGAATACTGCCACAGAAACATGCTGTTCACTGAT | 546 |
| Qy | 141 | LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly | 160 |
| Db | 547 | CTGAAGCCAGAAACTTGCTACTGCAATTCAAAGTAAATGTAAGCTTGCTGACTTGCT | 606 |
| Qy | 161 | LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr | 180 |
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| Qy | 181 | AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTyrSer | 200 |
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| Qy | 201 | CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle | 220 |
| Db | 727 | TGTGAGTGATCCTTATGCTCTCTTGTGTACTCTTCCATTGATGATGAGAAATATC | 786 |
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| Db | 787 | CCCAACTATTCAAAAAGATAAGGTTGATATATATCTCTCCCAAGTCATTATCTGCT | 846 |
| Qy | 241 | LeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle | 260 |
| Db | 847 | CTGGCCAGAGATTGATCCCAAGGATGCTTGTGTTGATCCAAATGAAGAGAAATCAAA | 906 |
| Qy | 261 | ArgGluIleArgGluHisGlnTyrPheGlnIleArgLeuProArgTyrLeuAlaValPro | 280 |
| Db | 907 | CGTGAATTCAGAGACATCAGTGGTTTCAAGATTCGCTTCCTCTGTTACTTAGCAGTGC | 966 |
| Qy | 281 | ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal | 300 |
| Db | 967 | CCACCAACACACAGACAGCAAGCCAAATGATTGATGAAGATACCTTCAAGATGTGTA | 1026 |
| Qy | 301 | AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu | 320 |
| Db | 1027 | AACCTGGGTTATGGAAGGACCAATGTGTGATCTCTGCGCAATAGACTGCAGAAATGAG | 1086 |
| Qy | 321 | AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSerGlyTyrLeu | 340 |
| Db | 1087 | GCAACTGTTGCATATATTACTTCTTGGAACAATCGATTCCGAGCTACCAAGTGCTATTG | 1146 |

QY 341 GLYAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer 360
Db 1147 GGAGCAGACTATCAAGAATCTTGGAGAGGAATTTTAATCGCTTTGCTTCATCGGAATCA 1206
QY 361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
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QY 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
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Db 1624 GACTTCCTTACCAAGCTGAGGGTTCTA 1650

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LOCUS D82036 2161 bp mRNA linear PLN 06-FEB-1999
DEFINITION Oryza sativa mRNA for OSK5, complete cds.
ACCESSION D82036
VERSION D82036.1 GI:4107002
KEYWORDS OSK5.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (sites)
AUTHORS Takano,M., Kajiya-Kanegae,H., Funatsuki,H. and Kikuchi,S.
TITLE Rice has two distinct classes of protein kinase genes related to SNF1 of Saccharomyces cerevisiae, which are differently regulated in early seed development
JOURNAL Mol. Gen. Genet. 260 (4), 388-394 (1998)
MEDLINE 99086251
PUBMED 9870704
REFERENCE 2 (bases 1 to 2161)
AUTHORS Takano,M.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1995) Makoto Takano, National Institute of Agrobiological Resources, Department of Molecular Genetics; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:mtakano@abr.affrc.go.jp, Tel:81-298-38-7446, Fax:81-298-38-7408)
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ORIGIN
Alignment Scores:
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Score: 2411.50 Matches: 453
Percent Similarity: 94.70% Conservative: 29
Best Local Similarity: 89.00% Mismatches: 26
Query Match: 89.55% Indels: 1
DB: 8 Gaps: 1
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QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
Db 187 AGAAGTTAGGTATTTGGCTCATTTGGAAGAAAGTGAAGATTGCAGACATAAAGCTTACAGA 246
QY 41 HisArgValAlaIleLysIleIleAsnCysAspGlnMetArgAsnMetGluMetGluGlu 60
Db 247 CACAGAGTTGCTATAAAGATCCTGACCCGCCCAATGAGAAATATGGAATGAGAGAG 306
QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
Db 307 AAAGCAAGACAGAAATCAAGATCTGAGATTGTTCAATTCATCCCATATCATTCGCCCTT 366
QY 81 TyrGluValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGly 100
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QY 101 GluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgArgIle 120
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QY 121 PheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValHisArgAsp 140
Db 487 TTCAGAGATATATATCTGGGGTTGAATACTGCCACAGAAACATGGTTCATCGTGAT 546
QY 141 LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly 160
Db 547 CTGAAGCCAGAAACTTGCTACTTGATTCAAAGTATAATGTAAGCTTGCTGACTTTGGT 606
QY 161 LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr 180
Db 607 TTGAGTAAAGTCATGATGATGGCAATTTTGAAGACAAAGCTGGGAGTCCAAACTAT 666
QY 181 AlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSer 200
Db 667 GCTGCTCCAGAGGTGATCTCTGTTAAATTATATGCTGAGCTGAGGTTGATGAGAGC 726
QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
Db 727 TGTGAGTGAATCCTTATGCTCTCTTGTGTGACTCTTCATTTGATGATGAGAAATATC 786
QY 221 ProAsnLeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAla 240

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| Db | 787 | CCCAACCTATTCAAAAAGATAAAGGGTGGTATATATACTCTCCCAAGTCATTATCTGCT | 846 |
| Oy | 241 | LeuAlaArgAspLeuIleProArgMetLeuValGluProMetLysArgIleThrIle | 260 |
| Db | 847 | CTGGCCAGAGATTGTGATCCCAAGGATGCTTGTGTGATCCAATGAAGAATCACAAATT | 906 |
| Oy | 261 | ArgGluIleArgGluHisGlnTrpPheGlnIleArgLeuProArgTyrLeuAlaValPro | 280 |
| Db | 907 | CGTGAATTTCGAGAGCATCAGTGGTTTCAGATTCCGCTTCCTCGTTACTTAGCAGTGCCCT | 966 |
| Oy | 281 | ProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArgAspValVal | 300 |
| Db | 967 | CCACCAGACACAGCACAGCAAGCCAAATGATTGATGAAGATACCCTTCAAGATGTCGTA | 1026 |
| Oy | 301 | AsnMetGlyPheAsnLysAsnHisValCysGluSerLeuCysSerArgLeuGlnAsnGlu | 320 |
| Db | 1027 | AACTGGGTTATGGAAGAAGACCATGTGTGTGATCTCTGCGCAATAGACTGCAGATGAG | 1086 |
| Oy | 321 | AlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSergLysTyrLeu | 340 |
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| Oy | 341 | GlyAlaAspTyrGlnGlnLysSerMetAspArgAsnLeuAsnGlnLeuAlaSerSergLys | 360 |
| Db | 1147 | GGAGCAGACTATCAAGAATCTTTGGAGAGGAATTTTAATCGCTTTGCTTCATCGGAATCA | 1206 |
| Oy | 361 | SerSergSergLysThrArgAsnTyrValProGlySerSergAspProHisSergSergLys | 380 |
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| Oy | 401 | ArgGluIleMetValGluValLeuLysAlaLeuGlnGlnLysLeuAsnValArgTrpLysLys | 420 |
| Db | 1327 | CGCGAGATATGATTGAGGCTCTTAAGGCACTTCAAGACTTAATGTCCTCGAAGAAG | 1386 |
| Oy | 421 | AsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsnAspThr | 440 |
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| Oy | 481 | TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla | 500 |
| Db | 1564 | TATCTGCTGATATGACAGAGATTACGGGGCTCAGCTCTTTCTTGAGCTTCTGTGCA | 1623 |
| Oy | 501 | AlaPheLeuThrLysLeuArgValLeu | 509 |
| Db | 1624 | GACTTCCTTACCAAGCTGAGGGTTCTA | 1650 |
| RESULT 6 | | | |
| AK069206 | AK069206 | 2927 bp | mRNA linear PLN 24-JUL-2003 |
| LOCUS | AK069206 | | Oryza sativa (japonica cultivar-group) cDNA clone:J023008117, full |
| DEFINITION | Oryza sativa (japonica cultivar-group) | | insert sequence. |
| ACCESSION | AK069206 | | |
| VERSION | AK069206.1 | | GI:32979230 |
| KEYWORDS | FLI_CDNA; CAP trapper. | | |
| SOURCE | Oryza sativa (japonica cultivar-group) | | |
| ORGANISM | Oryza sativa (japonica cultivar-group) | | |
| | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | |
| | Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; | | |
| | Ehrhartoideae; Oryzeae; Oryza. | | |
| REFERENCE | 1 | | |

| | |
|-----------|--|
| AUTHORS | The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team., Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Nikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN: Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y. |
| TITLE | Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice |
| JOURNAL | Science 301 (5631), 376-379 (2003) |
| MEDLINE | 22752273 |
| PUBMED | 12869764 |
| REFERENCE | 2 (bases 1 to 2927) |
| AUTHORS | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Nikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A. |
| TITLE | Direct Submission |
| JOURNAL | Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007) |
| COMMENT | This clone is one of the 28k full-length cDNA clones from japonica rice. URL : http://cdna01.dna.affrc.go.jp/cDNA/ NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M. FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., |

Ota,Y., Saichoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H.,
Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
Yasunishi,A. and Hayashizaki,Y.

FEATURES

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ORIGIN

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Query Match: 88.53% Indels: 4
DB: 8 Gaps: 2

US-09-857-522B-4 (1-509) x AK069206 (1-2927)

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DB 1372 AAAGCAAGAGAGAAATCAAGATACTGAGATTGTCATTATCCCATATCATTCGCCCTT 1431
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QY 201 CysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAspGluAsnIle 220
DB 1792 TGTGAGTGTATCTTATATGCTCTCTTGTGTACTCTTCATTGTGATGATGAGAATATC 1851
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QY 241 LeuAlaArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIle 260

DB 1912 CTGGCCAGAGATTGATTCACCAAGATGCTTGTGTGATCCAAAGAGATACAAATT 1971
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DB 1972 CGTGAATTCGAGAGCATCAGTGGTTTCAGATTGCGCTTCCTCGTTACTTAGCAGTGCCCT 2031
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DB 2092 AACTGGGTATGGAAGAGCAGCATGTGTGAATCTCTGCGCAATAGACTGCAGAAATGAG 2151
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DB 2152 GCAACTGTTCATATATTATTACTCTTGGAACAATCGATTCCGAGCTACAGTGCTATTG 2211
QY 341 GlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGluSer 360
DB 2212 GGAGCAGACTATCAAGAACTTTGGAGAGGAATTTTAATCGCTTTGCTTCATCGGAATCA 2271
QY 361 SerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSerSerGlyLeu 380
DB 2272 GCAAGTTCAATAACAAGCATATATCTCCAGAGACAGATGATCTCATGCCAGTGTTTG 2331
QY 381 ArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArgAlaHisPro 400
DB 2332 CGCCACACTATATCCCTGTTGAAGAATAAGGCTCTTGACCTGACGTACAGACTCAACCT 2391
QY 401 ArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArgTrpLysLys 420
DB 2392 CGCGAGATATAGATTGAGGTCCTTAAGGCACTTCAAGACTTAATGTCTCTGGAAGAAG 2451
QY 421 AsnGlyHisTyrAsnValLysCysArgTyrCysProGlyPheProGluValAsnAspThr 440
DB 2452 AATGACAGTACAAACATGAATGCAGATGGAAGCGTTGGG--ACTCAGGCCACTGATATG 2508
QY 441 LeuAspAlaSerAsnSerPheLeuGlyAspSerThrIleMetAspAsnAspAlaAsn 460
DB 2509 TTAGATGTTAACAAACAGCTTTGTTGATGACTCAATCATATGATTAACGGTGATGTAAT 2568
QY 461 GlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThrLysAspAspLys 480
DB 2569 GGGAGGCTACCTGCTGTGATCAAGTTTGAATCCAG-----ACCAGAGACGAGAAG 2619
QY 481 TyrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCysAla 500
DB 2620 TATCTGCTGATATGACAGAGAGTTACGGGGCTCAGCTCCTTTCTGGACTTCTGTGCA 2679
QY 501 AlaPheLeuThrLysLeuArgValLeu 509
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BT009004 1899 bp mRNA linear PLN 20-JUN-2003
LOCUS BT009004
DEFINITION Triticum aestivum clone wdr2c.pk018.c16.fis, full insert mRNA
sequence.
ACCESSION BT009004
VERSION BT009004.1 GI:32128555
KEYWORDS FLI_CDNA.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticaceae; Triticum.
REFERENCE 1 (bases 1 to 1899)
Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
AUTHORS Direct Submission
TITLE Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
JOURNAL

source 1. 1770
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ORIGIN

Alignment Scores:
Pred. No.: 1 09e-205 Length: 1770
Score: 2356.50 Matches: 444
Percent Similarity: 93.33% Conservative: 32
Best Local Similarity: 87.06% Mismatches: 33
Query Match: 87.50% Indels: 1
DB: 8 Gaps: 1

US-09-857-522B-4 (1-509) x OSU55768 (1-1770)

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DB 13 ATGATGGAATGCTAAAGCGGTGGCATTCAGAGCACTGAAGAACTACAACTTTGGA 72
QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
DB 73 AGAAGCTTAGGTAATGCTCATTTGGAAAAGTGAAGATTGCAGAGCATAGCTTACAGGA 132
QY 41 HisArgValAlaIleLysIleIleAsnCysArgGlnMetArgAsnMetGluMetGluGlu 60
DB 133 CACAGAGTGTCTATAAGATCCTGACCGCCGCAATGAGAATATGGAATGAGAGAG 192
QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPheIleHisProHisIleIleArgLeu 80
DB 193 AAAGCAAGAGAGAAATCAAGATACAGATTGTTTCATTCCTCCATATCATTCGCCCTT 252
QY 81 TyrgLuvAlIleTyThrProThrAspIleTyValValMetGluTyCysLysTyrgLys 100
DB 253 TATGAGGTTATATACACTCTACGATATATATGTTGTGATGAGTACTGCAAGTTTGA 312
QY 101 GluLeuPheAspTyriLeValGluLysGlyArgLeuGlnLysAspGlu---AlaArgArg 119
DB 313 GAACTGTTGATTACATTTGTTGAGAAAGCGAGTTGCAAGAAATCGAGTGGCTTCGCGA 372
QY 120 IlePheGlnGlnIleIleSerGlyValGluTyCysHisArgAsnMetValIleHisArg 139
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QY 140 AspLeuLysProGluAsnLeuLeuLeuAspSerLysTyraSnValLysLeuAlaAspPhe 159
DB 433 GATCTGAAGCCAGAAACTTGCTACTGATGCAAGTATATGTAAAGCTTGCTGACTTT 492
QY 160 GlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsn 179
DB 493 GGTGTGAGTACGTCATGCATGATGGCCATTTTGAAGACAAAGCTGTGGAGTCCAAAC 552

QY 180 TyraAlaAlaProGluValIleSerGlyLysLeuTyraAlaGlyProGluValAspValTrp 199
DB 553 TATGCTGTCTCCAGAGGTGATCTCTGTGTAATATATATGCTGACCTGACGAGTTGATGTATGG 612
QY 200 SerCysGlyValIleLeuTyraAlaLeuLeuCysGlyThrLeuProPheAspGluAsn 219
DB 613 AGCTGTGAGTGATCCTTATGCTCTCCCTTGTGTGACTCTTCATTTGATGATGAGAAT 672
QY 220 IleProAsnLeuPheLysIleLysGlyGlyIleTyThrLeuProSerHisLysSer 239
DB 673 ATCCCAACTTATTCAAAAAGATAAAGGCTGTATATATACTCTCCCAAGTCATTATCT 732
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DB 733 GCTGTGGCCAGAGATTGATCCCAAGATGCTTGTGTGATCCAAATGAAGAATCACA 792
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QY 320 GluAlaThrValAlaIleTyThrLeuLeuAspAsnArgPheArgAlaThrSerGlyTy 339
DB 973 GAGGCAACTGTTCATATATTACTTCTTGGACAATGATGATCCGACTACCAAGTGCTAT 1032
QY 340 LeuGlyAlaAspTyrgLingLysSerMetAspArgAsnLeuAsnGlnLeuAlaSerSerGlu 359
DB 1033 TTGGAGCAGACTATCAAGAACTTTGAGAGAGAAATTTAAATCGCTTGTGCTTCAGGAA 1092
QY 360 SerSerSerSerGlyThrArgAsnTyraValProGlySerSerAspProHisSerSerGly 379
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DB 1153 TTGGGGCCCATTAATCTCTGTGAAGAAATGGGCTCTTGACTTCAGTCAGAGCTCAA 1212
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DB 1393 AACGGAGGTTACCTGCTGTGATCAAGTTTGAATCCAGCTTTACAGAAGACAGAGAGAG 1452
QY 480 LysTyThrLeuLeuAspMetGlnArgValThrGlyProGlnLeuLeuPheLeuAspPheCys 499
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RESULT 9
HVU7990 HVU7990 1542 bp mRNA linear PLN 22-JUL-1998
LOCUS Hordeum vulgare mRNA for SNRK1-type protein kinase, partial.
DEFINITION
ACCESSION AJ007990

VERSION AJ007990.1 GI:3341451
KEYWORDS kin12a gene; SnRK1-type protein kinase.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1
AUTHORS Slocombe,S.P., Bertini,L., Beaudoin,F., Dickinson,J.R. and Halford,N.G.
TITLE Molecular cloning of Bsn1p1, a novel putative SNF4-related protein identified in a two-hybrid screen with barley seed SnRK1 protein kinase
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1542)
AUTHORS Slocombe,S.P.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1998) Slocombe S.P., Salamini Department, Max Planck Institut fuer Zuechtungsforschung, Carl-von-Linne Weg 10, D-50829 Koeln, GERMANY
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ORIGIN
Alignment Scores:
Pred. No.: 2.64e-182 Length: 1542
Score: 2100.00 Matches: 389
Percent Similarity: 87.72% Conservative: 61
Best Local Similarity: 75.83% Mismatches: 59
Query Match: 77.98% Indels: 4
DB: 8 Gaps: 2
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Qy 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40
Db 61 AAAACATTAGTTAGGAACATTGTGAGATGTGAAGTTGCAGAGCATAGCTTACGGGA 120
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Db 121 CAGAGAGTTGCTATAAGATTCTGAACCGTCGTAAATAATGGAACATATGGAAGAG 180

Qy 61 LysAlaLysArgGluPheLysIleLeuLysLeu-----PheIleHisProHisIle 77
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Qy 78 IleArgLeuTyrGluValIleTyrThrProThrAspIleTyrValMetGluTyrCys 97
Db 241 ATCCGGGTTATGAGTCAATAGACACCTTAAGATATATTCGTTGTGATGGAATATTCG 300
Qy 98 LysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnIuAspGluAla 117
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Qy 118 ArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValVal 137
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Qy 138 HisArgAspLeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAla 157
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Qy 278 AlaValProProProAspThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArg 297
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RESULT 10
LOCUS HVBKIN12M 1539 bp mRNA linear PLN 05-MAY-1995
DEFINITION H.vulgaris BKIN12 mRNA for protein kinase (partial).
ACCESSION X65604
VERSION X65604.1 GI:18933
KEYWORDS protein kinase.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1539)
AUTHORS Halford,N.G., Vicente-Carabajosa,J., Sabelli,P.A., Shewry,P.R.,
Hanappel,U. and Kreis,M.
TITLE Molecular analyses of a barley multigene family homologous to the
yeast protein kinase gene SNF1
JOURNAL Plant J. 2 (5), 791-797 (1992)
MEDLINE 93258420
PUBMED 1302632
REFERENCE 2 (bases 1 to 1539)
AUTHORS Halford,N.G.
TITLE Direct Submission
JOURNAL Submitted (16-APR-1992) N.G. Halford, long Ashton Research Station,
University of Bristol, Dept of Agricultural Sciences, long Ashton,
Bristol BS18 9AF, UK
FEATURES
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ORIGIN

Alignment Scores:
Pred. No.: 9.6e-180 Length: 1539
Score: 2072.00 Matches: 383
Percent Similarity: 87.13% Conservative: 64
Best Local Similarity: 74.66% Mismatches: 62
Query Match: 76.94% Indels: 4
DB: 8 Gaps: 2

US-09-857-522B-4 (1-509) x HVBKIN12M (1-1539)

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Db 61 AAACATTAGCTTTAGGAACATTGGAGATGTGAAGTTGCAGAGCGCTAACGTTACGGGA 120
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Db 421 CATCGTATCTTAAAGCCAGAAACCTGTTACTGATTCAGATATATGTGAACCTTGCT 480
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Db 901 GAGGTGTCAACCTAGATATGATAAAGATCATGTGTGAATCGCTGTGAATAGGCTG 960

QY 318 GlnAsnGluAlaThrValAlaTyrTyrLeuLeuAspAsnArgPheArgAlaThrSer 337

Db 961 CAAATGAGAGAACTGTTGCATATATCTGCTCTTGACGATCGGTTCCGATCTACTAGT 1020

QY 338 GltYrLeuGlyAlaAspTyrGlnGluSerMetAspArgAsnLeuAsnGlnLeuAlaSer 357

Db 1021 GGCTATTTGGGGGCTGACCAACCAACATCTCATGGATAGAGTTTAAATGAGTTTACCTTA 1080

QY 358 SerGluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSer 377

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QY 378 SerGlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeuGlnSerArg 397

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QY 398 AlaHisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnValArg 417

Db 1201 GCTCACCCCTCGTATATATGATTGAGGTTCTAAAGCACCTTAAGAAITTAATGTCCTGC 1260

QY 418 TrpLysLysAsnGlyHisTyrAsnValLysCysArgTrpCysProGlyPheProGluVal 437

Db 1261 TGAAGAAGAATGCACTCTACAACATGAATGCAAGTGTGCGCCCTGGGTTCTCCAGGTC 1320

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QY 457 AspAspAlaAsnGlyArgLeuProThrValIleLysPheGluPheGlnLeuTyrLysThr 476

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QY 497 AspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509

Db 1501 GAATTTTGTGGGGCTTCCTTACCAACCTTAGGGTTCTA 1539

RESULT 11

LOCUS RYERKIN1 1809 bp mRNA linear PLN 27-APR-1993

DEFINITION Secale cereale RKIN1 mRNA, complete CDS.

ACCESSION M74113

VERSION M74113.1 GI:169835

KEYWORDS protein serine/threonine kinase.

SOURCE Secale cereale (rye)

ORGANISM Secale cereale

REFERENCE 1 (bases 1 to 1809)

AUTHORS Alderson,A., Sabelli,P.A., Dickinson,J.R., Cole,D., Richardson,M., Kreis,M., Shewry,P.R. and Halford,N.G.

TITLE Complementation of snfl, a mutation affecting global regulation of carbon metabolism in yeast, by a plant protein kinase cDNA

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (19), 8602-8605 (1991)

MEDLINE 92020901

PUBMED 1924320

COMMENT Original source text: Secale cereale (cultivar Gazelle) seed

FEATURES

source

1. .1809

Location/Qualifiers

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CDS

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110. .1618

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ORIGIN

Alignment Scores:

Pred. No.: 8.83e-179 Length: 1809

Score: 2062.50 Matches: 401

Percent Similarity: 85.05% Conservative: 37

Best Local Similarity: 77.86% Mismatches: 58

Query Match: 76.59% Indels: 19

DB: 8 Gaps: 6

US-09-857-522B-4 (1-509) x RYERKIN1 (1-1809)

QY 1 MetAspGlySerSerLysGlySerGlyHisSerGluAlaLeuArgAsnTyrAsnLeuGly 20

Db 110 ATGATGGA-----GGAGCGCAACATCTGAAGCATTGAAAACTACTATCTGGGT 160

QY 21 ArgThrLeuGlyIleGlyThrPheGlyLysValLysIleAlaGluHisLysLeuThrGly 40

Db 161 AAAATATGTAGGTGTAGGCACATTTGCCAAAAGTAATTAATTGACAGCATAAAGCATACAAGA 220

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QY 61 LysAlaLysArgGluPheLysIleLeuLysLeuPhe-----IleHisProHisIle 77

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Db 341 ATCCGGGTTTATGAGGTCATTGTGACACCGGAAAGATATTTTGTGTTGATGGAATATTGC 400

QY 98 LysTyrGlyGluLeuPheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAla 117

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QY 118 ArgArgIlePheGlnGlnIleIleSerGlyValGluTyrCysHisArgAsnMetValVal 137

Db 461 CGTGAACCTTCCAGACAGATTATATCTGCTGTGAATACTGCGCACAGAAAACAAGTTGTT 520

QY 138 HisArgAspLeuLysProGluAsnLeuLeuAspSerLysTyrAsnValLysLeuAla 157

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QY 158 AspPheGlyLeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySer 177

Db 581 GACTTTGGGTTAAGTAATGTGATGATGCGCATTTTGTGAAGACTAGCTGCGGAGCT 640

QY 178 ProAsnTyrAlaAlaProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAsp 197

Db 641 CTAACATATGCTGCACAGAGGTCAITCTCAGGTAATTTGACGCTGGAACCTGAGATTGAT 700

QY 198 ValTrpSerCysGlyValIleLeuTyrAlaLeuLeuCysGlyThrLeuProPheAspAsp 217

Db 701 GTTGGAGCTGTGGGTGATATACTTATGCTCTTCTTGTGCTGTCTTCATTGATGAT 760

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Db 237

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Oy 258 IleThrIleArgGluIleArgGluHisGlnIleTrpPheGlnIleArgLeuProArgTyrLeu 277
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Oy 278 AlaValProProProArgThrThrGlnGlnAlaLysMetIleAspGluAspThrLeuArg 297
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Db 1001 GACGTTGTCAAACTGGGATATGATAAAGATCATGTGTGAATCGCTGTGCAATAGGCTG 1060
Oy 318 GlnAsnGluAlaThrValAlaTyrTyrLeuLeuLeuAspAsnArgPheArgAlaThrSer 337
Db 1061 CAAAACGAGAAACTGTTGCATATTACTTGTCTTGCAATCGGTTCCGGGCTACTAGT 1120
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Db 1121 GGCTATTGGGGCTCACTATCAACAACCAATG----- 1153
Oy 358 SerGluSerSerSerSerGlyThrArgAsnTyrValProGlySerSerAspProHisSer 377
Db 1154 ---GAATCAGCAAGCCCAAGTACCAAGAGTTATCTTCCAGGAAGCAATGATTCTCAAGGC 1210
Oy 378 SerGlyLeuArgProTyrTyrProValGluArgLysTrpAlaLeuGlyLeu---GlnSer 396
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Oy 397 ArgAlaHisProArgGluIleMetValGluValLeuLysAlaLeuGlnGluLeuAsnVal 416
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Db 1331 TGTGGAAGAAGATGAGACTGCTACACATGAAATGACAGGTGTCCTCGCTTCCCT 1390
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Db 1511 AAGACCAAGATGACAAAGTAACTGCTAGATATGACAGAGATTACTGACCTCAGCTCCTC 1570
Oy 495 PheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValLeu 509
Db 1571 TTCCTGGAATTTGTGCGGCTTCTTACCAACCTTAGGGTTCTA 1615
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D82037 D82037 2138 bp mRNA linear PLN 06-FEB-1999
DEFINITION Oryza sativa mRNA for OSK2, partial cds.
ACCESSION D82037
VERSION D82037.1 GI:4107004
KEYWORDS OSK2.
SOURCE Oryza sativa
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (sites)
AUTHORS Takano,M., Kajiya-Kanegae,H., Funatsuki,H. and Kikuchi,S.
TITLE Rice has two distinct classes of protein kinase genes related to

SNF1 of Saccharomyces cerevisiae, which are differently regulated
in early seed development
Mol. Gen. Genet. 260 (4), 388-394 (1998)
MEDLINE 99086251
PUBMED 9870704
REFERENCE 2 (bases 1 to 2138)
AUTHORS Takano,M.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-1995) Makoto Takano, National Institute of
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Kannondai, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:mtakano@abr.affrc.go.jp, Tel:81-298-38-7446,
Fax:81-298-38-7408)
FEATURES
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Best Local Similarity: 71.07% Mismatches: 21
Query Match: 76.35% Indels: 113
DB: 8 Gaps: 1
US-09-857-522B-4 (1-509) x D82037 (1-2138)
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Db 2 AAGAGAGAAATCAAGATATTGAGGTTGTTTCATTCAATCCCATATCATTCGCCCTTATGAG 61
Oy 83 ValIleTyrThrProThrAspIleTyrValValMetGluTyrCysLysTyrGlyGluLeu 102
Db 62 GTCATATACACTCTCTACGAGATATATATGTTGTGATGAGTACTGCAAGTTTGAGAACTG 121
Oy 103 PheAspTyrIleValGluLysGlyArgLeuGlnGluAspGluAlaArgIlePheGln 122
Db 122 TTGATTACATTGTTGAGAAAGCAGGTTGCAGGAAGATGAGGCTCGCGAATCTTCAG 181
Oy 123 GlnIleIleSerGlyValGluTyrCysHisArgAsnMetValAlaHisArgAspLeuLys 142
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Oy 143 ProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGlyLeuSer 162
Db 242 CCAGAAACTTGTCTACTCGATTCAAAAGTATAACGTAAGCTTGCTGCTTGAGT 301
Oy 163 AsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyrAlaAla 182
Db 302 AATGTCATGCATGATGCCCATTTTAAAGACAAAGCTGCGGAGTCCGAATATATGCTGCT 361
Oy 183 ProGluValIleSerGlyLysLeuTyrAlaGlyProGluValAspValTrpSerCysGly 202

| | | | | |
|----|------|--|-------------------------|------|
| Db | 362 | CCAGAGGTGATCTCTGGTAAATTATATGCTGACC | CGAGTTGATGTATGAGCTGTGGA | 421 |
| QY | 203 | ValIleuTyrAlaLeuLeuCySgIYThrLeuProPheAspSgIuAsnIleProAsn | | 222 |
| Db | 422 | GTGATCCTTTATGCTCTCCTTGTGGTACTCTTCCATTTGATGACGAAATATCCCCAAC | | 481 |
| QY | 223 | LeuPheLysLysIleLysGlyGlyIleTyrThrLeuProSerHisLeuSerAlaLeuAla | | 242 |
| Db | 482 | CTATTCAAAAAGATAAAGGGTGTATATATACTCTCCCAAGTCATTATCTGCTGGCC | | 541 |
| QY | 243 | ArgAspLeuIleProArgMetLeuValValGluProMetLysArgIleThrIleArgGlu | | 262 |
| Db | 542 | AGGGATTTGATCCCAAGGATGCTTGTGTGATCCAAATGAAGAATCACAAATTCGTGA | | 601 |
| QY | 263 | IleArgGluHisGlnTrpPheGlnIleArgLeuProArgIYrLeuAlaValProProPro | | 282 |
| Db | 602 | ATTGAGAGCATCAATGGTTTCAGATTGCGCTTCCTCGTTACTTAGCAGTGCCCTCCACCA | | 661 |
| QY | 283 | AspThrThrGlnGlnAlaLysMet | | 290 |
| Db | 662 | GACACAGCACAGCAAGCCAAANTGGTACTTTGTGCACATTCCTTAACGAGTTGTCATTA | | 721 |
| QY | 290 | | | 290 |
| Db | 722 | ATGTATCAAACTTATATACTAAATAATTTCTTGAGATATACTTATAGAGTATGATAA | | 781 |
| QY | 290 | | | 290 |
| Db | 782 | ATAATGTTTTGCCAACATAAACCGTATAAAGCAGTGGTGAAGCATTTGATAACAT | | 841 |
| QY | 290 | | | 290 |
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| QY | 290 | | | 290 |
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| QY | 290 | | | 290 |
| Db | 962 | TTGATTTTTTATTAATATATCTTGCCACTTTGCTAATATCTTGATATATGACCTTCTTGAA | | 1021 |
| QY | 291 | -IleAspGluAspThrLeuArgAspValValAsnMetGlyPheAsnLysAsnHisValCy | | 310 |
| Db | 1022 | GATTGATGAAGATACCCCTTCAGACGTGTGTAACCTTGGGTATGAAGAAGCATGTGTG | | 1081 |
| QY | 310 | sgIuSerLeuCySerArgLeuGlnAsnGluAlaThrValAlaTyrTyrLeuLeuLeuAs | | 330 |
| Db | 1082 | TGAATCTCTGCGCAATAGACTGCATAATGAGGCAACTGTTGCATATTATTGCTATTGGA | | 1141 |
| QY | 330 | PasnArgPheArgAlaThrSerGlyTyrLeuGlyAlaAspIYrGlnIuSerMetAspAr | | 350 |
| Db | 1142 | CAATCGATTCCGAGCTACCAGTGGCTATCTGGAGCAGACTATCAAGAATCATTGGAGAG | | 1201 |
| QY | 350 | GAsnLeuAsnGlnLeuAlaSerSerGluSerSerSerSerSerGlyThrArgAsnTyrValPr | | 370 |
| Db | 1202 | GAAITCTTAATCGCTTTGCTTCATCAGAAATCAGCAAGTTCAAAATACAAAGGCATTATCTCCC | | 1261 |
| QY | 370 | cgIuSerSerAspProHisSerSerGlyLeuArgProTyrTyrProValGluArgIYsTr | | 390 |
| Db | 1262 | AGGAAGCAGTGATCCTCATGCGAGTGGTTTGGCCCACATTAATCTGTTGAAAGAAAATG | | 1321 |
| QY | 390 | PalaleuGlnLeuGlnSerArgAlaHisProArgGluIleMetValGluValLeuLysAl | | 410 |
| Db | 1322 | GGCTCTTGGACTTCAGTCTCGAGCTCAGCCCTCGGAGATATGATGAGGTCTTAAGGC | | 1381 |
| QY | 410 | aleuGlnGluLeuAsnValArgTrpLysLysAsnGlyHisIYrAsnValLysCyBarGTr | | 430 |
| Db | 1382 | ACTTGAAGACTTAATGTCTGCTGGAAGAAGATGACAGATACACATGAAGTGCAGATG | | 1441 |
| QY | 430 | pCyAspProGlyPheProGluValAsnAspThrLeuAspAlaSerAsnSerPheLeuGlyAs | | 450 |
| Db | 1442 | GAGCGTTGGGTATCCTCAGGCCACTGATATGTTAGATGTCAACCAACAGCTTTGTTGATGA | | 1501 |

| | | | |
|-----------------|---|--|------|
| OY | 450 | pserThrIleMetAspAsnAspAlaSerGlyArgLeuProThrValIleLysPheG1 | 470 |
| Dd | 1502 | CTCAATTATTAATGAGTAATGCATGTAAACGGAGGTTACCTGCTGTGATCAAGTTGA | 1561 |
| OY | 470 | uPheGlnLeuTyrLysThrLysAspAspLysTyrLeuLeuAspMetGlnArgValThrg1 | 490 |
| Dd | 1562 | AATCCAGCTTTACAGACAGACAGACGAGAAGTACTGCTGATATGACAGAGTTACGGG | 1621 |
| OY | 490 | yProGlnLeuLeuPheLeuAspPheCysAlaAlaPheLeuThrLysLeuArgValIeu | 509 |
| Dd | 1622 | GCCTCAGCTCTTTCTTGCACTTCTGTGCAGCTTCCTTACCACAACGTGAGGTTCTA | 1679 |
| RESULT 13 | | | |
| AK067158 | | 2073 bp mRNA linear PLN 24-JUL-2003 | |
| LOCUS | | Oryza sativa (japonica cultivar-group) cDNA clone:J013094M16, full | |
| DEFINITION | | insert sequence. | |
| ACCESSION | AK067158 | | |
| VERSION | AK067158.1 | GI:32977176 | |
| KEYWORDS | FLI_CDNA; CAP trapper. | | |
| SOURCE | Oryza sativa (japonica cultivar-group) | | |
| ORGANISM | Oryza sativa (japonica cultivar-group) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriharoidae; Oryzaceae; Oryza. | | |
| REFERENCE | 1 | | |
| AUTHORS | The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yasaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Ninkura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN: Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y. Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice Science 301 (5631), 376-379 (2003) | | |
| JOURNAL MEDLINE | 22752273 | | |
| PUBMED | 12869764 | | |
| REFERENCE | 2 (bases 1 to 2073) | | |
| AUTHORS | Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Ninkura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Otomo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yasaki,J., Yokomizo,S. and Yoshimura,A. | | |
| TITLE | Direct Submission | | |
| JOURNAL | Submitted (05-DEC-2001) | Shoshi Kikuchi, National Institute of | |

Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica rice.

URL : http://cdna01.dna.affrc.go.jp/cDNA/

NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and Yamamoto,M.

FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Nikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

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US-09-857-522B-4 (1-509) x AK067158 (1-2073)

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VERSION     D82039.1  GI:4107008
KEYWORDS    OSK1.
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ORGANISM    Oryza sativa
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REFERENCE   1 (sites)
AUTHORS     Takano,M., Kajiya-Kanegae,H., Funatsuki,H. and Kikuchi,S.
TITLE       Rice has two distinct classes of protein kinase genes related to
            SNF1 of Saccharomyces cerevisiae, which are differently regulated
            in early seed development
JOURNAL     Mol. Gen. Genet. 260 (4), 388-394 (1998)
MEDLINE     99086251
PUBMED      9870704
REFERENCE   2 (bases 1 to 2209)
AUTHORS     Takano,M.
TITLE       Direct Submission
JOURNAL     Submitted (15-DEC-1995) Makoto Takano, National Institute of
            Agrobiological Resources, Department of Molecular Genetics, 2-1-2
            Kannondai, Tsukuba, Ibaraki 305-8602, Japan
            (E-mail:mtakano@abr.affrc.go.jp, Tel:81-298-38-7446,
            Fax:81-298-38-7408)

FEATURES
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ORIGIN
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Pred. No.:      7.67e-171      Length:      2209
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Percent Similarity: 84.28%      Conservative: 52
Best Local Similarity: 74.07%      Mismatches:  76
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US-09-857-522B-4 (1-509) x D82039 (1-2209)

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| Qy | 141 | LeuLysProGluAsnLeuLeuLeuAspSerLysTyrAsnValLysLeuAlaAspPheGly | 160 |
| Db | 595 | CTTAAGCCAGAGAACCTTCTTTGGACTCCAATGCAATGTTAAGATTGCAGACTTGGC | 654 |
| Qy | 161 | LeuSerAsnValMetHisAspGlyHisPheLeuLysThrSerCysGlySerProAsnTyr | 180 |
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| | PAT 27-SEP-2002 |

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| KEYWORDS | . | . |

| SOURCE ORGANISM | Arabidopsis thaliana (thale cress) |
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| Arabidopsis thaliana | |

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

| REFERENCE | AUTHORS | TITLE | JOURNAL |
|-----------|---|---|--|
| 1 | Harper, J.F., Kreps, J., Wang, X. and Zhu, T. | Stress-regulated genes of plants, transgenic plants containing same, and methods of use | Patent: WO 021655-A 2657 28-FEB-2002; The Scripps Research Institute (US) ; Syngenta Participations AG (CH) |

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US-09-857-522B-4 (1-509) X AX507962 (1-1539)

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Qy 452 ThrIleMetaspAspAspAlaAsnGlyArgIleuProThrValIleLysPheGluPhe 471
Db 1363 TCCAGCATATATAGAGAACGAAGCAGCTGTTAAGTCGCCCAATGTTGTCAAGTTGAAATT 1422
Qy 472 GlnLeuTyrLysThrLysAspAspLysTyrIleuLeuAspMetGlnArgValThrGlyPro 491
Db 1423 CAGTTGTATATAAACTCGGACGACCAAGTATCTACTGATTGCAGAGATACAAAGTTCCT 1482
Qy 492 GlnLeuPheIleuAspPheCysAlaAlaPheIleuThrLysIleuArgValIleu 509
Db 1483 CAGTTCTTGTCTTGGATCTGTGTGCTGCTTTCTTGTCTCAGCTCCGAGTCCTC 1536

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